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(US). **LEWIS, Marcia, E.** [US/US]; 67 Wheelwright
Farm, Cohasset, MA 02025 (US).

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(74) Agent: **EVANS, Paula, Campbell**; Palmer & Dodge, LLP,
One Beacon Street, Boston, MA 02108 (US).

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(71) Applicant (*for all designated States except US*): **BAYER
CORPORATION** [US/US]; 33 Coney Street, East
Walpole, MA 02032 (US).

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(72) Inventors; and

(75) Inventors/Applicants (*for US only*): **BURGESS,
Christopher** [US/US]; 97 Canton Terrace, Westwood,
MA 02090 (US). **ASTLE, Jon, H.** [US/US]; 42 Short
Street, Taunton, MA 02780 (US). **CARROLL, Eddie,
III** [US/US]; 1175 Washington Street, Norwood, MA
02062 (US). **CATINO, Theodore, J.** [US/US]; 18 Jo Paul
Drive, Attleboro, MA 02702 (US). **DWIVEDI, Poornima**
[US/US]; 2054 Pebble Drive, Alamo, CA 94507 (US).
MOLINO, Gary, A. [US/US]; 3 Essex Street, Nor-
folk, MA 02056 (US). **THIAGALINGAM, Arunthathi**
[US/US]; 26 Winchester Drive, Lexington, MA 02420

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(54) Title: NUCLEIC ACID SEQUENCES DIFFERENTIALLY EXPRESSED IN CANCER TISSUE

(57) Abstract: This invention relates to novel nucleic acid sequences which are differentially expressed in cancer cells. The invention also relates to proteins and peptides encoded by the sequences, to diagnostic assays and therapeutic agents based on the sequences and proteins, and to probes, antisense constructs, and antibodies derived from the sequences and proteins or peptides. The subject nucleic acids have been found to be differentially expressed by tumor cells, particularly in colon cancer tissue.

INTERNATIONAL SEARCH REPORT

International application No.

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A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12Q 1/68; A61K 38/00; C07H 21/02

US CL : 435/6; 530/300; 536/23.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6; 530/300; 536/23.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Continuation Sheet**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X.P	WO 01/22920 A2 (HUMAN GENOME SCIENCES, INC.) 05 April 2001 (05.04.2002), pages 1-10, 1868-1871, 1891-2157, especially 1931-1933, 1950-1959.	14, 15, and 17-19



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:		*T	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
*A	document defining the general state of the art which is not considered to be of particular relevance	*X	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
*B	earlier application or patent published on or after the international filing date	*Y	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
*L	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*&	document member of the same patent family
*O	document referring to an oral disclosure, use, exhibition or other means		
*P	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

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Facsimile No. (703)305-3230

Authorized officer

Young J. Kim

Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/30732

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.: 14, 15, 17-19 and SEQ ID Number 4483 and 4484
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐
☒

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/30732

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1, 2, 9-12, 20-28, 30-35, 37, 39, and 40, drawn to an isolated nucleic acid, gene comprising the nucleic acid, nucleic acid with degrees of homology, a host cell comprising the nucleic acid, a pharmaceutical composition comprising the nucleic acid, probes, array comprising the probes, polypeptide, antisense, primer, a kit, and method of detecting cancer by hybridization.

Group II, claim(s) 6-8, drawn to a method of identifying a modulating agent.

Group III, claim(s) 3-5, 13, 36, and 41, drawn to an antibody, pharmaceutical composition comprising the antibody, a kit comprising the antibody, and a method of detection using the antibody.

Group IV, claim(s) 14 and 15, drawn to a method of determining a phenotype via nucleic acid expression profiling.

Group V, claim(s) 16-19, drawn to a method of determining a phenotype via protein expression profiling.

Group VI, claim(s) 29, drawn to a transgenic animal.

Group VII, claim(s) 38, drawn to a method of detecting the presence or absence of a polypeptide.

In addition, each Group detailed above reads on distinct Groups drawn to multiple sequences. The sequences are distinct because they are unrelated sequences, and a further lack of unity is applied to each Group. The Applicants must further elect one nucleic acid sequence and a corresponding polypeptide sequence (as applicable) for examination in the elected Group detailed above. Payment of fees for an additional invention will entitle the Applicants to examination of one additional sequence.

Total Number of Invention was calculated by the formula below:

Each Group x number of SEQ IDs present.

Groups I-III each have 4470 SEQ ID Numbers, therefore: $3 \times 4470 = 13410$ inventions

Groups IV and V have 4482 SEQ ID Numbers, therefore: $2 \times 4482 = 8964$ inventions

Groups VI and VII have 503 SEQ ID Numbers, therefore: $2 \times 503 = 1006$ inventions

Therefore, the total number of inventions is: $13410 + 8964 + 1006 = 23380$ inventions.

The inventions listed as Groups I-VII do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Groups I, III, and VI lack unity of invention with regard to each other because they are drawn to physically distinct products not sharing a common technical feature. For example, although the antibody is derived from polypeptide of I, the polypeptide itself is not present in the product, thereby failing to "share" a special technical feature.

Groups I, lacks unity of invention with regard to Groups II, IV, V, and VII because PCT Rule 13.1 and Annex B do not provide for unity of invention between two or more products or methods of use that share a special technical feature. As the methods of Groups II, IV, V, and VII are an additional method for the use of Group I, lack of unity held.

Groups II, IV, V, and VII lack unity of invention with regard to each other because the methods are different achieving different outcome. Further, PCT Rule 13.1 and Annex B do not provide for unity of invention between two or more products or methods of use that share a special technical feature.

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Groups III and VI lack unity of invention with regard to Groups II, IV, V, and VII because the methods of Groups II, IV, V, and VII do not require the products of Groups III and VI, thereby failing to share a special technical feature.

Finally, Groups I-VII are drawn to unrelated nucleic acid/amino acid sequences, rendering the groups further lacking in unity of invention with respect to each SEQ ID Numbers disclosed (See MPEP 1850, Lack of Unity of Invention).

Continuation of B. FIELDS SEARCHED Item 3:

Sequence search on Electronic Database Genbank, Patent Database

Search term: SEQ ID Number 4484 and 4484

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- (51) International Patent Classification⁷: **C12Q** (US). **LEWIS, Marcia, E.** [US/US]; 67 Wheelwright Farm, Cohasset, MA 02025 (US).
- (21) International Application Number: PCT/US01/30732
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60/237,271 2 October 2000 (02.10.2000) US
- (71) Applicant (for all designated States except US): **BAYER CORPORATION** [US/US]; 33 Coney Street, East Walpole, MA 02032 (US).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): **BURGESS, Christopher** [US/US]; 97 Canton Terrace, Westwood, MA 02090 (US). **ASTLE, John, H.** [US/US]; 42 Short Sreet, Taunton, MA 02780 (US). **CARROLL, Eddie, III** [US/US]; 1175 Washington Street, Norwood, MA 02062 (US). **CATINO, Theodore, J.** [US/US]; 18 Jo Paul Drive, Attleboro, MA 02702 (US). **DWIVEDI, Poornima** [US/US]; 10 Haven Road, Medfield, MA 02052 (US). **MOLINO, Gary, A.** [US/US]; 3 Essex Street, Norfolk, MA 02056 (US). **THIAGLINGAM, Arunthathi** [US/US]; 26 Winchestrer Drive, Lexington, MA 02420
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
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- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 02/29086 A2

(54) Title: NUCLEIC ACID SEQUENCES DIFFERENTIALLY EXPRESSED IN CANCER TISSUE

(57) Abstract: This invention relates to novel nucleic acid sequences which are differentially expressed in cancer cells. The invention also relates to proteins and peptides encoded by the sequences, to diagnostic assays and therapeutic agents based on the sequences and proteins, and to probes, antisense constructs, and antibodies derived from the sequences and proteins or peptides. The subject nucleic acids have been found to be differentially expressed by tumor cells, particularly in colon cancer tissue.

NUCLEIC ACID SEQUENCES DIFFERENTIALLY EXPRESSED IN CANCER TISSUEField of the Invention

The present invention provides nucleic acid sequences and proteins encoded thereby
5 which are differentially expressed in cancer tissues, as well as probes derived from the nucleic
acid sequences, antibodies directed to the encoded proteins, and diagnostic methods for
determining the presence and state of cancerous cells, especially colon cancer cells.

Background of the Invention

Colorectal carcinoma is a malignant neoplastic disease. There is a high incidence of
10 colorectal carcinoma in the Western world, particularly in the United States. Tumors of this type
often metastasize through lymphatic and vascular channels. Many patients with colorectal
carcinoma eventually die from this disease. In fact, it is estimated that 62,000 persons in the
United States alone die of colorectal carcinoma annually.

However, if diagnosed early, colon cancer may be treated effectively by surgical removal
15 of the cancerous tissue. Colorectal cancers originate in the colorectal epithelium and typically
are not extensively vascularized (and therefore not invasive) during the early stages of
development. Colorectal cancer is thought to result from the clonal expansion of a single mutant
cell in the epithelial lining of the colon or rectum. The transition to a highly vascularized,
invasive and ultimately metastatic cancer which spreads throughout the body commonly takes
20 ten years or longer. If the cancer is detected prior to invasion, surgical removal of the cancerous
tissue is an effective cure. However, colorectal cancer is often detected only upon manifestation
of clinical symptoms, such as pain and black tarry stool. Generally, such symptoms are present
only when the disease is well established, often after metastasis has occurred, and the prognosis
for the patient is poor, even after surgical resection of the cancerous tissue. Early detection of
25 colorectal cancer therefore is important in that detection may significantly reduce its morbidity.

Invasive diagnostic methods such as endoscopic examination allow for direct visual
identification, removal, and biopsy of potentially cancerous growths such as polyps. Endoscopy
is expensive, uncomfortable, inherently risky, and therefore not a practical tool for screening
populations to identify those with colorectal cancer. Non-invasive analysis of stool samples for
30 characteristics indicative of the presence of colorectal cancer or precancer is a preferred

alternative for early diagnosis, but no known diagnostic method is available which reliably achieves this goal.

Summary of the Invention

5 The present invention provides nucleic acid sequences and proteins encoded thereby, as well as probes derived from the nucleic acid sequences, antibodies directed to the encoded proteins, and diagnostic methods for detecting cancerous cells, especially colon cancer cells. The sequences disclosed herein have been found to be differentially expressed in colon cancer cell lines and/or colon cancer tissue.

10 In one aspect, the invention provides an isolated nucleic acid sequence comprising SEQ ID Nos 1-503, or a sequence complementary thereto.

In another aspect, the invention provides an isolated nucleic acid comprising a nucleotide sequence which hybridizes under stringent conditions to a sequence of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence complementary thereto.

15 In another embodiment, the nucleic acid is at least about 80% to about 100% identical to a sequence corresponding to at least about 12, at least about 15, at least about 25, or at least about 40 consecutive nucleotides up to the full length of one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence complementary thereto.

20 In another aspect, the invention provides an isolated nucleic acid comprising a nucleotide sequence which hybridizes under stringent conditions to a sequence of SEQ ID Nos. 1-1103, preferably SEQ ID Nos. 1-503, or a sequence complementary thereto. In a related embodiment, the nucleic acid is at least about 80% or about 100% identical to a sequence corresponding to at least about 12, at least about 15, at least about 25, or at least about 40 consecutive nucleotides up
25 to the full length of one of SEQ ID Nos. 1-1103, preferably SEQ ID Nos. 1-503 or a sequence complementary thereto.

In one embodiment, the invention provides a nucleic acid comprising a nucleotide sequence which hybridizes under stringent conditions to a sequence of SEQ ID Nos. 1-1103, preferably SEQ ID Nos. 1-503, or a sequence complementary thereto, and a transcriptional
30 regulatory sequence operably linked to the nucleotide sequence to render the nucleotide sequence suitable for use as an expression vector. In another embodiment, the nucleic acid may be

included in an expression vector capable of replicating in a prokaryotic or eukaryotic cell. In a related embodiment, the invention provides a host cell transfected with the expression vector.

In another embodiment, the invention provides a transgenic animal having a transgene of a nucleic acid comprising a nucleotide sequence which hybridizes under stringent conditions to a sequence of SEQ ID Nos. 1-1103, preferably SEQ ID Nos 1-503, or a sequence complementary thereto incorporated in cells thereof. The transgene modifies the level of expression of the nucleic acid, the stability of a mRNA transcript of the nucleic acid, or the activity of the encoded product of the nucleic acid.

In yet another embodiment, the invention provides a substantially pure nucleic acid comprising the nucleotide sequence of SEQ ID Nos 1-1103, or a sequence complementary thereto.

In yet another embodiment, the invention provides a substantially pure nucleic acid which hybridizes under stringent conditions to a nucleic acid probe corresponding to at least about 12, at least about 15, at least about 25, or at least about 40 consecutive nucleotides up to the full length of one of SEQ ID Nos. 1-1103, preferably SEQ ID Nos 1-503, or a sequence complementary thereto.

The invention also provides an antisense oligonucleotide analog which hybridizes under stringent conditions to at least 12, at least 25, or at least 50 consecutive nucleotides of one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 up to the full length of one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence complementary thereto, and which is resistant to cleavage by a nuclease, preferably an endogenous endonuclease or exonuclease.

In another embodiment, the invention provides a probe/primer comprising a substantially purified oligonucleotide comprising at least about 12, at least about 15, at least about 25, or at least about 40 consecutive nucleotides of SEQ ID Nos 1-1103, or a sequence complementary thereto.

In another embodiment, the invention provides a probe/primer comprising a substantially purified oligonucleotide, said oligonucleotide containing a region of nucleotide sequence which hybridizes under stringent conditions to at least about 12, at least about 15, at least about 25, or at least about 40 consecutive nucleotides of sense or antisense sequence selected from SEQ ID Nos. 1-1103 up to the full length of one of SEQ ID Nos. 1-1103 or a sequence complementary thereto. In preferred embodiments, the probe selectively hybridizes with a target nucleic acid. In

another embodiment, the probe may include a label group attached thereto and able to be detected. The label group may be selected from radioisotopes, fluorescent compounds, enzymes, and enzyme co-factors. The invention further provides arrays of at least about 10, at least about 25, at least about 50, or at least about 100 different probes as described above attached to a solid support.

In yet another embodiment, the invention pertains to a method of determining the phenotype of a cell comprising detecting the differential expression, relative to a normal cell, of at least one nucleic acid of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, wherein the nucleic acid is differentially expressed by at least a factor of two, at least a factor of five, at least a factor of twenty, or at least a factor of fifty.

In a still further embodiment, the invention pertains to a method of determining the phenotype of cell, comprising detecting the differential expression, relative to a normal cell, of at least one protein encoded by a nucleic acid which hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, wherein the protein is differentially expressed by at least a factor of two, at least a factor of five, at least a factor of twenty, an up to at least a factor of 50.

The invention further provides a method of determining the phenotype of cell, comprising detecting the differential expression, relative to a normal cell, of at least one polypeptide selected from the group of polypeptides of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493, wherein the polypeptide is differentially expressed by at least a factor of two, at least a factor of five, at least a factor of twenty, an up to at least a factor of 50.

In yet another embodiment, the invention pertains to a method of determining the phenotype of a cell comprising detecting the differential expression, relative to a normal cell, of at least one nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, wherein the nucleic acid is differentially expressed by at least a factor of two, at least a factor of five, at least a factor of twenty, or at least a factor of fifty.

In another aspect, the invention provides polypeptides encoded by the subject nucleic acids. In one embodiment, the invention pertains to a polypeptide including an amino acid sequence encoded by a nucleic acid comprising a nucleotide sequence which hybridizes under stringent conditions to a sequence of SEQ ID Nos. 1-1103 or a sequence complementary thereto,

or a fragment comprising at least about 25, or at least about 40 amino acids thereof. Further provided are antibodies immunoreactive with these polypeptides.

In a further aspect the invention pertains to a polypeptide encoded by one or more of the sequences of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492,
5 and 4494.

In a still further aspect the invention pertains to a polypeptide having the sequence of one or SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 44857, 4489, 4491, and 4493.

In still another aspect, the invention provides diagnostic methods. In one embodiment, the invention pertains to a method for determining the phenotype of cells from a patient by
10 providing a nucleic acid probe comprising a nucleotide sequence having at least 10, at least about 15, at least about 25, or at least about 40 consecutive nucleotides represented in a sequence of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 up to the full length of one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence complementary thereto, obtaining a
15 sample of cells from a patient, optionally providing a second sample of cells substantially all of which are non-cancerous, contacting the nucleic acid probe under stringent conditions with mRNA of each of said first and second cell samples, and comparing (a) the amount of hybridization of the probe with mRNA of the first cell sample, with (b) the amount of hybridization of the probe with mRNA of the second cell sample, wherein a difference of at least
20 a factor of two, at least a factor of five, at least a factor of twenty, or at least a factor of fifty in the amount of hybridization with the mRNA of the first cell sample as compared to the amount of hybridization with the mRNA of the second cell sample is indicative of the phenotype of cells in the first cell sample. Determining the phenotype includes determining the genotype, as the term is used herein.

25 In another embodiment, the invention provides a test kit for identifying the presence of cancerous cells or tissues, comprising a probe/primer as described above, for measuring a level of a nucleic acid which hybridizes under stringent conditions to a nucleic acid of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 in a sample of cells isolated from a patient. In certain embodiments, the kit may further include instructions
30 for using the kit, solutions for suspending or fixing the cells, detectable tags or labels, solutions for rendering a nucleic acid susceptible to hybridization, solutions for lysing cells, or solutions for the purification of nucleic acids.

In another embodiment, the invention provides a method of determining the phenotype of a cell, comprising detecting the differential expression, relative to a normal or control cell, of at least one protein encoded by a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto, wherein the protein is differentially expressed by at least a factor of two, at least a factor of five, at least a factor of twenty, or at least a factor of fifty. In one embodiment, the level of the protein is detected in an immunoassay. The invention also pertains to a method for determining the presence or absence of a nucleic acid, such as mRNA, which hybridizes under stringent conditions to one of SEQ ID Nos. 1-1103 in a cell, comprising contacting the cell with a probe as described above. The invention further provides a method for determining the presence or absence of a subject polypeptide encoded by a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-1103 in a cell, comprising contacting the cell with an antibody as described above.

In yet another embodiment, the invention provides a method for determining the presence of an aberrant mutation (e.g., deletion, insertion, or substitution of nucleic acids) or aberrant methylation in a sequence which hybridizes under stringent conditions to a sequence of SEQ ID Nos. 1-1103 or a sequence complementary thereto, comprising collecting a sample of cells from a patient, isolating nucleic acid from the cells of the sample, contacting the nucleic acid sample with one or more probe/primers which specifically hybridize to a nucleic acid sequence of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto, under conditions such that hybridization and/or amplification of the nucleic acid occurs, and comparing the presence, absence, or size of an amplification product to the amplification product of a normal cell.

In one embodiment, the invention provides a test kit for identifying the presence of cancer cells, comprising an antibody specific for a protein encoded by a nucleic acid which hybridizes under stringent conditions to any one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto. In certain embodiments, the kit further includes instructions for using the kit. In certain embodiments, the kit may further include solutions for suspending or fixing the cells, detectable tags or labels, solutions for rendering a polypeptide susceptible to the binding of an antibody, solutions for lysing cells, or solutions for the purification of polypeptides.

In yet another aspect, the invention provides pharmaceutical compositions including the subject nucleic acids. In one embodiment, an agent which alters the level of expression in a cell

of a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence complementary thereto is identified by providing a cell, treating the cell with a test agent, determining the level of expression in the cell of a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence complementary thereto, and comparing the level of expression of the nucleic acid in the treated cell with the level of expression of the nucleic acid in an untreated cell, wherein a change in the level of expression of the nucleic acid in the treated cell relative to the level of expression of the nucleic acid in the untreated cell is indicative of an agent which alters the level of expression of the nucleic acid in a cell. The invention further provides a pharmaceutical composition comprising an agent identified by this method. In another embodiment, the invention provides a pharmaceutical composition which includes a polypeptide encoded by a nucleic acid having a nucleotide sequence that hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence complementary thereto. In one embodiment, the invention pertains to a pharmaceutical composition comprising a nucleic acid including a sequence which hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence complementary thereto.

In yet another aspect, the invention provides pharmaceutical compositions including the subject nucleic acids. In one embodiment, an agent which alters the level of expression in a cell of a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence complementary thereto is identified by providing a cell, treating the cell with a test agent, determining the level of expression in the cell of a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence complementary thereto, and comparing the level of expression of the nucleic acid in the treated cell with the level of expression of the nucleic acid in an untreated cell, wherein a change in the level of expression of the nucleic acid in the treated cell relative to the level of expression of the nucleic acid in the untreated cell is indicative of an agent which alters the level of expression of the nucleic acid in a cell.

The invention further provides a method for identifying an agent which alters the level of expression in a cell of a polypeptide having a sequence of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493 comprising providing a cell; treating the

cell with the test agent; determining the level of expression of one or more polypeptides of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493 in the cell by reacting the cell with an antibody specific for one or more of the polypeptides of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493; and

- 5 comparing the level of expression of the polypeptide in the treated cell with the level of expression of the same polypeptide in an untreated cell, wherein a change in the level of expression of the nucleic acid in the treated cell relative to the level of expression of the nucleic acid in the untreated cell is indicative of an agent which alters the level of expression of the polypeptide in a cell.

- 10 The invention further provides a pharmaceutical composition comprising an agent identified by the above methods. In another embodiment, the invention provides a pharmaceutical composition which includes a polypeptide encoded by a nucleic acid having a nucleotide sequence that hybridizes under stringent conditions to one of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence
- 15 complementary thereto. In a further embodiment the invention provides a pharmaceutical composition comprising one or more antibodies which bind to a polypeptide encoded by one or more of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494. In a still further embodiment, the invention provides a pharmaceutical composition comprising one or more antibodies which binds to a polypeptide of one or more of SEQ ID Nos.
- 20 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493. In one embodiment, the invention pertains to a pharmaceutical composition comprising a nucleic acid including a sequence which hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence complementary thereto.

- 25 In one embodiment the invention relates to a method for detecting cancer in a patient sample in which an antibody to a protein encoded by SEQ ID Nos 1-4470 is used to react with proteins in the patient sample. In a further embodiment, the invention relates to a method for detecting cancer in a patient sample in which an antibody to a protein encoded by one or more of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 is
- 30 used to react with proteins in the patient sample. In a still further embodiment, the invention provides a method for detecting cancer in a patient sample in which an antibody to a protein having the sequence of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493 is used to react with protein in the patient sample.

Brief Description of the Figure

Figure 1 depicts the nucleic acid sequence of SEQ ID Nos: 1-4470.

Figure 2 depicts the nucleic acid sequence of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494.

5 Figure 3 depicts the amino acid sequence of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493.

Detailed Description of the Invention

The invention relates to nucleic acids having the disclosed nucleotide sequences (SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494), as
10 well as full length cDNA, mRNA, and genes corresponding to these sequences, and to polypeptides and proteins encoded by these nucleic acids and genes, and portions thereof. In particular the invention relates to the full length cDNA sequence of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 and the polypeptide sequence encoded thereby and shown in SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485,
15 4487, 4489, 4491, and 4493, respectively. The 4494 sequences disclosed herein were analyzed by comparing the sequences to those disclosed in publicly available databases. Based upon the search results, it was found that SEQ ID Nos: 1-503 contained novel sequences, SEQ ID Nos: 504-1103 contained known EST sequences, and SEQ ID Nos: 1104-4494 contained known sequences.

20 Also included in the present invention are polypeptides and proteins encoded by the nucleic acids of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, and in particular the polypeptide sequences of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493. The various nucleic acids that can encode these polypeptides and proteins differ because of the degeneracy of the genetic code,
25 in that most amino acids are encoded by more than one triplet codon. The identity of such codons is well known in this art, and this information can be used for the construction of the nucleic acids within the scope of the invention. In one embodiment, the polypeptide sequences of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493 are encoded by the full length cDNA sequences of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480,
30 4482, 4484, 4486, 4488, 4490, 4492, and 4494, respectively.

Nucleic acids encoding polypeptides and proteins that are variants of the polypeptides and proteins encoded by the present nucleic acids and related cDNA and genes are also within the scope of the invention. The variants differ from wild-type protein in having one or more amino acid substitutions that either enhance, add, or diminish a biological activity of the wild-type protein. Once the amino acid change is selected, a nucleic acid encoding that variant is constructed according to the invention.

The following detailed description discloses how to obtain or make full-length cDNA and human genes corresponding to the nucleic acids, how to express these nucleic acids and genes, how to identify structural motifs of the genes, how to identify the function of a protein encoded by a gene corresponding to an nucleic acid, how to use nucleic acids as probes in mapping and in tissue profiling, how to use the corresponding polypeptides and proteins to raise antibodies, and how to use the nucleic acids, polypeptides, and proteins for diagnostic purposes.

The sequences disclosed herein have been found to be differentially expressed in colon cancer cell lines and/or colon cancer tissue, and thus are useful for determining the presence of colon cancer in a cell or tissue sample. The present sequences also have utility for determining the presence or state of other types of cancer.

Accordingly, a preferred aspect of the present invention relates to nucleic acids differentially expressed in tumor cells or tissue, especially colon cancer tissue or cells, polypeptides encoded by such nucleic acids, and antibodies immunoreactive with these polypeptides, and preparations of such compositions. Moreover, the present invention provides diagnostic and therapeutic assays and reagents for detecting and treating disorders involving, for example, expression of the subject nucleic acids.

I. General

This invention relates to compositions and methods for identifying and/or classifying cancerous cells present in a human tumors, particularly in solid tumors, e.g., carcinomas and sarcomas, such as, for example, breast or colon cancers. In its broadest aspect, the method uses nucleic acids that are differentially expressed in cancer cell lines and/or cancer tissue, compared with related normal cells or tissue, and using them to identify or classify tumor cells by the upregulation and/or downregulation of expression of particular genes, an event which is implicated in tumorigenesis.

Upregulation or increased expression of certain genes such as oncogenes, act to promote malignant growth. Downregulation or decreased expression of genes, such as tumor suppressor

genes, also promotes malignant growth. Thus, alteration in the expression of either type of gene is a potential diagnostic indicator for determining whether a subject is at risk of developing or has cancer, e.g., colon cancer.

Accordingly, in one aspect, the invention also provides biomarkers, such as nucleic acid markers, for human tumor cells and tissue, particularly for colon cancer cells and tissue. The invention also provides proteins encoded by these nucleic acid markers. The invention also features methods for identifying drugs useful for treatment of such cancer cells, and for treatment of a cancerous condition, such as colon cancer. Unlike prior methods, the invention provides a means for identifying cancer cells at an early stage of development, so that premalignant cells can be identified prior to their spreading throughout the human body. This allows early detection of potentially cancerous conditions, and treatment of those cancerous conditions prior to spread of the cancerous cells throughout the body, or prior to development of an irreversible cancerous condition.

II. Definitions

For convenience, the meaning of certain terms and phrases used in the specification, examples, and appended claims, are provided below.

The term “an aberrant expression”, as applied to a nucleic acid of the present invention, refers to level of expression of that nucleic acid which differs from the level of expression of that nucleic acid in healthy tissue, or which differs from the activity of the polypeptide present in a healthy subject. An activity of a polypeptide can be aberrant because it is stronger than the activity of its native counterpart. Alternatively, an activity can be aberrant because it is weaker or absent relative to the activity of its native counterpart. An aberrant activity can also be a change in the activity; for example, an aberrant polypeptide can interact with a different target peptide. A cell can have an aberrant expression level of a gene due to overexpression or underexpression of that gene.

The term “agonist”, as used herein, is meant to refer to an agent that mimics or upregulates (e.g., potentiates or supplements) the bioactivity of a protein. An agonist can be a wild-type protein or derivative thereof having at least one bioactivity of the wild-type protein. An agonist can also be a compound that upregulates expression of a gene or which increases at least one bioactivity of a protein. An agonist can also be a compound which increases the interaction of a polypeptide with another molecule, e.g., a target peptide or nucleic acid.

The term "allele", which is used interchangeably herein with "allelic variant", refers to alternative forms of a gene or portions thereof. Alleles occupy the same locus or position on homologous chromosomes. When a subject has two identical alleles of a gene, the subject is said to be homozygous for that gene or allele. When a subject has two different alleles of a gene, the subject is said to be heterozygous for the gene. Alleles of a specific gene can differ from each other in a single nucleotide, or several nucleotides, and can include substitutions, deletions, and/or insertions of nucleotides. An allele of a gene can also be a form of a gene containing mutations.

The term "allelic variant of a polymorphic region of a gene" refers to a region of a gene having one of several nucleotide sequences found in that region of the gene in other individuals.

The term "antagonist" as used herein is meant to refer to an agent that downregulates (e.g., suppresses or inhibits) at least one bioactivity of a protein. An antagonist can be a compound which inhibits or decreases the interaction between a protein and another molecule, e.g., a target peptide or enzyme substrate. An antagonist can also be a compound that downregulates expression of a gene or which reduces the amount of expressed protein present.

The term "antibody" as used herein is intended to include whole antibodies, e.g., of any isotype (IgG, IgA, IgM, IgE, etc), and includes fragments thereof which are also specifically reactive with a vertebrate, e.g., mammalian, protein. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as described above for whole antibodies. Thus, the term includes segments of proteolytically-cleaved or recombinantly-prepared portions of an antibody molecule that are capable of selectively reacting with a certain protein. Nonlimiting examples of such proteolytic and/or recombinant fragments include Fab, F(ab')₂, Fab', Fv, and single chain antibodies (scFv) containing a V[L] and/or V[H] domain joined by a peptide linker. The scFv's may be covalently or non-covalently linked to form antibodies having two or more binding sites. The subject invention includes polyclonal, monoclonal, or other purified preparations of antibodies and recombinant antibodies.

The phenomenon of "apoptosis" is well known, and can be described as a programmed death of cells. As is known, apoptosis is contrasted with "necrosis", a phenomenon when cells die as a result of being killed by a toxic material, or other external effect. Apoptosis involves chromatic condensation, membrane blebbing, and fragmentation of DNA, all of which are generally visible upon microscopic examination.

A disease, disorder, or condition “associated with” or “characterized by” an aberrant expression of a nucleic acid refers to a disease, disorder, or condition in a subject which can be statistically correlated with the expression of a nucleic acid.

As used herein the term “bioactive fragment of a polypeptide” refers to a fragment of a full-length polypeptide, wherein the fragment specifically agonizes (mimics) or antagonizes (inhibits) the activity of a wild-type polypeptide. The bioactive fragment preferably is a fragment capable of interacting with at least one other molecule, e.g., protein, small molecule, or DNA, which a full length protein can bind.

“Biological activity” or “bioactivity” or “activity” or “biological function”, which are used interchangeably, herein mean an effector or antigenic function that is directly or indirectly performed by a polypeptide (whether in its native or denatured conformation), or by any subsequence thereof. Biological activities include binding to polypeptides, binding to other proteins or molecules, activity as a DNA binding protein, as a transcription regulator, ability to bind damaged DNA, etc. A bioactivity can be modulated by directly affecting the subject polypeptide. Alternatively, a bioactivity can be altered by modulating the level of the polypeptide, such as by modulating expression of the corresponding gene.

The term “biomarker” refers a biological molecule, e.g., a nucleic acid, including DNA, cDNA, RNA, mRNA, tRNA, or rRNA, peptide, polypeptide, protein, hormone, etc., whose presence or concentration can be detected and correlated with a known condition, such as a disease state.

“Cells,” “host cells”, or “recombinant host cells” are terms used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A “chimeric polypeptide” or “fusion polypeptide” is a fusion of a first amino acid sequence encoding one of the subject polypeptides with a second amino acid sequence defining a domain (e.g., polypeptide portion) foreign to and not substantially homologous with any domain of the subject polypeptide. A chimeric polypeptide may present a foreign domain which is found (albeit in a different polypeptide) in an organism which also expresses the first polypeptide, or it may be an “interspecies,” “intergenic,” etc., fusion of polypeptide structures expressed by different kinds of organisms. In general, a fusion polypeptide can be represented by the general

formula $(X)_n-(Y)_m-(Z)_n$, wherein Y represents a portion of the subject polypeptide, and X and Z are each independently absent or represent amino acid sequences which are not related to the native sequence found in an organism, or which are not found as a polypeptide chain contiguous with the subject sequence, where m is an integer greater than or equal to one, and each
5 occurrence of n is, independently, 0 or an integer greater than or equal to 1 (n and m are preferably no greater than 5 or 10).

A "delivery complex" shall mean a targeting means (e.g., a molecule that results in higher affinity binding of a nucleic acid, protein, polypeptide or peptide to a target cell surface and/or increased cellular or nuclear uptake by a target cell). Examples of targeting means
10 include: sterols (e.g., cholesterol), lipids (e.g., a cationic lipid, virosome or liposome), viruses (e.g., adenovirus, adeno-associated virus, and retrovirus), or target cell-specific binding agents (e.g., ligands recognized by target cell specific receptors). Preferred complexes are sufficiently stable *in vivo* to prevent significant uncoupling prior to internalization by the target cell. However, the complex is cleavable under appropriate conditions within the cell so that the
15 nucleic acid, protein, polypeptide or peptide is released in a functional form.

As is well known, genes or a particular polypeptide may exist in single or multiple copies within the genome of an individual. Such duplicate genes may be identical or may have certain modifications, including nucleotide substitutions, additions or deletions, which all still code for polypeptides having substantially the same activity. The term "DNA sequence encoding a
20 polypeptide" may thus refer to one or more genes within a particular individual. Moreover, certain differences in nucleotide sequences may exist between individual organisms, which are called alleles. Such allelic differences may or may not result in differences in amino acid sequence of the encoded polypeptide yet still encode a polypeptide with the same biological activity.

25 The term "equivalent" is understood to include nucleotide sequences encoding functionally equivalent polypeptides. Equivalent nucleotide sequences will include sequences that differ by one or more nucleotide substitutions, additions or deletions, such as allelic variants; and will, therefore, include sequences that differ from the nucleotide sequence of the nucleic acids shown in SEQ ID NOs: 1-4494 due to the degeneracy of the genetic code.

30 As used herein, the terms "gene", "recombinant gene", and "gene construct" refer to a nucleic acid of the present invention associated with an open reading frame, including both exon and, optionally, intron sequences.

A "recombinant gene" refers to nucleic acid encoding a polypeptide and comprising exon sequences, though it may optionally include intron sequences which are derived from, for example, a related or unrelated chromosomal gene. The term "intron" refers to a DNA sequence present in a given gene which is not translated into protein and is generally found between exons.

5 The term "growth" or "growth state" of a cell refers to the proliferative state of a cell as well as to its differentiative state. Accordingly, the term refers to the phase of the cell cycle in which the cell is, e.g., G₀, G₁, G₂, or prophase, metaphase, or telophase, or anaphase, as well as to its state of differentiation, e.g., undifferentiated, partially differentiated, or fully differentiated. Without wanting to be limited, differentiation of a cell is usually accompanied by a decrease in
10 the proliferative rate of a cell.

"Homology" or "identity" or "similarity" refers to sequence similarity between two peptides or between two nucleic acid molecules, with identity being a more strict comparison. Homology and identity can each be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When a position in the compared sequence is
15 occupied by the same base or amino acid, then the molecules are identical at that position. A degree of homology or similarity or identity between nucleic acid sequences is a function of the number of identical or matching nucleotides at positions shared by the nucleic acid sequences. A degree of identity of amino acid sequences is a function of the number of identical amino acids at positions shared by the amino acid sequences. A degree of homology or similarity of amino acid
20 sequences is a function of the number of amino acids, i.e., structurally related, at positions shared by the amino acid sequences. An "unrelated" or "non-homologous" sequence shares less than 40% identity, though preferably less than 25% identity, with one of the sequences of the present invention.

The term "percent identical" refers to sequence identity between two amino acid
25 sequences or between two nucleotide sequences. Identity can each be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When an equivalent position in the compared sequences is occupied by the same base or amino acid, then the molecules are identical at that position; when the equivalent site occupied by the same or a similar amino acid residue (e.g., similar in steric and/or electronic nature), then the molecules
30 can be referred to as homologous (similar) at that position. Expression as a percentage of homology, similarity, or identity refers to a function of the number of identical or similar amino acids at positions shared by the compared sequences. Various alignment algorithms and/or programs may be used, including FASTA, BLAST, or ENTREZ. FASTA and BLAST are

available as a part of the GCG sequence analysis package (University of Wisconsin, Madison, Wis.), and can be used with, e.g., default settings. ENTREZ is available through the National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, Md. In one embodiment, the percent identity of two sequences can be
5 determined by the GCG program with a gap weight of 1, e.g., each amino acid gap is weighted as if it were a single amino acid or nucleotide mismatch between the two sequences.

Other techniques for alignment are described in Methods in Enzymology, vol. 266: Computer Methods for Macromolecular Sequence Analysis (1996), ed. Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co., San Diego, California, USA. Preferably, an
10 alignment program that permits gaps in the sequence is utilized to align the sequences. The Smith-Waterman is one type of algorithm that permits gaps in sequence alignments. See Meth. Mol. 70-187 (1997). Also, the GAP program using the Needleman and Wunsch alignment method can be utilized to align sequences. An alternative search strategy uses MPSRCH software, which runs on a MASPAR computer. MPSRCH uses a Smith-Waterman algorithm to
15 score sequences on a massively parallel computer. This approach improves ability to pick up distantly related matches, and is especially tolerant of small gaps and nucleotide sequence errors. Nucleic acid-encoded amino acid sequences can be used to search both protein and DNA databases.

Databases with individual sequences are described in Methods in Enzymology, ed.
20 Doolittle, *supra*. Databases include, for example, Genbank, EMBL, and DNA Database of Japan (DDBJ).

Preferred nucleic acids have a sequence at least 70%, and more preferably 80% identical and more preferably 90% and even more preferably at least 95% identical to a nucleic acid sequence of a sequence shown in one of SEQ ID NOS: 1-4494. Nucleic acids at least 90%, more
25 preferably 95%, and most preferably at least about 98-99% identical with a nucleic sequence represented in one of SEQ ID NOS: 1-4494 are of course also within the scope of the invention. In preferred embodiments, the nucleic acid is mammalian.

The term "interact" as used herein is meant to include detectable interactions (e.g., biochemical interactions) between molecules, such as interaction between protein-protein,
30 protein-nucleic acid, nucleic acid-nucleic acid, and protein-small molecule or nucleic acid-small molecule in nature. Examples of interactions between protein-protein, protein-nucleic acid, nucleic acid-nucleic acid, and protein-small molecule or nucleic acid-small molecule can include binding, modifying, cleaving, processing, or catalyzing.

The term "isolated" as used herein with respect to nucleic acids, such as DNA or RNA, refers to molecules separated from other DNAs, or RNAs, respectively, that are present in the natural source of the macromolecule. The term isolated as used herein also refers to a nucleic acid or peptide that is substantially free of cellular material, viral material, or culture medium when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. Moreover, an "isolated nucleic acid" is meant to include nucleic acid fragments which are not naturally occurring as fragments and would not be found in the natural state. The term "isolated" is also used herein to refer to polypeptides which are isolated from other cellular proteins and is meant to encompass both purified and recombinant polypeptides.

The terms "modulated" and "differentially regulated" as used herein refer to both upregulation (i.e., activation or stimulation e.g., by agonizing or potentiating) and downregulation (i.e., inhibition or suppression e.g., by antagonizing, decreasing or inhibiting).

The term "mutated gene" refers to an allelic form of a gene, which is capable of altering the phenotype of a subject having the mutated gene relative to a subject which does not have the mutated gene. If a subject must be homozygous for this mutation to have an altered phenotype, the mutation is said to be recessive. If one copy of the mutated gene is sufficient to alter the genotype of the subject, the mutation is said to be dominant. If a subject has one copy of the mutated gene and has a phenotype that is intermediate between that of a homozygous and that of a heterozygous subject (for that gene), the mutation is said to be co-dominant.

The designation "N", where it appears in the accompanying Sequence Listing, indicates that the identity of the corresponding nucleotide is unknown. "N" should therefore not necessarily be interpreted as permitting substitution with any nucleotide, e.g., A, T, C, or G, but rather as holding the place of a nucleotide whose identity has not been conclusively determined.

The "non-human animals" of the invention include mammals such as rodents, non-human primates, sheep, dog, cow, pigs, chickens, amphibians, reptiles, etc. Preferred non-human animals are selected from the rodent family including rat and mouse, most preferably mouse, though transgenic amphibians, such as members of the *Xenopus* genus, and transgenic chickens can also provide important tools for understanding and identifying agents which can affect, for example, embryogenesis and tissue formation. The term "chimeric animal" is used herein to refer to animals in which the recombinant gene is found, or in which the recombinant gene is expressed in some but not all cells of the animal. The term "tissue-specific chimeric

animal” indicates that one of the recombinant genes is present and/or expressed or disrupted in some tissues but not others.

As used herein, the term “nucleic acid” refers to polynucleotides such as deoxyribonucleic acid (DNA), and, where appropriate, ribonucleic acid (RNA). The term should
5 also be understood to include, as equivalents, analogs of either RNA or DNA made from nucleotide analogs, and, as applicable to the embodiment being described, single (sense or antisense) and double-stranded polynucleotides. ESTs, chromosomes, cDNAs, mRNAs, and rRNAs are representative examples of molecules that may be referred to as nucleic acids.

The term “nucleotide sequence complementary to the nucleotide sequence of SEQ ID
10 NO. x” refers to the nucleotide sequence of the complementary strand of a nucleic acid strand having SEQ ID NO. x. The term “complementary strand” is used herein interchangeably with the term “complement”. The complement of a nucleic acid strand can be the complement of a coding strand or the complement of a non-coding strand. As used herein, a “complementary strand” to SEQ ID NO. x is a nucleic acid sequence which hybridizes under stringent conditions
15 to SEQ ID NO. x.

The term “polymorphism” refers to the coexistence of more than one form of a gene or portion (e.g., allelic variant) thereof. A portion of a gene of which there are at least two different forms, i.e., two different nucleotide sequences, is referred to as a “polymorphic region of a gene”. A polymorphic region can be a single nucleotide, the identity of which differs in different
20 alleles. A polymorphic region can also be several nucleotides long.

A “polymorphic gene” refers to a gene having at least one polymorphic region.

As used herein, the term “promoter” means a DNA sequence that regulates expression of a selected DNA sequence operably linked to the promoter, and which effects expression of the selected DNA sequence in cells. The term encompasses “tissue specific” promoters, i.e.,
25 promoters which effect expression of the selected DNA sequence only in specific cells (e.g., cells of a specific tissue). The term also covers so-called “leaky” promoters, which regulate expression of a selected DNA primarily in one tissue, but cause expression in other tissues as well. The term also encompasses non-tissue specific promoters and promoters that constitutively expressed or that are inducible (i.e., expression levels can be controlled).

30 The terms “protein”, “polypeptide”, and “peptide” are used interchangeably herein when referring to a gene product.

The term "recombinant protein" refers to a polypeptide of the present invention which is produced by recombinant DNA techniques, wherein generally, DNA encoding a polypeptide is inserted into a suitable expression vector which is in turn used to transform a host cell to produce the heterologous protein. Moreover, the phrase "derived from", with respect to a recombinant gene, is meant to include within the meaning of "recombinant protein" those proteins having an amino acid sequence of a native polypeptide, or an amino acid sequence similar thereto which is generated by mutations including substitutions and deletions (including truncation) of a naturally occurring form of the polypeptide.

"Small molecule" as used herein, is meant to refer to a composition, which has a molecular weight of less than about 5 kD and most preferably less than about 4 kD. Small molecules can be nucleic acids, peptides, polypeptides, peptidomimetics, carbohydrates, lipids or other organic (carbon-containing) or inorganic molecules. Many pharmaceutical companies have extensive libraries of chemical and/or biological mixtures, often fungal, bacterial, or algal extracts, which can be screened with any of the assays of the invention to identify compounds that modulate a bioactivity.

As used herein, the term "specifically hybridizes" or "specifically detects" refers to the ability of a nucleic acid molecule of the invention to hybridize to at least a portion of, for example approximately 6, 12, 15, 20, 30, 50, 100, 150, 200, 300, 350, 400, 500, 750, or 1000 contiguous nucleotides of a nucleic acid designated in any one of SEQ ID Nos: 1-4494, or a sequence complementary thereto, or naturally occurring mutants thereof, such that it has less than 15%, preferably less than 10%, and more preferably less than 5% background hybridization to a cellular nucleic acid (e.g., mRNA or genomic DNA) encoding a different protein. In preferred embodiments, the oligonucleotide probe detects only a specific nucleic acid, e.g., it does not substantially hybridize to similar or related nucleic acids, or complements thereof.

"Transcriptional regulatory sequence" is a generic term used throughout the specification to refer to DNA sequences, such as initiation signals, enhancers, and promoters, which induce or control transcription of protein coding sequences with which they are operably linked. In preferred embodiments, transcription of one of the genes is under the control of a promoter sequence (or other transcriptional regulatory sequence) which controls the expression of the recombinant gene in a cell-type in which expression is intended. It will also be understood that the recombinant gene can be under the control of transcriptional regulatory sequences which are the same or which are different from those sequences which control transcription of the naturally occurring forms of the polypeptide.

As used herein, the term “transfection” means the introduction of a nucleic acid, e.g., via an expression vector, into a recipient cell by nucleic acid-mediated gene transfer.

“Transformation”, as used herein, refers to a process in which a cell’s genotype is changed as a result of the cellular uptake of exogenous DNA or RNA, and, for example, the transformed cell expresses a recombinant form of a polypeptide or, in the case of anti-sense expression from the transferred gene, the expression of the target gene is disrupted.

The term “treating” as used herein is intended to encompass curing as well as ameliorating at least one symptom of the condition or disease.

The term “vector” refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of preferred vector is an episome, i.e., a nucleic acid capable of extra-chromosomal replication. Preferred vectors are those capable of autonomous replication and/or expression of nucleic acids to which they are linked. Vectors capable of directing the expression of genes to which they are operatively linked are referred to herein as “expression vectors”. In general, expression vectors of utility in recombinant DNA techniques are often in the form of “plasmids” which refer generally to circular double stranded DNA loops which, in their vector form are not bound to the chromosome. In the present specification, “plasmid” and “vector” are used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors which serve equivalent functions and which become known in the art subsequently hereto.

The term “wild-type allele” refers to an allele of a gene which, when present in two copies in a subject results in a wild-type phenotype. There can be several different wild-type alleles of a specific gene, since certain nucleotide changes in a gene may not affect the phenotype of a subject having two copies of the gene with the nucleotide changes.

III. Nucleic Acids of the Present Invention

As described below, one aspect of the invention pertains to isolated nucleic acids, variants, and/or equivalents of such nucleic acids.

Nucleic acids of the present invention have been identified as differentially expressed in tumor cells, e.g., colon cancer-derived cell lines and colon cancer tissue (relative to the expression levels in normal cells or tissue, e.g., normal colon tissue and/or normal non-colon tissue). The present differentially expressed sequences comprise SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos.

1-1103, even more preferably SEQ ID Nos. 1-503, or sequence complementary thereto. In another embodiment, the invention comprises sequences which hybridize under stringent conditions with any of the sequences of SEQ ID Nos 1-4494. In a preferred aspect, sequences of the invention hybridize to SEQ ID Nos 1-4494 with about 50% identity, preferably about 70% identity, more preferably about 90% identity, and still more preferably about 100% identity. In preferred embodiments, the subject nucleic acids are differentially expressed by at least a factor of two, preferably at least a factor of five, even more preferably at least a factor of twenty, still more preferably at least a factor of fifty. Preferred nucleic acids are those sequences identified as differentially expressed both in colon cancer tissue and colon cancer cell lines. In preferred embodiments, nucleic acids of the present invention are upregulated in tumor cells, especially colon cancer tissue and/or colon cancer-derived cell lines. In another embodiment, nucleic acids of the present invention are downregulated in tumor cells, especially colon cancer tissue and/or colon cancer-derived cell lines.

Genes which are upregulated, such as oncogenes, or downregulated, such as tumor suppressors, in aberrantly proliferating cells can be used as targets for diagnostic or therapeutic applications. For example, upregulation of the *cdc2* gene induces mitosis. Overexpression of the *myt1* gene, a mitotic deactivator, negatively regulates the activity of *cdc2*. Aberrant proliferation may thus be induced either by upregulating *cdc2* or by downregulating *myt1*. Similarly, downregulation of tumor suppressors such as p53 and Rb have been implicated in tumorigenesis.

Particularly preferred polypeptides are those that are encoded by nucleic acid sequences at least about 70%, 75%, 80%, 90%, 95%, 97%, or 98% similar to a nucleic acid sequence of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494. Preferably, the nucleic acid includes all or a portion (e.g., at least about 10, at least about 15, at least about 25, or at least about 40 nucleotides) of the nucleotide sequence corresponding to the nucleic acid of SEQ ID Nos. 1-1103, most preferably SEQ ID Nos. 1-503, or a sequence complementary thereto.

Still other preferred nucleic acids of the present invention encode a polypeptide comprising at least a portion of a polypeptide encoded by one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494. For example, preferred nucleic acid molecules for use as probes/primers or antisense molecules (i.e., noncoding nucleic acid molecules) can comprise at least about 10, 20, 30, 50, 60, 70, 80, 90, or 100 base pairs in length up to the length of the complete sequence of any of SEQ ID Nos 1-4494. Coding nucleic

acid molecules can comprise, for example, from about 50, 60,70,80,90, or 100 base pairs up to the full length of the entire sequence of any of SEQ ID Nos 1-4494.

Another aspect of the invention provides a nucleic acid which hybridizes under low, medium, or high stringency conditions to a nucleic acid sequence represented by one of SEQ ID
5 Nos. 1-1103, preferably SEQ ID Nos. 1-503, or a sequence complementary thereto. Appropriate stringency conditions which promote DNA hybridization, for example, about 6.0 x sodium chloride/sodium citrate (SSC) at about 45 °C, followed by a wash of about 2.0 x SSC at about 50°C, are known to those skilled in the art or can be found in Current Protocols in Molecular
10 Biology, John Wiley & Sons, N.Y. (1989), 6.3.1-12.3.6. For example, the salt concentration in the wash step can be selected from a low stringency of about 2.0 x SSC at about 50°C to a high stringency of about 0.2 x SSC at about 50°C. In addition, the temperature in the wash step can be increased from low stringency conditions at room temperature, about 22 °C, to high stringency conditions at about 65 °C. Both temperature and salt may be varied, or temperature or salt concentration may be held constant while the other variable is changed. In a preferred
15 embodiment, a nucleic acid of the present invention will bind to one of SEQ ID Nos. 1-1103, preferably SEQ ID Nos. 1-503, or a sequence complementary thereto, under moderately stringent conditions, for example at about 2.0 x SSC and about 40°C. In a particularly preferred embodiment, a nucleic acid of the present invention will bind to one of SEQ ID Nos. 1-1103, preferably SEQ ID Nos. 1-503, or a sequence complementary thereto, under high stringency
20 conditions.

In one embodiment, the invention provides nucleic acids which hybridize under low stringency conditions of about 6 x SSC at about room temperature followed by a wash at about 2 x SSC at about room temperature.

In another embodiment, the invention provides nucleic acids which hybridize under high
25 , stringency conditions of about 2 x SSC at about 65 °C followed by a wash at about 0.2 x SSC at about 65 °C.

Nucleic acids having a sequence that differs from the nucleotide sequences shown in one of SEQ ID Nos. 1-1103, preferably SEQ ID Nos. 1-503, or a sequence complementary thereto, due to degeneracy in the genetic code, are also within the scope of the invention. Such nucleic
30 acids encode functionally equivalent peptides (i.e., a peptide having equivalent or similar biological activity) but differ in sequence from the sequence shown in the sequence listing due to degeneracy in the genetic code. For example, a number of amino acids are designated by more than one triplet. Codons that specify the same amino acid, or synonyms (for example, CAU and

CAC each encode histidine) may result in "silent" mutations which do not affect the amino acid sequence of a polypeptide. However, it is expected that DNA sequence polymorphisms that do lead to changes in the amino acid sequences of the subject polypeptides will exist among mammals. One skilled in the art will appreciate that these variations in one or more nucleotides (e.g., up to about 3-5% of the nucleotides) of the nucleic acids encoding polypeptides having an activity of a polypeptide may exist among individuals of a given species due to natural allelic variation.

Also within the scope of the invention are nucleic acids encoding splicing variants of proteins encoded by a nucleic acid of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, or a sequence complementary thereto, or natural homologs of such proteins. Such homologs can be cloned by hybridization or PCR, as further described herein.

The polynucleotide sequence may also encode for a leader sequence, e.g., the natural leader sequence or a heterologous leader sequence, for a subject polypeptide. For example, the desired DNA sequence may be fused in the same reading frame to a DNA sequence which aids in expression and secretion of the polypeptide from the host cell, for example, a leader sequence which functions as a secretory sequence for controlling transport of the polypeptide from the cell. The protein having a leader sequence is a preprotein and may have the leader sequence cleaved by the host cell to form the mature form of the protein.

The polynucleotide of the present invention may also be fused in frame to a marker sequence, also referred to herein as "Tag sequence" encoding a "Tag peptide", which allows for marking and/or purification of the present invention. In a preferred embodiment, the marker sequence is a hexahistidine tag, e.g., supplied by a PQE-9 vector. Numerous other Tag peptides are available commercially. Other frequently used Tags include myc-epitopes (e.g., see Ellison et al. (1991) J Biol Chem 266:21150-21157) which includes a 10-residue sequence from c-myc, the pFLAG system (International Biotechnologies, Inc.), the pEZZ-protein A system (Pharmacia, NJ), and a 16 amino acid portion of the Haemophilus influenza hemagglutinin protein. Furthermore, any polypeptide can be used as a Tag so long as a reagent, e.g., an antibody interacting specifically with the Tag polypeptide is available or can be prepared or identified.

As indicated by the examples set out below, nucleic acids can be obtained from mRNA present in any of a number of eukaryotic cells or tissue, e.g., and are preferably obtained from metazoan cells or tissue, more preferably from vertebrate cells or tissue, and even more preferably from mammalian cells and tissue, and most preferably from human cells or tissue. It

also is possible to obtain nucleic acids of the present invention from genomic DNA from both adults and embryos. For example, a gene can be cloned from either a cDNA or a genomic library in accordance with protocols generally known to persons skilled in the art. cDNA can be obtained by isolating total mRNA from a cell, e.g., a vertebrate cell, a mammalian cell, or a human cell, including embryonic cells. Double stranded cDNAs can then be prepared from the total mRNA, and subsequently inserted into a suitable plasmid or bacteriophage vector using any one of a number of known techniques. The gene can also be cloned using established polymerase chain reaction techniques in accordance with the nucleotide sequence information provided by the invention.

The invention includes within its scope a polynucleotide having the nucleotide sequence of nucleic acid obtained from this biological material, wherein the nucleic acid hybridizes under stringent conditions (at least about 4 x SSC at 65 °C, or at least about 4 x SSC at 42 °C; see, for example, U.S. Patent No. 5,707,829, incorporated herein by reference) with at least 15 contiguous nucleotides of at least one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494. By this is intended that when at least 15 contiguous nucleotides of one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 is used as a probe, the probe will preferentially hybridize with a gene or mRNA (of the biological material) comprising the complementary sequence, allowing the identification and retrieval of the nucleic acids of the biological material that uniquely hybridize to the selected probe. Probes from more than one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 will hybridize with the same gene or mRNA if the cDNA from which they were derived corresponds to one mRNA. Probes of more than 15 nucleotides can be used, but 15 nucleotides represents enough sequence for unique identification.

Because the present nucleic acids are cDNAs which represent partial mRNA transcripts, two or more nucleic acids of the invention may represent different regions of the same mRNA transcript and the same gene. Thus, if two or more of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 are identified as belonging to the same clone, then either sequence can be used to obtain the full-length mRNA or gene. Nucleic acid-related polynucleotides can also be isolated from cDNA libraries. These libraries are preferably prepared from mRNA of human colon cells, more preferably, human colon cancer specific tissue, designated as the 100-101, and 103-112 clones in Table 1. In another embodiment the nucleic acids are isolated from libraries prepared from normal colon specific tissue, designated herein as the 102 clones in Table 1. Alignment of SEQ ID Nos. 1-4470, 4472,

4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, as described above, indicated that a cell line or tissue source of a related protein or polynucleotide can also be used as a source of the nucleic acid-related cDNA.

Techniques for producing and probing nucleic acid sequence libraries are described, for example, in Sambrook et al., "Molecular Cloning: A Laboratory Manual" (New York, Cold Spring Harbor Laboratory, 1989). The cDNA can be prepared by using primers based on a sequence from SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494. In one embodiment, the cDNA library can be made from only polyadenylated mRNA. Thus, poly-T primers can be used to prepare cDNA from the mRNA. Alignment of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 can result in identification of a related polypeptide or polynucleotide. Some of the polynucleotides disclosed herein contains repetitive regions that were subject to masking during the search procedures. The information about the repetitive regions is discussed below.

Constructs of polynucleotides having sequences of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 can be generated synthetically. Alternatively, single-step assembly of a gene and entire plasmid from large numbers of oligodeoxyribonucleotides is described by Stemmer et al, Gene (Amsterdam) (1995) 164(i):49-53. In this method, assembly PCR (the synthesis of long DNA sequences from large numbers of oligodeoxyribonucleotides (oligos)) is described. The method is derived from DNA shuffling (Stemmer, Nature (1994) 370:389-391), and does not rely on DNA ligase, but instead relies on DNA polymerase to build increasingly longer DNA fragments during the assembly process. For example, a 1.1-kb fragment containing the TEM-1 beta-lactamase-encoding gene (bla) can be assembled in a single reaction from a total of 56 oligos, each 40 nucleotides (nt) in length. The synthetic gene can be PCR amplified and cloned in a vector containing the tetracycline-resistance gene (Tc-R) as the sole selectable marker. Without relying on ampicillin (Ap) selection, 76% of the Tc-R colonies were Ap-R, making this approach a general method for the rapid and cost-effective synthesis of any gene.

IV. Identification of Functional and Structural Motifs of Novel Genes Using Art-Recognized Methods

Translations of the nucleotide sequence of the nucleic acids, cDNAs, or full genes can be aligned with individual known sequences. Similarity with individual sequences can be used to determine the activity of the polypeptides encoded by the polynucleotides of the invention. For

example, sequences that show similarity with a chemokine sequence may exhibit chemokine activities. Also, sequences exhibiting similarity with more than one individual sequence may exhibit activities that are characteristic of either or both individual sequences.

5 The full length sequences and fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence of the nucleic acid. The nearest neighbors can indicate a tissue or cell type to be used to construct a library for the full-length sequences of the nucleic acid.

Typically, the nucleic acids are translated in all six frames to determine the best alignment with the individual sequences. The sequences disclosed herein in the Sequence
10 Listing are in a 5' to 3' orientation and translation in three frames can be sufficient (with a few specific exceptions as described in the Examples). These amino acid sequences are referred to, generally, as query sequences, which will be aligned with the individual sequences.

Nucleic acid sequences can be compared with known genes by any of the methods disclosed above. Results of individual and query sequence alignments can be divided into three
15 categories: high similarity, weak similarity, and no similarity. Individual alignment results ranging from high similarity to weak similarity provide a basis for determining polypeptide activity and/or structure.

Parameters for categorizing individual results include: percentage of the alignment region length where the strongest alignment is found, percent sequence identity, and p value.

20 The percentage of the alignment region length is calculated by counting the number of residues of the individual sequence found in the region of strongest alignment. This number is divided by the total residue length of the query sequence to find a percentage.

Percent sequence identity is calculated by counting the number of amino acid matches between the query and individual sequence and dividing total number of matches by the number
25 of residues of the individual sequence found in the region of strongest alignment. For the example above, the percent identity would be 10 matches divided by 11 amino acids, or approximately 90.9%.

P value is the probability that the alignment was produced by chance. For a single alignment, the p value can be calculated according to Karlin et al., Proc. Natl. Acad. Sci. 87:
30 2264 (1990) and Karlin et al., Proc. Natl. Acad. Sci. 90: (1993). The p value of multiple alignments using the same query sequence can be calculated using an heuristic approach

described in Altschul et al., Genet. 6:119(1994). Alignment programs such as BLAST program can calculate the p value.

The boundaries of the region where the sequences align can be determined according to Doolittle, Methods in Enzymology, *supra*; BLAST or FASTA programs; or by determining the
5 area where the sequence identity is highest.

Another factor to consider for determining identity or similarity is the location of the similarity or identity. Strong local alignment can indicate similarity even if the length of alignment is short. Sequence identity scattered throughout the length of the query sequence also can indicate a similarity between the query and profile sequences.

10 High Similarity

For the alignment results to be considered high similarity, the percent of the alignment region length, typically, is at least about 55% of total length query sequence; more typically, at least about 58%; even more typically; at least about 60% of the total residue length of the query sequence. Usually, percent length of the alignment region can be as much as about 62%; more
15 usually, as much as about 64%; even more usually, as much as about 66%.

Further, for high similarity, the region of alignment, typically, exhibits at least about 75% of sequence identity; more typically, at least about 78%; even more typically; at least about 80% sequence identity. Usually, percent sequence identity can be as much as about 82%; more usually, as much as about 84%; even more usually, as much as about 86%.

20 The p value is used in conjunction with these methods. If high similarity is found, the query sequence is considered to have high similarity with a profile sequence when the p value is less than or equal to about 10^{-2} ; more usually; less than or equal to about 10^{-3} even more usually; less than or equal to about 10^{-4} . More typically, the p value is no more than about 10^{-5} more typically; no more than or equal to about 10^{-10} ; even more typically; no more than or equal to
25 about 10^{-15} for the query sequence to be considered high similarity.

Weak Similarity

For the alignment results to be considered weak there is no minimum percent length of the alignment region no minimum length of alignment. A better showing of weak similarity is considered when the region of alignment is, typically, at least about 15 amino acid residues in
30 length; more typically, at least about 20; even more typically; at least about 25 amino acid

residues in length. Usually, length of the alignment region can be as much as about 30 amino acid residues; more usually, as much as about 40; even more usually, as much as about 60 amino acid residues.

Further, for weak similarity, the region of alignment, typically, exhibits at least about
5 35% of sequence identity; more typically, at least about 40%; even more typically; at least about 45% sequence identity. Usually, percent sequence identity can be as much as about 50%; more usually, as much as about 55%; even more usually, as much as about 60%.

If low similarity is found, the query sequence is considered to have weak similarity with a profile sequence when the p value is usually less than or equal to about 10^{-2} ; more usually; less
10 than or equal to about 10^{-3} even more usually; less than or equal to about 10^{-4} . More typically, the p value is no more than about 10^{-5} more usually; no more than or equal to about 10^{-10} ; even more usually; no more than or equal to about 10^{-15} for the query sequence to be considered weak similarity.

Similarity Determined by Sequence Identity

15 Sequence identity alone can be used to determine similarity of a query sequence to an individual sequence and can indicate the activity of the sequence. Such an alignment, preferably, permits gaps to align sequences. Typically, the query sequence is related to the profile sequence if the sequence identity over the entire query sequence is at least about 15%; more typically, at least about 20%; even more typically, at least about 25%; even more typically, at least about
20 50%. Sequence identity alone as a measure of similarity is most useful when the query sequence is usually, at least 80 residues in length; more usually, 90 residues; even more usually, at least 95 amino acid residues in length. More typically, similarity can be concluded based on sequence identity alone when the query sequence is preferably 100 residues in length; more preferably, 120 residues in length; even more preferably, 150 amino acid residues in length.

25 Determining Activity from Alignments with Profile and Multiple Aligned Sequences

Translations of the nucleic acids can be aligned with amino acid profiles that define either protein families or common motifs. Also, translations of the nucleic acids can be aligned to multiple sequence alignments (MSA) comprising the polypeptide sequences of members of protein families or motifs. Similarity or identity with profile sequences or MSAs can be used to
30 determine the activity of the polypeptides encoded by nucleic acids or corresponding cDNA or genes. For example, sequences that show an identity or similarity with a chemokine profile or MSA can exhibit chemokine activities.

Profiles can be designed manually by (1) creating a MSA, which is an alignment of the amino acid sequence of members that belong to the family and (2) constructing a statistical representation of the alignment. Such methods are described, for example, in Birney et al., Nucl. Acid Res. 25(14): 2730-2739 (1996).

5 MSAs of some protein families and motifs are publicly available. For example, these include MSAs of 547 different families and motifs. These MSAs are described also in Sonnhammer et al., Proteins 28: 405-420 (1997). Other sources are also available in the world wide web. A brief description of these MSAs is reported in Pascarella et al., Prot. Eng. 9(3): 249-251 (1996).

10 Techniques for building profiles from MSAs are described in Sonnhammer et al., *supra*; Birney et al., *supra*; and Methods in Enzymology, vol. 266: "Computer Methods for Macromolecular Sequence Analysis," 1996, ed. Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co., San Diego, California, USA.

Similarity between a query sequence and a protein family or motif can be determined by
15 (a) comparing the query sequence against the profile and/or (b) aligning the query sequence with the members of the family or motif.

Typically, a program such as Searchwise can be used to compare the query sequence to the statistical representation of the multiple alignment, also known as a profile. The program is described in Birney et al., *supra*. Other techniques to compare the sequence and profile are
20 described in Sonnhammer et al., *supra* and Doolittle, *supra*.

Next, methods described by Feng et al., J. Mol. Evol. 25:351-360 (1987) and Higgins et al., CABIOS 5:151-153 (1989) can be used to align the query sequence with the members of a family or motif, also known as a MSA. Computer programs, such as PILEUP, can be used. See Feng et al., *infra*.

25 The following factors are used to determine if a similarity between a query sequence and a profile or MSA exists: (1) number of conserved residues found in the query sequence, (2) percentage of conserved residues found in the query sequence, (3) number of frameshifts, and (4) spacing between conserved residues.

Some alignment programs that both translate and align sequences can make any number
30 of frameshifts when translating the nucleotide sequence to produce the best alignment. The fewer frameshifts needed to produce an alignment, the stronger the similarity or identity between

the query and profile or MSAs. For example, a weak similarity resulting from no frameshifts can be a better indication of activity or structure of a query sequence, than a strong similarity resulting from two frameshifts.

Preferably, three or fewer frameshifts are found in an alignment; more preferably two or fewer frameshifts; even more preferably, one or fewer frameshifts; even more preferably, no frameshifts are found in an alignment of query and profile or MSAs.

Conserved residues are those amino acids that are found at a particular position in all or some of the family or motif members. For example, most known chemokines contain four conserved cysteines. Alternatively, a position is considered conserved if only a certain class of amino acids is found in a particular position in all or some of the family members. For example, the N-terminal position may contain a positively charged amino acid, such as lysine, arginine, or histidine.

Typically, a residue of a polypeptide is conserved when a class of amino acids or a single amino acid is found at a particular position in at least about 40% of all class members; more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif; more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

A residue is considered conserved when three unrelated amino acids are found at a particular position in the some or all of the members; more usually, two unrelated amino acids. These residues are conserved when the unrelated amino acids are found at particular positions in at least about 40% of all class member, more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

A query sequence has similarity to a profile or MSA when the query sequence comprises at least about 25% of the conserved residues of the profile or MSA; more usually, at least about 30%; even more usually; at least about 40%. Typically, the query sequence has a stronger similarity to a profile sequence or MSA when the query sequence comprises at least about 45% of the conserved residues of the profile or MSA more typically, at least about 50%; even more typically; at least about 55%.

V. Probes and Primers

The nucleotide sequences determined from the cloning of genes from tumor cells, especially colon cancer cell lines and tissues will further allow for the generation of probes and primers designed for identifying and/or cloning homologs in other cell types, e.g., from other tissues, as well as homologs from other mammalian organisms. Nucleotide sequences useful as probes/primers may include all or a portion of the sequences listed in SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or sequences complementary thereto or sequences which hybridize under stringent conditions to all or a portion of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494. For instance, the present invention also provides a probe/primer comprising a substantially purified oligonucleotide, which oligonucleotide comprising a nucleotide sequence that hybridizes under stringent conditions to at least approximately 12, preferably 25, more preferably 40, 50, or 75 consecutive nucleotides up to the full length of the sense or anti-sense sequence selected from the group consisting of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, or a sequence complementary thereto, or naturally occurring mutants thereof. For instance, primers based on a nucleic acid represented in SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, and even still more preferred SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto, can be used in PCR reactions to clone homologs of that sequence.

In yet another embodiment, the invention provides probes/primers comprising a nucleotide sequence that hybridizes under moderately stringent conditions to at least approximately 12, 16, 25, 40, 50 or 75 consecutive nucleotides up to the full length of the sense or antisense sequence selected from the group consisting of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, or naturally occurring mutants thereof.

In particular, these probes are useful because they provide a method for detecting mutations in wild-type genes of the present invention. Nucleic acid probes which are complementary to a wild-type gene of the present invention and can form mismatches with mutant genes are provided, allowing for detection by enzymatic or chemical cleavage or by shifts in electrophoretic mobility. Likewise, probes based on the subject sequences can be used to

detect transcripts or genomic sequences encoding the same or homologous proteins, for use, for example, in prognostic or diagnostic assays. In preferred embodiments, the probe further comprises a label group attached thereto and able to be detected, e.g., the label group is selected from radioisotopes, fluorescent compounds, chemiluminescent compounds, enzymes, and
5 enzyme co-factors.

Full-length cDNA molecules comprising the disclosed nucleic acids are obtained as follows. In a preferred embodiment, the invention provides the full length cDNA sequence of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494. A subject nucleic acid or a portion thereof comprising at least about 12, 15, 18, or 20 nucleotides
10 up to the full length of a sequence represented in SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, or a sequence complementary thereto, may be used as a hybridization probe to detect hybridizing members of a cDNA library using probe design methods, cloning methods, and clone selection techniques as described in U.S. Patent No.
15 5,654,173, "Secreted Proteins and Polynucleotides Encoding Them," incorporated herein by reference. Libraries of cDNA may be made from selected tissues, such as normal or tumor tissue, or from tissues of a mammal treated with, for example, a pharmaceutical agent. Preferably, the tissue is the same as that used to generate the nucleic acids, as both the nucleic acid and the cDNA represent expressed genes. Most preferably, the cDNA library is made from
20 the biological material described herein in the Examples. Alternatively, many cDNA libraries are available commercially. (Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed. (Cold Spring Harbor Press, Cold Spring Harbor, NY 1989). The choice of cell type for library construction may be made after the identity of the protein encoded by the nucleic acid-related gene is known. This will indicate which tissue and cell types are likely to express the
25 related gene, thereby containing the mRNA for generating the cDNA.

Members of the library that are larger than the nucleic acid, and preferably that contain the whole sequence of the native message, may be obtained. To confirm that the entire cDNA has been obtained, RNA protection experiments may be performed as follows. Hybridization of a full-length cDNA to an mRNA may protect the RNA from RNase degradation. If the cDNA is
30 not full length, then the portions of the mRNA that are not hybridized may be subject to RNase degradation. This may be assayed, as is known in the art, by changes in electrophoretic mobility on polyacrylamide gels, or by detection of released monoribonucleotides. Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed. (Cold Spring Harbor Press, Cold Spring Harbor, NY 1989). In order to obtain additional sequences 5' to the end of a partial cDNA, 5'

RACE (PCR Protocols: A Guide to Methods and Applications (Academic Press, Inc. 1990)) may be performed.

Genomic DNA may be isolated using nucleic acids in a manner similar to the isolation of full-length cDNAs. Briefly, the nucleic acids, or portions thereof, may be used as probes to
5 libraries of genomic DNA. Preferably, the library is obtained from the cell type that was used to generate the nucleic acids. Most preferably, the genomic DNA is obtained from the biological material described herein in the Example. Such libraries may be in vectors suitable for carrying large segments of a genome, such as P1 or YAC, as described in detail in Sambrook et al., 9.4-9.30. In addition, genomic sequences can be isolated from human BAC libraries, which are
10 commercially available from Research Genetics, Inc., Huntsville, Alabama, USA, for example. In order to obtain additional 5' or 3' sequences, chromosome walking may be performed, as described in Sambrook et al., such that adjacent and overlapping fragments of genomic DNA are isolated. These may be mapped and pieced together, as is known in the art, using restriction digestion enzymes and DNA ligase.

15 Using the nucleic acids of the invention, corresponding full length genes can be isolated using both classical and PCR methods to construct and probe cDNA libraries. Using either method, Northern blots, preferably, may be performed on a number of cell types to determine which cell lines express the gene of interest at the highest rate.

Classical methods of constructing cDNA libraries in Sambrook et al., supra. With these
20 methods, cDNA can be produced from mRNA and inserted into viral or expression vectors. Typically, libraries of mRNA comprising poly(A) tails can be produced with poly(T) primers. Similarly, cDNA libraries can be produced using the instant sequences as primers.

PCR methods may be used to amplify the members of a cDNA library that comprise the desired insert. In this case, the desired insert may contain sequence from the full length cDNA
25 that corresponds to the instant nucleic acids. Such PCR methods include gene trapping and RACE methods.

Gene trapping may entail inserting a member of a cDNA library into a vector. The vector then may be denatured to produce single stranded molecules. Next, a substrate-bound probe, such a biotinylated oligo, may be used to trap cDNA inserts of interest. Biotinylated probes can
30 be linked to an avidin-bound solid substrate. PCR methods can be used to amplify the trapped cDNA. To trap sequences corresponding to the full length genes, the labeled probe sequence may be based on the nucleic acids of the invention, e.g., SEQ ID Nos. 1-1103, preferably SEQ

ID Nos. 1-503, or a sequence complementary thereto. Random primers or primers specific to the library vector can be used to amplify the trapped cDNA. Such gene trapping techniques are described in Gruber et al., PCT WO 95/04745 and Gruber et al., U.S. Pat. No. 5,500,356. Kits are commercially available to perform gene trapping experiments from, for example, Life
5 Technologies, Gaithersburg, Maryland, USA.

“Rapid amplification of cDNA ends,” or RACE, is a PCR method of amplifying cDNAs from a number of different RNAs. The cDNAs may be ligated to an oligonucleotide linker and amplified by PCR using two primers. One primer may be based on sequence from the instant nucleic acids, for which full length sequence is desired, and a second primer may comprise a
10 sequence that hybridizes to the oligonucleotide linker to amplify the cDNA. A description of this method is reported, for example, in PCT Pub. No. WO 97/19110.

In preferred embodiments of RACE, a common primer may be designed to anneal to an arbitrary adaptor sequence ligated to cDNA ends (Apte and Siebert, Biotechniques, 15:890-893, 1993; Edwards et al., Nuc. Acids Res., 19:5227-5232, 1991). When a single gene-specific
15 RACE primer is paired with the common primer, preferential amplification of sequences between the single gene specific primer and the common primer occurs. Commercial cDNA pools modified for use in RACE are available.

Another PCR-based method generates full-length cDNA library with anchored ends without specific knowledge of the cDNA sequence. The method uses lock-docking primers (1-
20 VI), where one primer, poly TV (I-III) locks over the polyA tail of eukaryotic mRNA producing first strand synthesis and a second primer, polyGH (IV-VI) locks onto the polyC tail added by terminal deoxynucleotidyl transferase (TdT). This method is described, for example, in PCT Pub. No. WO 96/40998.

The promoter region of a gene generally is located 5' to the initiation site for RNA
25 polymerase II. Hundreds of promoter regions contain the “TATA” box, a sequence such as TATTA or TATAA, which is sensitive to mutations. The promoter region can be obtained by performing 5' RACE using a primer from the coding region of the gene. Alternatively, the cDNA can be used as a probe for the genomic sequence, and the region 5' to the coding region is identified by “walking up.”

30 If the gene is highly expressed or differentially expressed, the promoter from the gene may be of use in a regulatory construct for a heterologous gene.

Once the full-length cDNA or gene is obtained, DNA encoding variants can be prepared by site-directed mutagenesis, described in detail in Sambrook 15.3-15.63. The choice of codon or nucleotide to be replaced can be based on the disclosure herein on optional changes in amino acids to achieve altered protein structure and/or function.

5 As an alternative method to obtaining DNA or RNA from a biological material, nucleic acid comprising nucleotides having the sequence of one or more nucleic acids of the invention can be synthesized. Thus, the invention encompasses nucleic acid molecules ranging in length from 12 nucleotides (corresponding to at least 12 contiguous nucleotides which hybridize under stringent conditions to or are at least 80% identical to a nucleic acid represented by one of SEQ
10 ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, or a sequence complementary thereto) up to a maximum length suitable for one or more biological manipulations, including replication and expression, of the nucleic acid molecule. The invention includes but is not limited to (a) nucleic acid having the size of a full gene, and comprising at
15 least one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, or a sequence complementary thereto; (b) the nucleic acid of (a) also comprising at least one additional gene, operably linked to permit expression of a fusion protein; (c) an expression vector comprising (a) or (b); (d) a plasmid comprising (a) or (b); and (e) a recombinant viral
20 particle comprising (a) or (b). Construction of (c) can be accomplished as described below in part VI.

The sequence of a nucleic acid of the present invention is not limited and can be any sequence of A, T, G, and/or C (for DNA) and A, U, G, and/or C (for RNA) or modified bases thereof, including inosine and pseudouridine. The choice of sequence will depend on the desired
25 function and can be dictated by coding regions desired, the intron-like regions desired, and the regulatory regions desired.

VI. Vectors Carrying Nucleic Acids of the Present Invention

The invention further provides plasmids and vectors, which can be used to express a gene in a host cell. The host cell may be any prokaryotic or eukaryotic cell. Thus, a nucleotide
30 sequence derived from any one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, and still more preferably SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto, encoding all or a

selected portion of a protein, can be used to produce a recombinant form of an polypeptide via microbial or eukaryotic cellular processes. Ligating the polynucleotide sequence into a gene construct, such as an expression vector, and transforming or transfecting into hosts, either eukaryotic (yeast, avian, insect or mammalian) or prokaryotic (bacterial cells), are standard
5 procedures well known in the art.

Vectors that allow expression of a nucleic acid in a cell are referred to as expression vectors. Typically, expression vectors contain a nucleic acid operably linked to at least one transcriptional regulatory sequence. Regulatory sequences are art-recognized and are selected to direct expression of the subject nucleic acids. Transcriptional regulatory sequences are described
10 in Goeddel; Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, CA (1990). In one embodiment, the expression vector includes a recombinant gene encoding a peptide having an agonistic activity of a subject polypeptide, or alternatively, encoding a peptide which is an antagonistic form of a subject polypeptide.

The choice of plasmid will depend on the type of cell in which propagation is desired and
15 the purpose of propagation. Certain vectors are useful for amplifying and making large amounts of the desired DNA sequence. Other vectors are suitable for expression in cells in culture. Still other vectors are suitable for transfer and expression in cells in a whole animal or person. The choice of appropriate vector is well within the skill of the art. Many such vectors are available commercially. The nucleic acid or full-length gene is inserted into a vector typically by means
20 of DNA ligase attachment to a cleaved restriction enzyme site in the vector. Alternatively, the desired nucleotide sequence may be inserted by homologous recombination in vivo. Typically this is accomplished by attaching regions of homology to the vector on the flanks of the desired nucleotide sequence. Regions of homology are added by ligation of oligonucleotides, or by polymerase chain reaction using primers comprising both the region of homology and a portion
25 of the desired nucleotide sequence.

Nucleic acids or full-length genes are linked to regulatory sequences as appropriate to obtain the desired expression properties. These may include promoters (attached either at the 5' end of the sense strand or at the 3' end of the antisense strand), enhancers, terminators, operators, repressors, and inducers. The promoters may be regulated or constitutive. In some situations it
30 may be desirable to use conditionally active promoters, such as tissue-specific or developmental stage-specific promoters. These are linked to the desired nucleotide sequence using the techniques described above for linkage to vectors. Any techniques known in the art may be used.

When any of the above host cells, or other appropriate host cells or organisms, are used to replicate and/or express the polynucleotides or nucleic acids of the invention, the resulting replicated nucleic acid, RNA, expressed protein or polypeptide, is within the scope of the invention as a product of the host cell or organism. The product is recovered by any appropriate means known in the art.

Once the gene corresponding to the nucleic acid is identified, its expression can be regulated in the cell to which the gene is native. For example, an endogenous gene of a cell can be regulated by an exogenous regulatory sequence as disclosed in U.S. Patent No. 5,641,670, "Protein Production and Protein Delivery."

A number of vectors exist for the expression of recombinant proteins in yeast (see, for example, Broach *et al* (1983) in *Experimental Manipulation of Gene Expression*, ed. M. Inouye, Academic Press, p. 83, incorporated by reference herein). In addition, drug resistance markers such as ampicillin can be used. In an illustrative embodiment, a polypeptide is produced recombinantly utilizing an expression vector generated by sub-cloning one of the nucleic acids represented in one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, or a sequence complementary thereto.

The preferred mammalian expression vectors contain both prokaryotic sequences, to facilitate the propagation of the vector in bacteria, and one or more eukaryotic transcription units that are expressed in eukaryotic cells. The various methods employed in the preparation of plasmids and transformation of host organisms are well known in the art. For other suitable expression systems for both prokaryotic and eukaryotic cells, as well as general recombinant procedures, see *Molecular Cloning: A Laboratory Manual*, 2nd Ed., ed. by Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory Press: 1989) Chapters 16 and 17.

When it is desirable to express only a portion of a gene, e.g., a truncation mutant, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from *E. coli* (Ben-Bassat *et al.*, (1987) *J. Bacteriol.* 169:751-757) and *Salmonella typhimurium* and its *in vitro* activity has been demonstrated on recombinant proteins (Miller *et al.* (1987) *PNAS* 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either *in vivo* by expressing polypeptides in a host which produces

MAP (e.g., *E. coli* or CM89 or *S. cerevisiae*), or *in vitro* by use of purified MAP (e.g., procedure of Miller *et al.*, *supra*).

Moreover, the nucleic acid constructs of the present invention can also be used as part of a gene therapy protocol to deliver nucleic acids such as antisense nucleic acids. Thus, another
5 aspect of the invention features expression vectors for *in vivo* or *in vitro* transfection with an antisense oligonucleotide.

In addition to viral transfer methods, non-viral methods can also be employed to introduce a subject nucleic acid, e.g., a sequence represented by one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ
10 ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, or a sequence complementary thereto, into the tissue of an animal. Most nonviral methods of gene transfer rely on normal mechanisms used by mammalian cells for the uptake and intracellular transport of macromolecules. In preferred embodiments, non-viral targeting means of the present invention rely on endocytic pathways for the uptake of the subject nucleic acid by the targeted cell.
15 Exemplary targeting means of this type include liposomal derived systems, polylysine conjugates, and artificial viral envelopes.

A nucleic acid of any of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, or a sequence complementary thereto, the corresponding cDNA, or the full-
20 length gene may be used to express the partial or complete gene product. Appropriate nucleic acid constructs are purified using standard recombinant DNA techniques as described in, for example, Sambrook *et al.*, (1989) *Molecular Cloning: A Laboratory Manual*, 2nd ed. (Cold Spring Harbor Press, Cold Spring Harbor, New York), and under current regulations described in United States Dept. of HHS, National Institute of Health (NIH) Guidelines for Recombinant
25 DNA research. The polypeptides encoded by the nucleic acid may be expressed in any expression system, including, for example, bacterial, yeast, insect, amphibian and mammalian systems. Suitable vectors and host cells are described, for example, in U.S. Patent No. 5,654,173.

Bacteria. Expression systems in bacteria include those described in Chang *et al.*, *Nature*
30 (1978) 275:615, Goeddel *et al.*, *Nature* (1979) 281 :544, Goeddel *et al.*, *Nucleic Acids Rec.* (1980) 8:4057; EP 0 036,776, U.S. Patent No. 4,551,433, DeBoer *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1983) 80:2125, and Siebenlist *et al.*, *Cell* (1980) 20:269.

- Yeast. Expression systems in yeast include those described in Hinnen *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1978) 75:1929; Ito *et al.*, *J. Bacteriol.* (1983) 153:163; Kurtz *et al.*, *Mol. Cell. Biol.* (1986) 6:142; Kunze *et al.*, *J. Basic Microbiol.* (1985) 25:141; Gleeson *et al.*, *J. Gen. Microbiol.* (1986) 132:3459, Roggenkamp *et al.*, *Mol. Gen. Genet.* (1986) 202:302) Das *et al.*, *J. Bacteriol.* (1984) 158:1165; De Louvencourt *et al.*, *J. Bacteriol.* (1983) 154:737, Van den Berg *et al.*, *Bio/Technology* (1990) 8:135; Kunze *et al.*, *J. Basic Microbiol.* (1985) 25:141; Cregg *et al.*, *Mol. Cell. Biol.* (1985) 5:3376, U.S. Patent Nos. 4,837,148 and 4,929,555; Beach and Nurse, *Nature* (1981) 300:706; Davidow *et al.*, *Curr. Genet.* (1985) 10:380, Gaillardin *et al.*, *Curr. Genet.* (1985) 10:49, Ballance *et al.*, *Biochem. Biophys. Res. Commun.* (1983) 112:284289;
- 5 *Tilburn et al.*, *Gene* (1983) 26:205221, Yelton *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1984) 81:14701474, Kelly and Hynes, *EMBO J.* (1985) 4:475479; EP 0 244,234, and WO 91/00357.

- Insect Cells. Expression of heterologous genes in insects is accomplished as described in U.S. Patent No. 4,745,051, Friesen *et al.*, (1986) "The Regulation of Baculovirus Gene Expression" in: *The Molecular Biology Of Baculoviruses* (W. Doerfler, ed.), EP 0 127,839, EP 0
- 15 155,476, and Vlak *et al.*, *J. Gen. Virol.* (1988) 69:765776, Miller *et al.*, *Ann. Rev. Microbiol.* (1988) 42:177, Carbonell *et al.*, *Gene* (1988) 73:409, Maeda *et al.*, *Nature* (1985) 315:592594, Lebacqz Verheyden *et al.*, *Mol. Cell. Biol.* (1988) 8:3129; Smith *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1985) 82:8404, Miyajima *et al.*, *Gene* (1987) 58:273; and Martinet *et al.*, *DNA* (1988) 7:99. Numerous baculoviral strains and variants and corresponding permissive insect host cells
- 20 from hosts are described in Luckow *et al.*, *Bio/Technology* (1988) 6:4755, Miller *et al.*, *Generic Engineering* (Setlow, J.K. *et al.* eds.), Vol. 8 (Plenum Publishing, 1986), pp. 277279, and Maeda *et al.*, *Nature*, (1985) 315:592-594.

- Mammalian Cells. Mammalian expression is accomplished as described in Dijkema *et al.*, *EMBO J.* (1985) 4:761, Gorman *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1982) 79:6777, Boshart
- 25 *et al.*, *Cell* (1985) 41:52 1 and U.S. Patent No. 4,399,216. Other features of mammalian expression are facilitated as described in Ham and Wallace, *Meth. Enz.* (1979) 58:44, Barnes and Sato, *Anal. Biochem.* (1980) 102:255, U.S. Patent Nos. 4,767,704, 4,657,866, 4,927,762, 4,560,655, WO 90/103430, WO 87/00195, and U.S. RE 30,985.

VII. Therapeutic Nucleic Acid Constructs

- 30 One aspect of the invention relates to the use of the isolated nucleic acid, e.g., SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, or a sequence complementary thereto, in antisense therapy. As used herein, antisense therapy refers to

administration or *in situ* generation of oligonucleotide molecules or their derivatives which specifically hybridize (e.g., bind) under cellular conditions with the cellular mRNA and/or genomic DNA, thereby inhibiting transcription and/or translation of that gene. The binding may be by conventional base pair complementarity, or, for example, in the case of binding to DNA
5 duplexes, through specific interactions in the major groove of the double helix. In general, antisense therapy refers to the range of techniques generally employed in the art, and includes any therapy which relies on specific binding to oligonucleotide sequences.

An antisense construct of the present invention can be delivered, for example, as an expression plasmid which, when transcribed in the cell, produces RNA which is complementary
10 to at least a unique portion of the cellular mRNA. Alternatively, the antisense construct is an oligonucleotide probe which is generated *ex vivo* and which, when introduced into the cell, causes inhibition of expression by hybridizing with the mRNA and/or genomic sequences of a subject nucleic acid. Such oligonucleotide probes are preferably modified oligonucleotides which are resistant to endogenous nucleases, e.g., exonucleases and/or endonucleases, and are
15 therefore stable *in vivo*. Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphorothioate and methylphosphonate analogs of DNA (see also U.S. Patents 5,176,996; 5,264,564; and 5,256,775). Additionally, general approaches to constructing oligomers useful in antisense therapy have been reviewed, for example, by Van der Krol *et al.* (1988) *BioTechniques* 6:958-976; and Stein *et al.* (1988) *Cancer Res* 48:2659-2668. With
20 respect to antisense DNA, oligodeoxyribonucleotides derived from the translation initiation site, e.g., between the -10 and +10 regions of the nucleotide sequence of interest, are preferred.

Antisense approaches involve the design of oligonucleotides (either DNA or RNA) that are complementary to mRNA. The antisense oligonucleotides will bind to the mRNA transcripts and prevent translation. Absolute complementarity, although preferred, is not required. In the
25 case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable
30 degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

Oligonucleotides that are complementary to the 5' end of the mRNA, e.g., the 5' untranslated sequence up to and including the AUG initiation codon, should work most

efficiently at inhibiting translation. However, sequences complementary to the 3' untranslated sequences of mRNAs have recently been shown to be effective at inhibiting translation of mRNAs as well. (Wagner, R. 1994. Nature 372:333). Therefore, oligonucleotides complementary to either the 5' or 3' untranslated, non-coding regions of a gene could be used in an antisense approach to inhibit translation of endogenous mRNA. Oligonucleotides complementary to the 5' untranslated region of the mRNA should include the complement of the AUG start codon. Antisense oligonucleotides complementary to mRNA coding regions are typically less efficient inhibitors of translation but could also be used in accordance with the invention. Whether designed to hybridize to the 5', 3', or coding region of subject mRNA, antisense nucleic acids should be at least six nucleotides in length, and are preferably less than about 100 and more preferably less than about 50, 25, 17 or 10 nucleotides in length.

Regardless of the choice of target sequence, it is preferred that *in vitro* studies are first performed to quantitate the ability of the antisense oligonucleotide to quantitate the ability of the antisense oligonucleotide to inhibit gene expression. It is preferred that these studies utilize controls that distinguish between antisense gene inhibition and nonspecific biological effects of oligonucleotides. It is also preferred that these studies compare levels of the target RNA or protein with that of an internal control RNA or protein. Additionally, it is envisioned that results obtained using the antisense oligonucleotide are compared with those obtained using a control oligonucleotide. It is preferred that the control oligonucleotide is of approximately the same length as the test oligonucleotide and that the nucleotide sequence of the oligonucleotide differs from the antisense sequence no more than is necessary to prevent specific hybridization to the target sequence.

The oligonucleotides can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors), or agents facilitating transport across the cell membrane (see, e.g., Letsinger *et al.*, 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre *et al.*, 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. WO 88/098 10, published December 15, 1988) or the blood-brain barrier (see, e.g., PCT Publication No. WO 89/10 134, published April 25, 1988), hybridization-triggered cleavage agents (See, e.g., Krol *et al.*, 1988, BioTechniques 6:958-976), or intercalating agents (See, e.g., Zon, 1988, Pharm. Res. 5:539-549). To this end, the oligonucleotide may be conjugated to

another molecule, e.g., a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The antisense oligonucleotide may comprise at least one modified base moiety which is selected from the group including but not limited to 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xantine, 4-acetylcytosine, 5-(carboxyhydroxytriethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)_w, and 2,6-diaminopurine.

The antisense oligonucleotide may also comprise at least one modified sugar moiety selected from the group including but not limited to arabinose, 2-fluoroarabinose, xylulose, and hexose.

The antisense oligonucleotide can also contain a neutral peptide-like backbone. Such molecules are termed peptide nucleic acid (PNA)-oligomers and are described, e.g., in Peny-O'Keefe *et al.* (1996) Proc. Natl. Acad. Sci. U.S.A. 93:14670 and in Eglom *et al.* (1993) Nature 365:566. One advantage of PNA oligomers is their capability to bind to complementary DNA essentially independently from the ionic strength of the medium due to the neutral backbone of the DNA. In yet another embodiment, the antisense oligonucleotide comprises at least one modified phosphate backbone selected from the group consisting of a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methyphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

In yet a further embodiment, the antisense oligonucleotide is an α -anomeric oligonucleotide. An α -anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gautier *et al.*, 1987, Nucl. Acids Res. 15:6625-6641). The oligonucleotide is a 2'-O-methylribonucleotide (Inoue *et al.*, 1987, Nucl. Acids Res. 15:6131-12148), or a chimeric RNA-DNA analogue (Inoue *et al.*, 1987, FEBS Lett. 215:327-330).

Oligonucleotides of the invention may be synthesized by standard methods known in the art, e.g., by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein *et al.* (1988, Nucl. Acids Res. 16:3209), methylphosphonate
5 oligonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin *et al.*, 1988, Proc. Natl. Acad. Sci. U.S.A. 85:7448-7451), etc.

While antisense nucleotides complementary to a coding region sequence can be used, those complementary to the transcribed untranslated region and to the region comprising the initiating methionine are most preferred.

10 The antisense molecules can be delivered to cells which express the target nucleic acid *in vivo*. A number of methods have been developed for delivering antisense DNA or RNA to cells; e.g., antisense molecules can be injected directly into the tissue site, or modified antisense molecules, designed to target the desired cells (e.g., antisense linked to peptides or antibodies that specifically bind receptors or antigens expressed on the target cell surface) can be
15 administered systemically.

However, it is often difficult to achieve intracellular concentrations of the antisense sufficient to suppress translation on endogenous mRNAs. Therefore, a preferred approach utilizes a recombinant DNA construct in which the antisense oligonucleotide is placed under the control of a strong pol III or pot II promoter. The use of such a construct to transfect target cells
20 in the patient will result in the transcription of sufficient amounts of single stranded RNAs that will form complementary base pairs with the endogenous transcripts and thereby prevent translation of the target mRNA. For example, a vector can be introduced *in vivo* such that it is taken up by a cell and directs the transcription of an antisense RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the
25 desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art for replication and expression in mammalian cells. Expression of the sequence encoding the antisense RNA can be by any promoter known in the art to act in mammalian, preferably human cells. Such promoters can be inducible or constitutive. Such promoters include but are not
30 limited to: the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290:304-3 10), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto *et al.*, 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner *et al.*, 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster

et al., 1982, Nature 296:39-42), etc. Any type of plasmid, cosmid, YAC or viral vector can be used to prepare the recombinant DNA construct which can be introduced directly into the tissue site; e.g., the choroid plexus or hypothalamus. Alternatively, viral vectors can be used which selectively infect the desired tissue (e.g., for brain, herpesvirus vectors may be used), in which
5 case administration may be accomplished by another route (e.g., systemically).

In another aspect of the invention, ribozyme molecules designed to catalytically cleave target mRNA transcripts can be used to prevent translation of target mRNA and expression of a target protein (See, e.g., PCT International Publication WO90/11364, published October 4, 1990; Sarver *et al.*, 1990, Science 247:1222-1225 and U.S. Patent No. 5,093,246). While ribozymes
10 that cleave mRNA at site specific recognition sequences can be used to destroy target mRNAs, the use of hammerhead ribozymes is preferred. Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. The sole requirement is that the target mRNA have the following sequence of two bases: 5'-UG-3'. The construction and production of hammerhead ribozymes is well known in the art
15 and is described more fully in Haseloff and Gerlach, 1988, Nature, 334:585-591. Preferably the ribozyme is engineered so that the cleavage recognition site is located near the 5' end of the target mRNA; i.e., to increase efficiency and minimize the intracellular accumulation of non-functional mRNA transcripts.

The ribozymes of the present invention also include RNA endoribonucleases (hereinafter
20 "Cech-type ribozymes") such as the one which occurs naturally in *Tetrahymena thermophila* (known as the IVS, or L-19 IVS RNA) and which has been extensively described by Thomas Cech and collaborators (Zaug, et al., 1984, Science, 224:574-578; Zaug and Cech, 1986, Science, 231:470-475; Zaug, et al., 1986, Nature, 324:429-433; published International patent application No. W088/04300 by University Patents Inc.; Been and Cech, 1986, Cell, 47:207-216). The
25 Cech-type ribozymes have an eight base pair active site which hybridizes to a target RNA sequence whereafter cleavage of the target RNA takes place. The invention encompasses those Cech-type ribozymes which target eight base-pair active site sequences that are present in a target gene.

As in the antisense approach, the ribozymes can be composed of modified
30 oligonucleotides (e.g., for improved stability, targeting, etc.) and should be delivered to cells which express the target gene *in vivo*. A preferred method of delivery involves using a DNA construct "encoding" the ribozyme under the control of a strong constitutive pol III or pol II promoter, so that transfected cells will produce sufficient quantities of the ribozyme to destroy

endogenous messages and inhibit translation. Because ribozymes, unlike antisense molecules, are catalytic, a lower intracellular concentration is required for efficiency.

Antisense RNA, DNA, and ribozyme molecules of the invention may be prepared by any method known in the art for the synthesis of DNA and RNA molecules. These include techniques for chemically synthesizing oligodeoxyribonucleotides and oligoribonucleotides well known in the art such as for example solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by *in vitro* and *in vivo* transcription of DNA sequences encoding the antisense RNA molecule. Such DNA sequences may be incorporated into a wide variety of vectors which incorporate suitable RNA polymerase promoters such as the T7 or SP6 polymerase promoters. Alternatively, antisense cDNA constructs that synthesize antisense RNA constitutively or inducibly, depending on the promoter used, can be introduced stably into cell lines.

Moreover, various well-known modifications to nucleic acid molecules may be introduced as a means of increasing intracellular stability and half-life. Possible modifications include but are not limited to the addition of flanking sequences of ribonucleotides or deoxyribonucleotides to the 5' and/or 3' ends of the molecule or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the oligodeoxyribonucleotide backbone.

VIII. Full-length cDNA Sequences of the Present Invention

The present invention also relates to full length cDNA sequences corresponding to one or more of the partial sequences of SEQ ID Nos. 1-4470. In particular the invention provides the full length cDNA sequences of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494. The full length sequences may be obtained as described above. These sequences are shown in Figure 2, and summarized below in Table 2. Also shown in Table 2 are the SEQ ID Nos and GenBank accession numbers for the polypeptides which are encoded by the full length cDNA sequences and which correspond to SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493.

cDNA SEQ ID NO.	Gene Name	GenBank Accession No.	Protein SEQ ID NO.	GenBank Accession No.
4472	Reg IV	NM 032044	4471	NP 114433
4474	XAG-2	NM 006408	4473	NP 006399

4476	SPARC/Osteonectin	NM 003118	4475	NP 003109
4478	GW112 protein	NM 006418	4477	NP 006409
4480	HSBP1	NM 001540	4479	NP 001531
4482	SKD1 Homolog	NP 004869	4481	NP 004860
4484	9-27	NM 003641	4483	NP 003632
4486	Defensin 5	NM 021010	4485	NP 066290
4488	p0071	NM 003628	4487	NP 003619
4490	UBE2I	NM 003345	4489	NP 003336
4492	Cytoplasmic dynein light chain	NM 003746	4491	NP 003737
4494	10Ckshs1	NM 001798	4493	NP 001789

IX. Polypeptides of the Present Invention

The present invention makes available isolated polypeptides which are isolated from, or otherwise substantially free of other cellular proteins, especially other signal transduction factors and/or transcription factors which may normally be associated with the polypeptide. Subject

5 polypeptides of the present invention include polypeptides encoded by the nucleic acids of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, and still more preferably SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and

10 4494, or a sequence complementary thereto, or polypeptides encoded by genes of which a sequence in SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, or a sequence complementary thereto, is a fragment. In a preferred embodiment, polypeptides, useful in the present invention have the amino acid sequence of one or more of SEQ ID Nos. 4471,

15 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493. Polypeptides of the present invention include those proteins which are differentially regulated in tumor cells, especially colon cancer-derived cell lines (relative to normal cells, e.g., normal colon tissue and

non-colon tissue). In a preferred embodiment the differentially regulated polypeptides are one or more of the polypeptides having the sequence set forth in SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493. In preferred embodiments, the polypeptides are upregulated in tumor cells, especially colon cancer cancer-derived cell lines. In other embodiments, the polypeptides are downregulated in tumor cells, especially colon cancer-derived cell lines. Proteins which are upregulated, such as oncogenes, or downregulated, such as tumor suppressors, in aberrantly proliferating cells may be targets for diagnostic or therapeutic techniques. For example, upregulation of the *cdc2* gene induces mitosis. Overexpression of the *myt1* gene, a mitotic deactivator, negatively regulates the activity of *cdc2*. Aberrant proliferation may thus be induced either by upregulating *cdc2* or by downregulating *myt1*.

The term "substantially free of other cellular proteins" (also referred to herein as "contaminating proteins") or "substantially pure or purified preparations" are defined as encompassing preparations of polypeptides having less than about 20% (by dry weight) contaminating protein, and preferably having less than about 5% contaminating protein. Functional forms of the subject polypeptides can be prepared, for the first time, as purified preparations by using a cloned nucleic acid as described herein. Full length proteins or fragments corresponding to one or more particular motifs and/or domains or to arbitrary sizes, for example, at least about 5, 10, 25, 50, 75, or 100 amino acids in length are within the scope of the present invention.

For example, isolated polypeptides can be encoded by all or a portion of a nucleic acid sequence shown in any of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503 and most preferably SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto. Isolated peptidyl portions of proteins can be obtained by screening peptides recombinantly produced from the corresponding fragment of the nucleic acid encoding such peptides. In addition, fragments can be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry. For example, a polypeptide of the present invention may be arbitrarily divided into fragments of desired length with no overlap of the fragments, or preferably divided into overlapping fragments of a desired length. The fragments can be produced (recombinantly or by chemical synthesis) and tested to identify those peptidyl fragments which can function as either agonists or antagonists of a wild-type (e.g., "authentic") protein.

Another aspect of the present invention concerns recombinant forms of the subject proteins. Recombinant polypeptides preferred by the present invention, in addition to native proteins, as described above are encoded by a nucleic acid, which is at least 60%, more preferably at least 80%, and more preferably 85%, and more preferably 90%, and more preferably 95% identical to an amino acid sequence encoded by SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494. Polypeptides which are encoded by a nucleic acid that is at least about 98-99% identical with the sequence of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 are also within the scope of the invention. Also included in the present invention are peptide fragments comprising at least a portion of such a protein.

In a preferred embodiment, a polypeptide of the present invention is a mammalian polypeptide and even more preferably a human polypeptide. In particularly preferred embodiment, the polypeptide retains wild-type bioactivity. It will be understood that certain post-translational modifications, e.g., phosphorylation and the like, can increase the apparent molecular weight of the polypeptide relative to the unmodified polypeptide chain.

The present invention further pertains to recombinant forms of one of the subject polypeptides. Such recombinant polypeptides preferably are capable of functioning in one of either role of agonist or antagonist of at least one biological activity of a wild-type ("authentic") polypeptide of the appended sequence listing. The term "evolutionarily related to", with respect to amino acid sequences of proteins, refers to both polypeptides having amino acid sequences which have arisen naturally, and also to mutational variants of human polypeptides which are derived, for example, by combinatorial mutagenesis.

In general, polypeptides referred to herein as having an activity (e.g., are "bioactive") of a protein are defined as polypeptides which include an amino acid sequence encoded by all or a portion of the nucleic acid sequences shown in one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, and most preferably SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493, or a sequence complementary thereto, and which mimic or antagonize all or a portion of the biological/biochemical activities of a naturally occurring protein. According to the present invention, a polypeptide has biological activity if it is a specific agonist or antagonist of a naturally occurring form of a protein.

Assays for determining whether a compound, e.g, a protein or variant thereof, has one or more of the above biological activities are well known in the art. In certain embodiments, the polypeptides of the present invention have activities such as those outlined above.

In another embodiment, the coding sequences for the polypeptide can be incorporated as a part of a fusion gene including a nucleotide sequence encoding a different polypeptide. This type of expression system can be useful under conditions where it is desirable to produce an immunogenic fragment of a polypeptide (see, for example, EP Publication No: 0259149; and Evans *et al.* (1989) *Nature* 339:3 85; Huang *et al.* (1988) *J. Virol.* 62:3 855; and Schlienger *et al.*, (1992) *J. Virol.* 66:2). In addition to utilizing fusion proteins to enhance immunogenicity, it is widely appreciated that fusion proteins can also facilitate the expression of proteins, and, accordingly, can be used in the expression of the polypeptides of the present invention (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* (N.Y. John Wiley & Sons, 1991)). In another embodiment, a fusion gene coding for a purification leader sequence, such as a poly-(His)/enterokinase cleavage site sequence at the N-terminus of the desired portion of the recombinant protein, can allow purification of the expressed fusion protein by affinity chromatography using a Ni²⁺ metal resin. The purification leader sequence can then be subsequently removed by treatment with enterokinase to provide the purified protein (e.g., see Hochuli *et al.* (1987) *J. Chromatography* 411:177; and Janknecht *et al.* *PNAS* 88:8972).

Techniques for making fusion genes are known to those skilled in the art. Essentially, the joining of various DNA fragments coding for different polypeptide sequences is performed in accordance with conventional techniques, employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of nucleic acid fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive nucleic acid fragments which can subsequently be annealed to generate a chimeric nucleic acid sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* John Wiley & Sons: 1992).

The present invention further pertains to methods of producing the subject polypeptides. For example, a host cell transfected with a nucleic acid vector directing expression of a nucleotide sequence encoding the subject polypeptides can be cultured under appropriate conditions to allow expression of the peptide to occur. Suitable media for cell culture are well

known in the art. The recombinant polypeptide can be isolated from cell culture medium, host cells, or both using techniques known in the art for purifying proteins including ion-exchange chromatography, gel filtration chromatography, ultrafiltration, electrophoresis, and immunoaffinity purification with antibodies specific for such peptide. In a preferred
5 embodiment, the recombinant polypeptide is a fusion protein containing a domain which facilitates its purification, such as GST fusion protein.

Moreover, it will be generally appreciated that, under certain circumstances, it may be advantageous to provide homologs of one of the subject polypeptides which function in a limited capacity as one of either an agonist (mimetic) or an antagonist, in order to promote or inhibit
10 only a subset of the biological activities of the naturally occurring form of the protein. Thus, specific biological effects can be elicited by treatment with a homolog of limited function, and with fewer side effects relative to treatment with agonists or antagonists which are directed to all of the biological activities of naturally occurring forms of subject proteins.

Homologs of each of the subject polypeptide can be generated by mutagenesis, such as
15 by discrete point mutation(s), or by truncation. For instance, mutation can give rise to homologs which retain substantially the same, or merely a subset, of the biological activity of the polypeptide from which it was derived. Alternatively, antagonistic forms of the polypeptide can be generated which are able to inhibit the function of the naturally occurring form of the protein, such as by competitively binding to a receptor.

20 The recombinant polypeptides of the present invention also include homologs of the wild-type proteins, such as versions of those proteins which are resistant to proteolytic cleavage, for example, due to mutations which alter ubiquitination or other enzymatic targeting associated with the protein.

Polypeptides may also be chemically modified to create derivatives by forming covalent
25 or aggregate conjugates with other chemical moieties, such as glycosyl groups, lipids, phosphate, acetyl groups and the like. Covalent derivatives of proteins can be prepared by linking the chemical moieties to functional groups on amino acid sidechains of the protein or at the N-terminus or at the C-terminus of the polypeptide.

Modification of the structure of the subject polypeptides can be for such purposes as
30 enhancing therapeutic or prophylactic efficacy, stability (e.g., *ex vivo* shelf life and resistance to proteolytic degradation), or post-translational modifications (e.g., to alter phosphorylation pattern of protein). Such modified peptides, when designed to retain at least one activity of the

naturally occurring form of the protein, or to produce specific antagonists thereof, are considered functional equivalents of the polypeptides described in more detail herein. Such modified peptides can be produced, for instance, by amino acid substitution, deletion, or addition. The substitutional variant may be a substituted conserved amino acid or a substituted non-conserved amino acid.

For example, it is reasonable to expect that an isolated replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, a threonine with a serine, or a similar replacement of an amino acid with a structurally related amino acid (i.e., isosteric and/or isoelectric mutations) will not have a major effect on the biological activity of the resulting molecule. Conservative replacements are those that take place within a family of amino acids that are related in their side chains. Genetically encoded amino acids can be divided into four families: (1) acidic = aspartate, glutamate; (2) basic = lysine, arginine, histidine; (3) nonpolar = alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan; and (4) uncharged polar = glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine. In similar fashion, the amino acid repertoire can be grouped as (1) acidic = aspartate, glutamate; (2) basic = lysine, arginine histidine, (3) aliphatic = glycine, alanine, valine, leucine, isoleucine, serine, threonine, with serine and threonine optionally be grouped separately as aliphatic-hydroxyl; (4) aromatic = phenylalanine, tyrosine, tryptophan; (5) amide = asparagine, glutamine; and (6) sulfur-containing = cysteine and methionine. (see, for example, *Biochemistry*, 2 ed., Ed. by L. Stryer, WH Freeman and Co.: 1981). Whether a change in the amino acid sequence of a peptide results in a functional homolog (e.g., functional in the sense that the resulting polypeptide mimics or antagonizes the wild-type form) can be readily determined by assessing the ability of the variant peptide to produce a response in cells in a fashion similar to the wild-type protein, or competitively inhibit such a response.

Polypeptides in which more than one replacement has taken place can readily be tested in the same manner. The variant may be designed so as to retain biological activity of a particular region of the protein. In a non-limiting example, Osawa et al., 1994, *Biochemistry and Molecular International* 34:1003-1009, discusses the actin binding region of a protein from several different species. The actin binding regions of the these species are considered homologous based on the fact that they have amino acids that fall within "homologous residue groups." Homologous residues are judged according to the following groups (using single letter amino acid designations): STAG; ILVMF; HRK; DEQN; and FYW. For example, an S, a T, an A or a G can be in a position and the function (in this case actin binding) is retained.

Additional guidance on amino acid substitution is available from studies of protein evolution. Go et al., 1980, *Int. J. Peptide Protein Res.* 15: 211-224, classified amino acid residue sites as interior or exterior depending on their accessibility. More frequent substitution on exterior sites was confirmed to be general in eight sets of homologous protein families regardless of their biological functions and the presence or absence of a prosthetic group. Virtually all types of amino acid residues had higher mutabilities on the exterior than in the interior. No correlation between mutability and polarity was observed of amino acid residues in the interior and exterior, respectively. Amino acid residues were classified into one of three groups depending on their polarity: polar (Arg, Lys, His, Gln, Asn, Asp, and Glu); weak polar (Ala, Pro, Gly, Thr, and Ser), and nonpolar (Cys, Val, Met, Ile, Leu, Phe, Tyr, and Trp). Amino acid replacements during protein evolution were very conservative: 88% and 76% of them in the interior or exterior, respectively, were within the same group of the three. Intergroup replacements are such that weak polar residues are replaced more often by nonpolar residues in the interior and more often by polar residues on the exterior.

Querol et al., 1996, *Prot. Eng.* 9:265-271, provides general rules for amino acid substitutions to enhance protein thermostability. New glycosylation sites can be introduced as discussed in Olsen and Thomsen, 1991, *J. Gen. Microbiol.* 137 :579-585. An additional disulfide bridge can be introduced, as discussed by Perry and Wetzel, 1984, *Science* 226:555-557; Pantoliano et al., 1987, *Biochemistry* 26:2077-2082; Matsumura et al., 1989, *Nature* 342:291-293; Nishikawa et al., 1990, *Protein Eng.* 3:443-448; Takagi et al., 1990, *J. Biol. Chem.* 265:6874-6878; Clarke et al., 1993, *Biochemistry* 32:4322-4329; and Wakarchuk et al., 1994, *Protein Eng.* 7:1379-1386.

An additional metal binding site can be introduced, according to Toma et al., 1991, *Biochemistry* 30:97-106, and Haezebrouck et al., 1993, *Protein Eng.* 6:643-649. Substitutions with prolines in loops can be made according to Masul et al., 1994, *Appl Env. Microbiol.* 60:3579-3584; and Hardy et al., *FEBS Lett.* 317:89-92.

Cysteine-depleted muteins are considered variants within the scope of the invention. These variants can be constructed according to methods disclosed in U.S. Patent No. 4,959,314, which discloses how to substitute other amino acids for cysteines, and how to determine biological activity and effect of the substitution. Such methods are suitable for proteins according to this invention that have cysteine residues suitable for such substitutions, for example to eliminate disulfide bond formation.

To learn the identity and function of the gene that correlates with an nucleic acid, the nucleic acids or corresponding amino acid sequences can be screened against profiles of protein families. Such profiles focus on common structural motifs among proteins of each family. Publicly available profiles are described above.

5 In comparing a new nucleic acid with known sequences, several alignment tools are available. Examples include PileUp, which creates a multiple sequence alignment, and is described in Feng *et al.*, *J. Mol. Evol.* (1987) 25:35 1-360. Another method, GAP, uses the alignment method of Needleman *et al.*, *J. Mol. Biol.* (1970) 48:443-453. GAP is best suited for global alignment of sequences. A third method, BestFit, functions by inserting gaps to maximize
10 the number of matches using the local homology algorithm of Smith and Waterman, *Adv. Appl. Math.* (1981) 2:482-489.

X. Diagnostic & Prognostic Assays and Drug Screening Methods

 The present invention provides method for determining whether a subject is at risk for developing a disease or condition characterized by unwanted cell proliferation by detecting the
15 disclosed biomarkers, i.e., the present nucleic acids (SEQ ID Nos: 1-4494) and/or polypeptide markers (preferably SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493) for colon cancer encoded thereby.

 In clinical applications, human tissue samples can be screened for the presence and/or absence of the biomarkers identified herein. Such samples could consist of needle biopsy cores,
20 surgical resection samples, lymph node tissue, or serum. For example, these methods include obtaining a biopsy, which is optionally fractionated by cryostat sectioning to enrich tumor cells to about 80% of the total cell population. In certain embodiments, nucleic acids extracted from these samples may be amplified using techniques well known in the art. The levels of selected markers detected would be compared with statistically valid groups of metastatic, non-metastatic
25 malignant, benign, or normal colon tissue samples.

 In one embodiment, the diagnostic method comprises determining whether a subject has an abnormal mRNA and/or protein level of the disclosed markers, such as by Northern blot analysis, reverse transcription-polymerase chain reaction (RT-PCR), in situ hybridization, immunoprecipitation, Western blot hybridization, or immunohistochemistry. According to the
30 method, cells are obtained from a subject and the levels of the disclosed biomarkers, protein or mRNA level, is determined and compared to the level of these markers in a healthy subject. An

abnormal level of the biomarker polypeptide or mRNA levels is likely to be indicative of cancer such as colon cancer.

Accordingly, in one aspect, the invention provides probes and primers that are specific to the unique nucleic acid markers disclosed herein. Accordingly, the nucleic acid probes comprise
5 a nucleotide sequence at least 10 nucleotides in length, preferably at least 15 nucleotides, more preferably, 25 nucleotides, and most preferably at least 40 nucleotides, and up to all or nearly all of the coding sequence which is complementary to a portion of the coding sequence of a marker nucleic acid sequence, which nucleic acid sequence is represented by SEQ ID Nos: 1-4494 or a sequence complementary thereto.

- 10 In one embodiment, the method comprises using a nucleic acid probe to determine the presence of cancerous cells in a tissue from a patient. Specifically, the method comprises:
1. providing a nucleic acid probe comprising a nucleotide sequence at least 10 nucleotides in length, preferably at least 15 nucleotides, more preferably, 25
15 nucleotides, and most preferably at least 40 nucleotides, and up to all or nearly all of the coding sequence which is complementary to a portion of the coding sequence of a nucleic acid sequence represented by SEQ ID Nos: 1-4494 or a sequence complementary thereto and is differentially expressed in tumors cells, such as colon cancer cells;
 2. obtaining a tissue sample from a patient potentially comprising cancerous cells;
 - 20 3. providing a second tissue sample containing cells substantially all of which are non-cancerous;
 4. contacting the nucleic acid probe under stringent conditions with RNA of each of said first and second tissue samples (e.g., in a Northern blot or in situ hybridization assay); and
 - 25 5. comparing (a) the amount of hybridization of the probe with RNA of the first tissue sample, with (b) the amount of hybridization of the probe with RNA of the second tissue sample; wherein a statistically significant difference in the amount of hybridization with the RNA of the first tissue sample as compared to the amount of hybridization with the RNA of the second tissue sample is indicative of
30 the presence of cancerous cells in the first tissue sample.

In one aspect, the method comprises *in situ* hybridization with a probe derived from a given marker nucleic acid sequence, which nucleic acid sequence is represented by SEQ ID Nos: 1-4494 or a sequence complementary thereto. The method comprises contacting the labeled hybridization probe with a sample of a given type of tissue potentially containing cancerous or pre-cancerous cells as well as normal cells, and determining whether the probe labels some cells of the given tissue type to a degree significantly different (e.g., by at least a factor of two, or at least a factor of five, or at least a factor of twenty, or at least a factor of fifty) than the degree to which it labels other cells of the same tissue type.

Also within the invention is a method of determining the phenotype of a test cell from a given human tissue, e.g., whether the cell is (a) normal, or (b) cancerous or precancerous, by contacting the mRNA of a test cell with a nucleic acid probe at least 12 nucleotides in length, preferably at least 15 nucleotides, more preferably at least 25 nucleotides, and most preferably at least 40 nucleotides, and up to all or nearly all of a sequence which is complementary to a portion of the coding sequence of a nucleic acid sequence represented by SEQ ID Nos: 1-4494 or a sequence complementary thereto, and which is differentially expressed in tumor cells as compared to normal cells of the given tissue type; and determining the approximate amount of hybridization of the probe to the mRNA, an amount of hybridization either more or less than that seen with the mRNA of a normal cell of that tissue type being indicative that the test cell is cancerous or pre-cancerous.

Alternatively, the above diagnostic assays may be carried out using antibodies to detect the protein product encoded by the marker nucleic acid sequence, which nucleic acid sequence is represented by SEQ ID Nos: 1-4494 or a sequence complementary thereto. Accordingly, in one embodiment, the assay would include contacting the proteins of the test cell with an antibody specific for the gene product of a nucleic acid represented by SEQ ID Nos: 1-4494, preferably SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto, the marker nucleic acid being one which is expressed at a given control level in normal cells of the same tissue type as the test cell, and determining the approximate amount of immunocomplex formation by the antibody and the proteins of the test cell, wherein a statistically significant difference in the amount of the immunocomplex formed with the proteins of a test cell as compared to a normal cell of the same tissue type is an indication that the test cell is cancerous or pre-cancerous. Preferably, the antibody is specific for one of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493.

The method for producing polyclonal and/or monoclonal antibodies which specifically bind to polypeptides useful in the present invention is known to those of skill in the art and can be found in, for example Dymecki et al., 1992, J. Biol. Chem., 267:4815; Boersma & Van Leeuwen, 1994, J. Neurosci. Methods, 51:317; Green et al., 1982, Cell, 28:477; and Arnheiter et al., 1981, Nature, 294:278.

Another such method includes the steps of: providing an antibody specific for the gene product of a marker nucleic acid sequence represented by SEQ ID Nos 1-4494, the gene product being present in cancerous tissue of a given tissue type (e.g., colon tissue) at a level more or less than the level of the gene product in non-cancerous tissue of the same tissue type; obtaining from a patient a first sample of tissue of the given tissue type, which sample potentially includes cancerous cells; providing a second sample of tissue of the same tissue type (which may be from the same patient or from a normal control, e.g. another individual or cultured cells), this second sample containing normal cells and essentially no cancerous cells; contacting the antibody with protein (which may be partially purified, in lysed but unfractionated cells, or in situ) of the first and second samples under conditions permitting immunocomplex formation between the antibody and the marker nucleic acid sequence product present in the samples; and comparing (a) the amount of immunocomplex formation in the first sample, with (b) the amount of immunocomplex formation in the second sample, wherein a statistically significant difference in the amount of immunocomplex formation in the first sample less as compared to the amount of immunocomplex formation in the second sample is indicative of the presence of cancerous cells in the first sample of tissue.

The subject invention further provides a method of determining whether a cell sample obtained from a subject possesses an abnormal amount of marker polypeptide which comprises (a) obtaining a cell sample from the subject, (b) quantitatively determining the amount of the marker polypeptide in the sample so obtained, and (c) comparing the amount of the marker polypeptide so determined with a known standard, so as to thereby determine whether the cell sample obtained from the subject possesses an abnormal amount of the marker polypeptide. Such marker polypeptides may be detected by immunohistochemical assays, dot-blot assays, ELISA and the like.

Immunoassays are commonly used to quantitate the levels of proteins in cell samples, and many other immunoassay techniques are known in the art. The invention is not limited to a particular assay procedure, and therefore is intended to include both homogeneous and heterogeneous procedures. Exemplary immunoassays which can be conducted according to the

invention include fluorescence polarization immunoassay (FPIA), fluorescence immunoassay (FIA), enzyme immunoassay (EIA), nephelometric inhibition immunoassay (NIA), enzyme linked immunosorbent assay (ELISA), and radioimmunoassay (RIA). An indicator moiety, or label group, can be attached to the subject antibodies and is selected so as to meet the needs of various uses of the method which are often dictated by the availability of assay equipment and compatible immunoassay procedures. General techniques to be used in performing the various immunoassays noted above are known to those of ordinary skill in the art.

In another embodiment, the level of the encoded product, i.e., the product encoded by SEQ ID Nos 1-4494 or a sequence complementary thereto, or alternatively the level of the polypeptide of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493, in a biological fluid (e.g., blood or urine) of a patient may be determined as a way of monitoring the level of expression of the marker nucleic acid sequence in cells of that patient. Such a method would include the steps of obtaining a sample of a biological fluid from the patient, contacting the sample (or proteins from the sample) with an antibody specific for a encoded marker polypeptide, and determining the amount of immune complex formation by the antibody, with the amount of immune complex formation being indicative of the level of the marker encoded product in the sample. This determination is particularly instructive when compared to the amount of immune complex formation by the same antibody in a control sample taken from a normal individual or in one or more samples previously or subsequently obtained from the same person.

In another embodiment, the method can be used to determine the amount of marker polypeptide present in a cell, which in turn can be correlated with progression of a hyperproliferative disorder, e.g., colon cancer. The level of the marker polypeptide can be used predictively to evaluate whether a sample of cells contains cells which are, or are predisposed towards becoming, transformed cells. Moreover, the subject method can be used to assess the phenotype of cells which are known to be transformed, the phenotyping results being useful in planning a particular therapeutic regimen. For instance, very high levels of the marker polypeptide in sample cells is a powerful diagnostic and prognostic marker for a cancer, such as colon cancer. The observation of marker polypeptide level can be utilized in decisions regarding, e.g., the use of more aggressive therapies.

As set out above, one aspect of the present invention relates to diagnostic assays for determining, in the context of cells isolated from a patient, if the level of a marker polypeptide is significantly reduced in the sample cells. The term "significantly reduced" refers to a cell

phenotype wherein the cell possesses a reduced cellular amount of the marker polypeptide relative to a normal cell of similar tissue origin. For example, a cell may have less than about 50%, 25%, 10%, or 5% of the marker polypeptide that a normal control cell. In particular, the assay evaluates the level of marker polypeptide in the test cells, and, preferably, compares the measured level with marker polypeptide detected in at least one control cell, e.g., a normal cell and/or a transformed cell of known phenotype.

Of particular importance to the subject invention is the ability to quantitate the level of marker polypeptide as determined by the number of cells associated with a normal or abnormal marker polypeptide level. The number of cells with a particular marker polypeptide phenotype may then be correlated with patient prognosis. In one embodiment of the invention, the marker polypeptide phenotype of the lesion is determined as a percentage of cells in a biopsy which are found to have abnormally high/low levels of the marker polypeptide. Such expression may be detected by immunohistochemical assays, dot-blot assays, ELISA and the like.

Where tissue samples are employed, immunohistochemical staining may be used to determine the number of cells having the marker polypeptide phenotype. For such staining, a multiblock of tissue is taken from the biopsy or other tissue sample and subjected to proteolytic hydrolysis, employing such agents as protease K or pepsin. In certain embodiments, it may be desirable to isolate a nuclear fraction from the sample cells and detect the level of the marker polypeptide in the nuclear fraction.

The tissue samples are fixed by treatment with a reagent such as formalin, glutaraldehyde, methanol, or the like. The samples are then incubated with an antibody, preferably a monoclonal antibody, with binding specificity for the marker polypeptides. This antibody may be conjugated to a label for subsequent detection of binding. Samples are incubated for a time sufficient for formation of the immunocomplexes. Binding of the antibody is then detected by virtue of a label conjugated to this antibody. Where the antibody is unlabeled, a second labeled antibody may be employed, e.g., which is specific for the isotype of the anti-marker polypeptide antibody. Examples of labels which may be employed include radionuclides, fluorescers, chemilumescers, enzymes and the like.

Where enzymes are employed, the substrate for the enzyme may be added to the samples to provide a colored or fluorescent product. Examples of suitable enzymes for use in conjugates include horseradish peroxidase, alkaline phosphatase, malate dehydrogenase and the like. Where not commercially available, such antibody-enzyme conjugates are readily produced by techniques known to those skilled in the art.

In one embodiment, the assay is performed as a dot blot assay. The dot blot assay finds particular application where tissue samples are employed as it allows determination of the average amount of the marker polypeptide associated with a single cell by correlating the amount of marker polypeptide in a cell-free extract produced from a predetermined number of cells.

- 5 It is well established in the cancer literature that tumor cells of the same type (e.g., breast and/or colon tumor cells) may not show uniformly increased expression of individual oncogenes or uniformly decreased expression of individual tumor suppressor genes. There may also be varying levels of expression of a given marker gene even between cells of a given type of cancer, further emphasizing the need for reliance on a battery of tests rather than a single test.
- 10 Accordingly, in one aspect, the invention provides for a battery of tests utilizing a number of probes of the invention, in order to improve the reliability and/or accuracy of the diagnostic test.

- In one embodiment, the present invention also provides a method wherein nucleic acid probes are immobilized on a DNA chip in an organized array. Oligonucleotides can be bound to a solid support by a variety of processes, including lithography. For example a chip can hold up
- 15 to 250,000 oligonucleotides (GeneChip, Affymetrix). These nucleic acid probes comprise a nucleotide sequence at least about 12 nucleotides in length, preferably at least about 15 nucleotides, more preferably at least about 25 nucleotides, and most preferably at least about 40 nucleotides, and up to all or nearly all of a sequence which is complementary to a portion of the coding sequence of a marker nucleic acid sequence represented by SEQ ID Nos: 1-4494 and is
- 20 differentially expressed in tumor cells, such as colon cancer cells. The present invention provides significant advantages over the available tests for various cancers, such as colon cancer, because it increases the reliability of the test by providing an array of nucleic acid markers on a single chip.

- The method includes obtaining a biopsy, which is optionally fractionated by cryostat
- 25 sectioning to enrich tumor cells to about 80% of the total cell population. The DNA or RNA is then extracted, amplified, and analyzed with a DNA chip to determine the presence of absence of the marker nucleic acid sequences.

- In one embodiment, the nucleic acid probes are spotted onto a substrate in a two-dimensional matrix or array. Samples of nucleic acids can be labeled and then hybridized to the
- 30 probes. Double-stranded nucleic acids, comprising the labeled sample nucleic acids bound to probe nucleic acids, can be detected once the unbound portion of the sample is washed away.

The probe nucleic acids can be spotted on substrates including glass, nitrocellulose, etc. The probes can be bound to the substrate by either covalent bonds or by non-specific interactions, such as hydrophobic interactions. The sample nucleic acids can be labeled using radioactive labels, fluorophores, chromophores, etc.

5 Techniques for constructing arrays and methods of using these arrays are described, for example, in EP No. 0 799 897; PCT No. WO 97/292 12; PCT No. WO 97/27317; EP No. 0 785 280; PCT No. WO 97/02357; U.S. Pat. No. 5,593,839; U.S. Pat. No. 5,578,832; EP No. 0 728 520; U.S. Pat. No. 5,599,695; EP No. 0 721 016; U.S. Pat. No. 5,556,752; PCT No. WO 95/22058; and U.S. Pat. No. 5,631,734.

10 Further, arrays can be used to examine differential expression of genes and can be used to determine gene function. For example, arrays of the instant nucleic acid sequences can be used to determine if any of the nucleic acid sequences are differentially expressed between normal cells and cancer cells, for example. High expression of a particular message in a cancer cell, which is not observed in a corresponding normal cell, can indicate a cancer specific protein.

15 In one embodiment nucleic acid molecules useful in the present invention, such as those of SEQ ID Nos 1-4494, preferably those of SEQ ID Nos 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, may be used to generate macroarrays on a solid surface such as a membrane such that the arrayed nucleic acid molecules can be used to determine if any of the nucleic acids are differentially expressed between normal cells or tissue and cancerous
20 cells or tissue. In one embodiment, the nucleic acid molecules of the invention are either cDNA or may be used to generate cDNA molecules to be subsequently amplified by PCR and spotted on nylon membranes. The membranes are then reacted with radiolabeled target nucleic acid molecules obtained from equivalent samples of cancerous and normal tissue or cells. Methods of cDNA generation and macroarray preparation are known to those of skill in the art and may be
25 found, for example in Bertucci et al., 1999 *Hum. Mol. Genet.* 8:2129; Nguyen et al., 1995, *Genomics*, 29: 207; Zhao et al., *Gene*, 156:207; Gress et al., 1992, *Mammalian Genome*, 3:609; Zhumabayeva et al., 2001, *Biotechniques*, 30:158; and Lennon et al., 1991, *Trends Genet.* 7:314.

 In yet another embodiment, the invention contemplates using a panel of antibodies which are generated against the marker polypeptides of this invention, which polypeptides are encoded
30 by one or more of SEQ ID Nos: 1-4494, preferably SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494. Preferably, the antibodies are generated against one or more polypeptides having the sequence of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493. Such a panel of antibodies may be used as a

reliable diagnostic probe for colon cancer. The assay of the present invention comprises contacting a biopsy sample containing cells, e.g., colon cells, with a panel of antibodies to one or more of the encoded products to determine the presence or absence of the marker polypeptides.

5 The diagnostic methods of the subject invention may also be employed as follow-up to treatment, e.g., quantitation of the level of marker polypeptides may be indicative of the effectiveness of current or previously employed cancer therapies as well as the effect of these therapies upon patient prognosis.

Accordingly, the present invention makes available diagnostic assays and reagents for detecting gain and/or loss of marker polypeptides from a cell in order to aid in the diagnosis and
10 phenotyping of proliferative disorders arising from, for example, tumorigenic transformation of cells.

The diagnostic assays described above can be adapted to be used as prognostic assays, as well. Such an application takes advantage of the sensitivity of the assays of the invention to events which take place at characteristic stages in the progression of a tumor. For example, a
15 given marker gene may be up- or downregulated at a very early stage, perhaps before the cell is irreversibly committed to developing into a malignancy, while another marker gene may be characteristically up or down regulated only at a much later stage. Such a method could involve the steps of contacting the mRNA of a test cell with a nucleic acid probe derived from a given marker nucleic acid which is expressed at different characteristic levels in cancerous or
20 precancerous cells at different stages of tumor progression, and determining the approximate amount of hybridization of the probe to the mRNA of the cell, such amount being an indication of the level of expression of the gene in the cell, and thus an indication of the stage of tumor progression of the cell; alternatively, the assay can be carried out with an antibody specific for the gene product of the given marker nucleic acid, contacted with the proteins of the test cell. A
25 battery of such tests will disclose not only the existence and location of a tumor, but also will allow the clinician to select the mode of treatment most appropriate for the tumor, and to predict the likelihood of success of that treatment.

The methods of the invention can also be used to follow the clinical course of a tumor. For example, the assay of the invention can be applied to a tissue sample from a patient;
30 following treatment of the patient for the cancer, another tissue sample is taken and the test repeated. Successful treatment will result in either removal of all cells which demonstrate differential expression characteristic of the cancerous or precancerous cells, or a substantial

increase in expression of the gene in those cells, perhaps approaching or even surpassing normal levels.

In yet another embodiment, the invention provides methods for determining whether a subject is at risk for developing a disease, such as a predisposition to develop cancer, for example colon cancer, associated with an aberrant activity of any one of the polypeptides encoded by nucleic acids of SEQ ID Nos: 1-4494, preferably, any one of the polypeptides of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493, wherein the aberrant activity of the polypeptide is characterized by detecting the presence or absence of a genetic lesion characterized by at least one of (i) an alteration affecting the integrity of a gene encoding a marker polypeptides, or (ii) the mis-expression of the encoding nucleic acid. To illustrate, such genetic lesions can be detected by ascertaining the existence of at least one of (i) a deletion of one or more nucleotides from the nucleic acid sequence, (ii) an addition of one or more nucleotides to the nucleic acid sequence, (iii) a substitution of one or more nucleotides of the nucleic acid sequence, (iv) a gross chromosomal rearrangement of the nucleic acid sequence, (v) a gross alteration in the level of a messenger RNA transcript of the nucleic acid sequence, (vi) aberrant modification of the nucleic acid sequence, such as of the methylation pattern of the genomic DNA, (vii) the presence of a non-wild type splicing pattern of a messenger RNA transcript of the gene, (viii) a non-wild type level of the marker polypeptide, (ix) allelic loss of the gene, and/or (x) inappropriate post-translational modification of the marker polypeptide.

The present invention provides assay techniques for detecting lesions in the encoding nucleic acid sequence. These methods include, but are not limited to, methods involving sequence analysis, Southern blot hybridization, restriction enzyme site mapping, and methods involving detection of absence of nucleotide pairing between the nucleic acid to be analyzed and a probe.

Specific diseases or disorders, e.g., genetic diseases or disorders, are associated with specific allelic variants of polymorphic regions of certain genes, which do not necessarily encode a mutated protein. Thus, the presence of a specific allelic variant of a polymorphic region of a gene in a subject can render the subject susceptible to developing a specific disease or disorder. Polymorphic regions in genes, can be identified, by determining the nucleotide sequence of genes in populations of individuals. If a polymorphic region is identified, then the link with a specific disease can be determined by studying specific populations of individuals, e.g, individuals which developed a specific disease, such as colon cancer. A polymorphic region can

be located in any region of a gene, e.g., exons, in coding or non coding regions of exons, introns, and promoter region.

In an exemplary embodiment, there is provided a nucleic acid composition comprising a nucleic acid probe including a region of nucleotide sequence which is capable of hybridizing to a sense or antisense sequence of a gene or naturally occurring mutants thereof, or 5' or 3' flanking sequences or intronic sequences naturally associated with the subject genes or naturally occurring mutants thereof. The nucleic acid of a cell is rendered accessible for hybridization, the probe is contacted with the nucleic acid of the sample, and the hybridization of the probe to the sample nucleic acid is detected. Such techniques can be used to detect lesions or allelic variants at either the genomic or mRNA level, including deletions, substitutions, etc., as well as to determine mRNA transcript levels.

A preferred detection method is allele specific hybridization using probes overlapping the mutation or polymorphic site and having about 5, 10, 20, 25, or 30 nucleotides around the mutation or polymorphic region. In a preferred embodiment of the invention, several probes capable of hybridizing specifically to allelic variants are attached to a solid phase support, e.g., a "chip". Mutation detection analysis using these chips comprising oligonucleotides, also termed "DNA probe arrays" is described e.g., in Cronin et al. (1996) *Human Mutation* 7:244. In one embodiment, a chip comprises all the allelic variants of at least one polymorphic region of a gene. The solid phase support is then contacted with a test nucleic acid and hybridization to the specific probes is detected. Accordingly, the identity of numerous allelic variants of one or more genes can be identified in a simple hybridization experiment.

In certain embodiments, detection of the lesion comprises utilizing the probe/primer in a polymerase chain reaction (PCR) (see, e.g. U.S. Patent Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligase chain reaction (LCR) (see, e.g., Landegran et al. (1988) *Science* 241:1077-1080; and Nakazawa et al. (1994) *PNAS* 91:360-364), the latter of which can be particularly useful for detecting point mutations in the gene (see Abravaya et al. (1995) *Nuc Acid Res* 23:675-682). In a merely illustrative embodiment, the method includes the steps of (i) collecting a sample of cells from a patient, (ii) isolating nucleic acid (e.g., genomic, mRNA or both) from the cells of the sample, (iii) contacting the nucleic acid sample with one or more primers which specifically hybridize to a nucleic acid sequence under conditions such that hybridization and amplification of the nucleic acid (if present) occurs, and (iv) detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR

and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (Guatelli, J.C. *et al.*, 1990, Proc. Natl. Acad. Sci. USA 87:1874-1878), transcriptional amplification system (Kwoh, D.Y. *et al.*, 1989, Proc. Natl. Acad. Sci. USA 86:1173-1177), Q-Beta Replicase (Lizardi, P.M. *et al.*, 1988, Bio/Technology 6:1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

10 In a preferred embodiment of the subject assay, mutations in, or allelic variants, of a gene from a sample cell are identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis. Moreover, the use of sequence specific ribozymes (see, for example, U.S. Patent No. 5,498,531) 15 can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

Another aspect of the invention is directed to the identification of agents capable of modulating the differentiation and proliferation of cells characterized by aberrant proliferation. In this regard, the invention provides assays for determining compounds that modulate the 20 expression of the marker nucleic acids (SEQ ID Nos: 1-4494, preferably SEQ ID Nos 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494) and/or alter for example, inhibit the bioactivity of the encoded polypeptide such as those of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493.

Several *in vivo* methods can be used to identify compounds that modulate expression of 25 the marker nucleic acids (SEQ ID Nos: 1-4494) and/or alter for example, inhibit the bioactivity of the encoded polypeptide.

Drug screening is performed by adding a test compound to a sample of cells, and monitoring the effect. A parallel sample which does not receive the test compound is also monitored as a control. The treated and untreated cells are then compared by any suitable 30 phenotypic criteria, including but not limited to microscopic analysis, viability testing, ability to replicate, histological examination, the level of a particular RNA or polypeptide associated with the cells, the level of enzymatic activity expressed by the cells or cell lysates, and the ability of

the cells to interact with other cells or compounds. Differences between treated and untreated cells indicates effects attributable to the test compound.

Desirable effects of a test compound include an effect on any phenotype that was conferred by the cancer-associated marker nucleic acid sequence. Examples include a test
5 compound that limits the overabundance of mRNA, limits production of the encoded protein, or limits the functional effect of the protein. The effect of the test compound would be apparent when comparing results between treated and untreated cells.

The invention thus also encompasses methods of screening for agents which inhibit expression of the nucleic acid markers (SEQ ID Nos: 1-4494, preferably SEQ ID Nos. 4472,
10 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494) *in vitro*, comprising exposing a cell or tissue in which the marker nucleic acid mRNA is detectable in cultured cells to an agent in order to determine whether the agent is capable of inhibiting production of the mRNA; and determining the level of mRNA in the exposed cells or tissue, wherein a decrease in the level of the mRNA after exposure of the cell line to the agent is indicative of inhibition of the
15 marker nucleic acid mRNA production.

Alternatively, the screening method may include *in vitro* screening of a cell or tissue in which marker protein is detectable in cultured cells to an agent suspected of inhibiting production of the marker protein; and determining the level of the marker protein in the cells or tissue, wherein a decrease in the level of marker protein after exposure of the cells or tissue to
20 the agent is indicative of inhibition of marker protein production.

The invention also encompasses *in vivo* methods of screening for agents which inhibit expression of the marker nucleic acids, comprising exposing a mammal having tumor cells in which marker mRNA or protein is detectable to an agent suspected of inhibiting production of marker mRNA or protein; and determining the level of marker mRNA or protein in tumor cells
25 of the exposed mammal. A decrease in the level of marker mRNA or protein after exposure of the mammal to the agent is indicative of inhibition of marker nucleic acid expression.

Accordingly, the invention provides a method comprising incubating a cell expressing the marker nucleic acids (SEQ ID Nos: 1-4494) with a test compound and measuring the mRNA or protein level. The invention further provides a method for quantitatively determining the level of
30 expression of the marker nucleic acids in a cell population, and a method for determining whether an agent is capable of increasing or decreasing the level of expression of the marker nucleic acids in a cell population. The method for determining whether an agent is capable of

increasing or decreasing the level of expression of the marker nucleic acids in a cell population comprises the steps of (a) preparing cell extracts from control and agent-treated cell populations, (b) isolating the marker polypeptides from the cell extracts, (c) quantifying (e.g., in parallel) the amount of an immunocomplex formed between the marker polypeptide and an antibody specific to said polypeptide. The marker polypeptides of this invention may also be quantified by
5 assaying for its bioactivity. Agents that induce increased the marker nucleic acid expression may be identified by their ability to increase the amount of immunocomplex formed in the treated cell as compared with the amount of the immunocomplex formed in the control cell. In a similar manner, agents that decrease expression of the marker nucleic acid may be identified by their
10 ability to decrease the amount of the immunocomplex formed in the treated cell extract as compared to the control cell.

mRNA levels can be determined by Northern blot hybridization. mRNA levels can also be determined by methods involving PCR. Other sensitive methods for measuring mRNA, which can be used in high throughput assays, e.g., a method using a DELFIA endpoint detection and
15 quantification method, are described, e.g., in Webb and Hurskainen (1996) *Journal of Biomolecular Screening* 1:119. Marker protein levels can be determined by immunoprecipitations or immunohistochemistry using an antibody that specifically recognizes the protein product encoded by SEQ ID Nos: 1- 4494, and preferably one or more of the proteins having the sequence of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487,
20 4489, 4491, and 4493.

Agents that are identified as active in the drug screening assay are candidates to be tested for their capacity to block cell proliferation activity. These agents would be useful for treating a disorder involving aberrant growth of cells, especially colon cells.

A variety of assay formats will suffice and, in light of the present disclosure, those not
25 expressly described herein will nevertheless be comprehended by one of ordinary skill in the art. For instance, the assay can be generated in many different formats, and include assays based on cell-free systems, e.g., purified proteins or cell lysates, as well as cell-based assays which utilize intact cells.

In many drug screening programs which test libraries of compounds and natural extracts,
30 high throughput assays are desirable in order to maximize the number of compounds surveyed in a given period of time. Assays of the present invention which are performed in cell-free systems, such as may be derived with purified or semi-purified proteins or with lysates, are often preferred as "primary" screens in that they can be generated to permit rapid development and relatively

easy detection of an alteration in a molecular target which is mediated by a test compound. Moreover, the effects of cellular toxicity and/or bioavailability of the test compound can be generally ignored in the *in vitro* system, the assay instead being focused primarily on the effect of the drug on the molecular target as may be manifest in an alteration of binding affinity with
5 other proteins or changes in enzymatic properties of the molecular target.

A. Use of Nucleic Acids as Probes in Mapping and in Tissue Profiling Probes

Polynucleotide probes as described above, e.g., comprising at least 12 contiguous nucleotides selected from the nucleotide SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more
10 preferably SEQ ID Nos. 1-503, and still more preferably SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto, are used for a variety of purposes, including identification of human chromosomes and determining transcription levels. Additional disclosure about preferred regions of the nucleic acid sequences is found in the accompanying tables.

15 The nucleotide probes are labeled, for example, with a radioactive, fluorescent, biotinylated, or chemiluminescent label, and detected by well known methods appropriate for the particular label selected. Protocols for hybridizing nucleotide probes to preparations of metaphase chromosomes are also well known in the art. A nucleotide probe will hybridize specifically to nucleotide sequences in the chromosome preparations which are complementary
20 to the nucleotide sequence of the probe. A probe that hybridizes specifically to a nucleic acid should provide a detection signal at least 5-, 10-, or 20-fold higher than the background hybridization provided with other unrelated sequences.

In a non-limiting example, commercial programs are available for identifying regions of chromosomes commonly associated with disease, such as cancer. Nucleic acids of the invention
25 can be used to probe these regions. For example, if, through profile searching, a nucleic acid is identified as corresponding to a gene encoding a kinase, its ability to bind to a cancer-related chromosomal region will suggest its role as a kinase in one or more stages of tumor cell development/growth. Although some experimentation would be required to elucidate the role, the nucleic acid constitutes a new material for isolating a specific protein that has potential for
30 developing a cancer diagnostic or therapeutic.

Nucleotide probes are used to detect expression of a gene corresponding to the nucleic acid. For example, in Northern blots, mRNA is separated electrophoretically and contacted with

a probe. A probe is detected as hybridizing to an mRNA species of a particular size. The amount of hybridization is quantitated to determine relative amounts of expression, for example under a particular condition. Probes are also used to detect products of amplification by polymerase chain reaction. The products of the reaction are hybridized to the probe and hybrids are detected.

5 Probes are used for *in situ* hybridization to cells to detect expression. Probes can also be used *in vivo* for diagnostic detection of hybridizing sequences. Probes are typically labeled with a radioactive isotope. Other types of detectable labels may be used such as chromophores, fluorophores, and enzymes.

Expression of specific mRNA can vary in different cell types and can be tissue specific.

10 This variation of mRNA levels in different cell types can be exploited with nucleic acid probe assays to determine tissue types. For example, PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes substantially identical or complementary to nucleic acids of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, and still more

15 preferably SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto, can determine the presence or absence of target cDNA or mRNA.

Examples of a nucleotide hybridization assay are described in Urdea *et al.*, PCT W092/02526 and Urdea *et al.*, U.S. Patent No. 5,124,246, both incorporated herein by reference.

20 The references describe an example of a sandwich nucleotide hybridization assay.

Alternatively, the Polymerase Chain Reaction (PCR) is another means for detecting small amounts of target nucleic acids, as described in Mullis *et al.*, *Met/i. Enzymol.* (1987) 155:335-350; U.S. Patent No. 4,683,195; and U.S. Patent No. 4,683,202, all incorporated herein by reference. Two primer polynucleotides nucleotides hybridize with the target nucleic acids and

25 are used to prime the reaction. The primers may be composed of sequence within or 3' and 5' to the polynucleotides of the Sequence Listing. Alternatively, if the primers are 3' and 5' to these polynucleotides, they need not hybridize to them or the complements. A thermostable polymerase creates copies of target nucleic acids from the primers using the original target nucleic acids as a template. After a large amount of target nucleic acids is generated by the

30 polymerase, it is detected by methods such as Southern blots. When using the Southern blot method, the labeled probe will hybridize to a polynucleotide of the Sequence Listing or complement.

Furthermore, mRNA or cDNA can be detected by traditional blotting techniques described in Sambrook *et al.*, "Molecular Cloning: A Laboratory Manual" (New York, Cold Spring Harbor Laboratory, 1989). mRNA or cDNA generated from mRNA using a polymerase enzyme can be purified and separated using gel electrophoresis. The nucleic acids on the gel are
5 then blotted onto a solid support, such as nitrocellulose. The solid support is exposed to a labeled probe and then washed to remove any unhybridized probe. Next, the duplexes containing the labeled probe are detected. Typically, the probe is labeled with radioactivity.

Mapping

Nucleic acids of the present invention are used to identify a chromosome on which the
10 corresponding gene resides. Using fluorescence *in situ* hybridization (FISH) on normal metaphase spreads, comparative genomic hybridization allows total genome assessment of changes in relative copy number of DNA sequences. See Schwartz and Samad, *Current Opinions in Biotechnology* (1994) 8:70-74; Kallioniemi *et al.*, *Seminars in Cancer Biology* (1993) 4:41-46; Valdes and Tagle, *Methods in Molecular Biology* (1997) 68:1, Boultonwood, ed., Human Press,
15 Totowa, NJ.

Preparations of human metaphase chromosomes are prepared using standard cytogenetic techniques from human primary tissues or cell lines. Nucleotide probes comprising at least 12 contiguous nucleotides selected from the nucleotide sequence of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos.
20 1-1103, even more preferably SEQ ID Nos. 1-503, and still more preferably SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto, are used to identify the corresponding chromosome. The nucleotide probes are labeled, for example, with a radioactive, fluorescent, biotinylated, or chemiluminescent label, and detected by well known methods appropriate for the particular label
25 selected. Protocols for hybridizing nucleotide probes to preparations of metaphase chromosomes are also well known in the art. A nucleotide probe will hybridize specifically to nucleotide sequences in the chromosome preparations that are complementary to the nucleotide sequence of the probe. A probe that hybridizes specifically to a target gene provides a detection signal at least 5-, 10-, or 20-fold higher than the background hybridization provided with unrelated coding
30 sequences.

Nucleic acids are mapped to particular chromosomes using, for example, radiation hybrids or chromosome-specific hybrid panels. See Leach *et al.*, *Advances in Genetics*, (1995) 33:63-99; Walter *et al.*, *Nature Genetics* (1994) 7:22-28; Walter and Goodfellow, *Trends in*

Genetics (1992) 9:352. Panels for radiation hybrid mapping are available from Research Genetics, Inc., Huntsville, Alabama, USA. Databases for markers using various panels are available via the world wide web at <http://F/shgc-www.stanford.edu>, and other locations. The statistical program RHMAP can be used to construct a map based on the data from radiation
5 hybridization with a measure of the relative likelihood of one order versus another, RHMAP is available via the world wide web at <http://www.sph.umich.edu/group/statgen/software>.

Such mapping can be useful in identifying the function of the target gene by its proximity to other genes with known function. Function can also be assigned to the target gene when particular syndromes or diseases map to the same chromosome.

10 Tissue Profiling

The nucleic acids of the present invention can be used to determine the tissue type from which a given sample is derived. For example, a metastatic lesion is identified by its developmental organ or tissue source by identifying the expression of a particular marker of that organ or tissue. If a nucleic acid is expressed only in a specific tissue type, and a metastatic
15 lesion is found to express that nucleic acid, then the developmental source of the lesion has been identified. Expression of a particular nucleic acid is assayed by detection of either the corresponding mRNA or the protein product. Immunological methods, such as antibody staining, are used to detect a particular protein product. Hybridization methods may be used to detect particular mRNA species, including but not limited to *in situ* hybridization and Northern
20 blotting.

Use of Polymorphisms

A nucleic acid will be useful in forensics, genetic analysis, mapping, and diagnostic applications if the corresponding region of a gene is polymorphic in the human population. A particular polymorphic form of the nucleic acid may be used to either identify a sample as
25 deriving from a suspect or rule out the possibility that the sample derives from the suspect. Any means for detecting a polymorphism in a gene are used, including but not limited to electrophoresis of protein polymorphic variants, differential sensitivity to restriction enzyme cleavage, and hybridization to an allele-specific probe.

B. Use of Nucleic Acids and Encoded Polypeptides to Raise Antibodies

30 Expression products of a nucleic acid, the corresponding mRNA or cDNA, or the corresponding complete gene are prepared and used for raising antibodies for experimental,

diagnostic, and therapeutic purposes. For nucleic acids to which a corresponding gene has not been assigned, this provides an additional method of identifying the corresponding gene. The nucleic acid or related cDNA is expressed as described above, and antibodies are prepared. These antibodies are specific to an epitope on the encoded polypeptide, and can precipitate or
5 bind to the corresponding native protein in a cell or tissue preparation or in a cell-free extract of an *in vitro* expression system.

Immunogens for raising antibodies are prepared by mixing the polypeptides encoded by the nucleic acids of the present invention with adjuvants. Alternatively, polypeptides are made as fusion proteins to larger immunogenic proteins. Polypeptides are also covalently linked to other
10 larger immunogenic proteins, such as keyhole limpet hemocyanin. Immunogens are typically administered intradermally, subcutaneously, or intramuscularly. Immunogens are administered to experimental animals such as rabbits, sheep, and mice, to generate antibodies. Optionally, the animal spleen cells are isolated and fused with myeloma cells to form hybridomas which secrete monoclonal antibodies. Such methods are well known in the art. According to another method
15 known in the art, the nucleic acid is administered directly, such as by intramuscular injection, and expressed *in vivo*. The expressed protein generates a variety of protein-specific immune responses, including production of antibodies, comparable to administration of the protein.

Preparations of polyclonal and monoclonal antibodies specific for nucleic acid-encoded proteins and polypeptides are made using standard methods known in the art. The antibodies
20 specifically bind to epitopes present in the polypeptides encoded by a nucleic acid of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, and still more preferably SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto. In a preferred embodiment the antibodies bind to
25 epitopes on the polypeptides of SEQ ID Nos. 4471, 4473, 4475, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493. Typically, at least about 6, 8, 10, or 12 contiguous amino acids are required to form an epitope. However, epitopes which involve noncontiguous amino acids may require more, for example, at least about 15, 25, or 50 amino acids. A short sequence of a nucleic acid may then be unsuitable for use as an epitope to raise antibodies for identifying the
30 corresponding novel protein, because of the potential for cross-reactivity with a known protein. However, the antibodies may be useful for other purposes, particularly if they identify common structural features of a known protein and a novel polypeptide encoded by a nucleic acid of the invention.

Antibodies that specifically bind to human nucleic acid-encoded polypeptides should provide a detection signal at least about 5-, 10-, or 20-fold higher than a detection signal provided with other proteins when used in Western blots or other immunochemical assays. Preferably, antibodies that specifically bind nucleic acid T-encoded polypeptides do not detect
5 other proteins in immunochemical assays and can immunoprecipitate nucleic acid-encoded proteins from solution.

To test for the presence of serum antibodies to the nucleic acid-encoded polypeptide in a human population, human antibodies are purified by methods well known in the art. Preferably, the antibodies are affinity purified by passing antiserum over a column to which a nucleic acid-
10 encoded protein, polypeptide, or fusion protein is bound. The bound antibodies can then be eluted from the column, for example using a buffer with a high salt concentration.

In addition to the antibodies discussed above, genetically engineered antibody derivatives are made, such as single chain antibodies.

Antibodies may be made by using standard protocols known in the art (See, for example,
15 Antibodies: A Laboratory Manual ed. by Harlow and Lane (Cold Spring Harbor Press: 1988)). A mammal, such as a mouse, hamster, or rabbit can be immunized with an immunogenic form of the peptide (e.g., a mammalian polypeptide or an antigenic fragment which is capable of eliciting an antibody response, or a fusion protein as described above).

In one aspect, this invention includes monoclonal antibodies that show a subject
20 polypeptide is highly expressed in colorectal tissue or tumor tissue, especially colon cancer tissue or colon cancer-derived cell lines. Therefore, in one embodiment, this invention provides a diagnostic tool for the analysis of expression of a subject polypeptide in general, and in particular, as a diagnostic for colon cancer.

Techniques for conferring immunogenicity on a protein or peptide include conjugation to
25 carriers or other techniques well known in the art. An immunogenic portion of a protein can be administered in the presence of adjuvant. The progress of immunization can be monitored by detection of antibody titers in plasma or serum. Standard ELISA or other immunoassays can be used with the immunogen as antigen to assess the levels of antibodies. In a preferred embodiment, the subject antibodies are immunospecific for antigenic determinants of a protein
30 of a mammal, e.g., antigenic determinants of a protein encoded by one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or closely related homologs (e.g., at least 90% identical, and more preferably at least 95% identical).

Following immunization of an animal with an antigenic preparation of a polypeptide, antisera can be obtained and, if desired, polyclonal antibodies isolated from the serum. To produce monoclonal antibodies, antibody-producing cells (lymphocytes) can be harvested from an immunized animal and fused by standard somatic cell fusion procedures with immortalizing cells such as myeloma cells to yield hybridoma cells. Such techniques are well known in the art, and include, for example, the hybridoma technique (originally developed by Kohler and Milstein, (1975) *Nature*, 256: 495-497), the human B cell hybridoma technique (Kozbar *et al.*, (1983) *Immunology Today*, 4: 72), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole *et al.*, (1985) *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc. pp. 77-96). Hybridoma cells can be screened immunochemically for production of antibodies specifically reactive with a polypeptide of the present invention and monoclonal antibodies isolated from a culture comprising such hybridoma cells.

The term antibody as used herein is intended to include fragments thereof which are also specifically reactive with one of the subject polypeptides. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as described above for whole antibodies. For example, F(ab)₂ fragments can be generated by treating antibody with pepsin. The resulting F(ab)₂ fragment can be treated to reduce disulfide bridges to produce Fab fragments. The antibody of the present invention is further intended to include bispecific, single-chain, and chimeric and humanized molecules having affinity for a polypeptide conferred by at least one CDR region of the antibody. In preferred embodiments, the antibodies, the antibody further comprises a label attached thereto and able to be detected, (e.g., the label can be a radioisotope, fluorescent compound, chemiluminescent compound, enzyme, or enzyme co-factor).

Antibodies can be used, e.g., to monitor protein levels in an individual for determining, e.g., whether a subject has a disease or condition, such as colon cancer, associated with an aberrant protein level, or allowing determination of the efficacy of a given treatment regimen for an individual afflicted with such a disorder. The level of polypeptides may be measured from cells in bodily fluid, such as in blood samples.

Another application of antibodies of the present invention is in the immunological screening of cDNA libraries constructed in expression vectors such as gt11, gt18-23, ZAP, and ORF8. Messenger libraries of this type, having coding sequences inserted in the correct reading frame and orientation, can produce fusion proteins. For instance, gt11 will produce fusion proteins whose amino termini consist of β -galactosidase amino acid sequences and whose

carboxyl termini consist of a foreign polypeptide. Antigenic epitopes of a protein, e.g., other orthologs of a particular protein or other paralogs from the same species, can then be detected with antibodies, as, for example, reacting nitrocellulose filters lifted from infected plates with antibodies. Positive phage detected by this assay can then be isolated from the infected plate.

- 5 Thus, the presence of homologs can be detected and cloned from other animals, as can alternate isoforms (including splicing variants) from humans.

In another embodiment, a panel of monoclonal antibodies may be used, wherein each of the epitope's involved functions are represented by a monoclonal antibody. Loss or perturbation of binding of a monoclonal antibody in the panel would be indicative of a mutational alteration of the protein and thus of the corresponding gene.

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C. Differential Expression

The present invention also provides a method to identify abnormal or diseased tissue in a human. For nucleic acids corresponding to profiles of protein families as described above, the choice of tissue may be dictated by the putative biological function. The expression of a gene corresponding to a specific nucleic acid is compared between a first tissue that is suspected of being diseased and a second, normal tissue of the human. The normal tissue is any tissue of the human, especially those that express the target gene including, but not limited to, brain, thymus, testis, heart, prostate, placenta, spleen, small intestine, skeletal muscle, pancreas, and the mucosal lining of the colon.

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20 The tissue suspected of being abnormal or diseased can be derived from a different tissue type of the human, but preferably it is derived from the same tissue type; for example an intestinal polyp or other abnormal growth should be compared with normal intestinal tissue. A difference between the target gene, mRNA, or protein in the two tissues which are compared, for example in molecular weight, amino acid or nucleotide sequence, or relative abundance, indicates a change in the gene, or a gene which regulates it, in the tissue of the human that was suspected of being diseased.

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The target genes in the two tissues are compared by any means known in the art. For example, the two genes are sequenced, and the sequence of the gene in the tissue suspected of being diseased is compared with the gene sequence in the normal tissue. The target genes, or portions thereof, in the two tissues are amplified, for example using nucleotide primers based on the nucleotide sequence shown in the Sequence Listing, using the polymerase chain reaction. The amplified genes or portions of genes are hybridized to nucleotide probes selected from a

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corresponding nucleotide sequence shown SEQ ID No. 1-4494. A difference in the nucleotide sequence of the target gene in the tissue suspected of being diseased compared with the normal nucleotide sequence suggests a role of the nucleic acid-encoded proteins in the disease, and provides a lead for preparing a therapeutic agent. The nucleotide probes are labeled by a variety of methods, such as radiolabeling, biotinylation, or labeling with fluorescent or chemiluminescent tags, and detected by standard methods known in the art.

Alternatively, target mRNA in the two tissues is compared. PolyA⁺RNA is isolated from the two tissues as is known in the art. For example, one of skill in the art can readily determine differences in the size or amount of target mRNA transcripts between the two tissues using Northern blots and nucleotide probes selected from the nucleotide sequence shown in the Sequence Listing. Increased or decreased expression of a target mRNA in a tissue sample suspected of being diseased, compared with the expression of the same target mRNA in a normal tissue, suggests that the expressed protein has a role in the disease, and also provides a lead for preparing a therapeutic agent.

Any method for analyzing proteins is used to compare two nucleic acid-encoded proteins from matched samples. The sizes of the proteins in the two tissues are compared, for example, using antibodies of the present invention to detect nucleic acid-encoded proteins in Western blots of protein extracts from the two tissues. Other changes, such as expression levels and subcellular localization, can also be detected immunologically, using antibodies to the corresponding protein. A higher or lower level of nucleic acid-encoded protein expression in a tissue suspected of being diseased, compared with the same nucleic acid-encoded protein expression level in a normal tissue, is indicative that the expressed protein has a role in the disease, and provides another lead for preparing a therapeutic agent.

Similarly, comparison of gene sequences or of gene expression products, e.g., mRNA and protein, between a human tissue that is suspected of being diseased and a normal tissue of a human, are used to follow disease progression or remission in the human. Such comparisons of genes, mRNA, or protein are made as described above.

For example, increased or decreased expression of the target gene in the tissue suspected of being neoplastic can indicate the presence of neoplastic cells in the tissue. The degree of increased expression of the target gene in the neoplastic tissue relative to expression of the gene in normal tissue, or differences in the amount of increased expression of the target gene in the neoplastic tissue over time, is used to assess the progression of the neoplasia in that tissue or to monitor the response of the neoplastic tissue to a therapeutic protocol over time.

The expression pattern of any two cell types can be compared, such as low and high metastatic tumor cell lines, or cells from tissue which have and have not been exposed to a therapeutic agent. A genetic predisposition to disease in a human is detected by comparing an target gene, mRNA, or protein in a fetal tissue with a normal target gene, mRNA, or protein.

5 Fetal tissues that are used for this purpose include, but are not limited to, amniotic fluid, chorionic villi, blood, and the blastomere of an *in vitro*-fertilized embryo. The comparable normal target gene is obtained from any tissue. The mRNA or protein is obtained from a normal tissue of a human in which the target gene is expressed. Differences such as alterations in the nucleotide sequence or size of the fetal target gene or mRNA, or alterations in the molecular

10 weight, amino acid sequence, or relative abundance of fetal target protein, can indicate a germline mutation in the target gene of the fetus, which indicates a genetic predisposition to disease.

In a preferred embodiment nucleic acid macroarrays comprising the one or more of the sequences of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488,

15 4490, 4492, and 4494 may be used to evaluate differential expression of nucleic acid sequences in cancerous cells or tissue relative to the expression of the same sequences in normal cells or tissue as described above. Preferably, such sequences are differentially expressed by at least 3 fold in cancerous cells or tissue relative to normal cells or tissue. More specifically, the present invention provides the full length sequences of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480,

20 4482, 4484, 4486, 4488, 4490, 4492, and 4494 which are differentially expressed in cancerous colonic cells/tissue by at least 3 fold relative to normal patient samples. Thus, the sequences of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, as well as the encoded polypeptides (SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493, respectively) serve as valuable diagnostic markers for

25 identifying and screening for colon cancer in a patient.

D. Use of Nucleic Acids, and Encoded Polypeptides to Screen for Peptide Analogs and Antagonists

Polypeptides encoded by the instant nucleic acids, e.g., SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, and most preferably SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto, and corresponding full length genes can be used to screen peptide libraries to identify binding partners, such as receptors, from among the encoded polypeptides. Preferably, the

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polypeptides of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493 may be used screen for binding partners.

A library of peptides may be synthesized following the methods disclosed in U.S. Pat. No. 5,010,175, and in PCT WO 91/17823. As described below in brief, one prepares a mixture of peptides, which is then screened to identify the peptides exhibiting the desired signal transduction and receptor binding activity. In the '175 method, a suitable peptide synthesis support (e.g., a resin) is coupled to a mixture of appropriately protected, activated amino acids. The concentration of each amino acid in the reaction mixture is balanced or adjusted in inverse proportion to its coupling reaction rate so that the product is an equimolar mixture of amino acids coupled to the starting resin. The bound amino acids are then deprotected, and reacted with another balanced amino acid mixture to form an equimolar mixture of all possible dipeptides. This process is repeated until a mixture of peptides of the desired length (e.g., hexamers) is formed. Note that one need not include all amino acids in each step: one may include only one or two amino acids in some steps (e.g., where it is known that a particular amino acid is essential in a given position), thus reducing the complexity of the mixture. After the synthesis of the peptide library is completed, the mixture of peptides is screened for binding to the selected polypeptide. The peptides are then tested for their ability to inhibit or enhance activity. Peptides exhibiting the desired activity are then isolated and sequenced.

The method described in WO 91/17823 is similar. However, instead of reacting the synthesis resin with a mixture of activated amino acids, the resin is divided into twenty equal portions (or into a number of portions corresponding to the number of different amino acids to be added in that step), and each amino acid is coupled individually to its portion of resin. The resin portions are then combined, mixed, and again divided into a number of equal portions for reaction with the second amino acid. In this manner, each reaction may be easily driven to completion. Additionally, one may maintain separate "subpools" by treating portions in parallel, rather than combining all resins at each step. This simplifies the process of determining which peptides are responsible for any observed receptor binding or signal transduction activity.

In such cases, the subpools containing, e.g., 1-2,000 candidates each are exposed to one or more polypeptides of the invention. Each subpool that produces a positive result is then resynthesized as a group of smaller subpools (sub-subpools) containing, e.g., 20-100 candidates, and reassayed. Positive sub-subpools may be resynthesized as individual compounds, and assayed finally to determine the peptides that exhibit a high binding constant. These peptides can be tested for their ability to inhibit or enhance the native activity. The methods described in WO

91/7823 and U.S. Patent No. 5,194,392 (herein incorporated by reference) enable the preparation of such pools and subpools by automated techniques in parallel, such that all synthesis and resynthesis may be performed in a matter of days.

Peptide agonists or antagonists are screened using any available method, such as signal
5 transduction, antibody binding, receptor binding, mitogenic assays, chemotaxis assays, etc. The methods described herein are presently preferred. The assay conditions ideally should resemble the conditions under which the native activity is exhibited *in vivo*, that is, under physiologic pH, temperature, and ionic strength. Suitable agonists or antagonists will exhibit strong inhibition or enhancement of the native activity at concentrations that do not cause toxic side effects in the
10 subject. Agonists or antagonists that compete for binding to the native polypeptide may require concentrations equal to or greater than the native concentration, while inhibitors capable of binding irreversibly to the polypeptide may be added in concentrations on the order of the native concentration.

The end results of such screening and experimentation will be at least one novel
15 polypeptide binding partner, such as a receptor, encoded by a nucleic acid of the invention, and at least one peptide agonist or antagonist of the novel binding partner. Such agonists and antagonists can be used to modulate, enhance, or inhibit receptor function in cells to which the receptor is native, or in cells that possess the receptor as a result of genetic engineering. Further, if the novel receptor shares biologically important characteristics with a known receptor,
20 information about agonist/antagonist binding may help in developing improved agonists/antagonists of the known receptor.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of cell biology, cell culture, molecular biology, transgenic biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such
25 techniques are explained fully in the literature. See, for example, *Molecular Cloning A Laboratory Manual*, 2nd Ed., ed. by Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory Press:1989); *DNA Cloning*, Volumes I and II (D.N. Glover ed., 1985); *Oligonucleotide Synthesis* (M. J. Gait ed., 1984); Mullis *et al.* U.S. Patent No. 4,683,195; *Nucleic Acid Hybridization* (B.D. Hames & S. J. Higgins eds. 1984); *Transcription And Translation* (B. D. Hames & S. J. Higgins eds. 1984); *Culture Of Animal Cells* (R. I. Freshney, Alan R. Liss, Inc., 1987); *Immobilized Cells And Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide To Molecular Cloning* (1984); the treatise, *Methods in Enzymology* (Academic Press, Inc., N.Y.); *Gene Transfer Vectors For Mammalian Cells* (J. H. Miller and M.P. Calos

- eds., 1987, Cold Spring Harbor Laboratory); *Methods In Enzymology*, Vols. 154 and 155 (Wu et al. eds.), *Immunochemical Methods In Cell And Molecular Biology* (Mayer and Walker, eds., Academic Press, London, 1987); *Handbook Of Experimental Immunology*, Volumes I-IV (D. M. Weir and C.C. Blackwell, eds., 1986); *Manipulating the Mouse Embryo*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986).

As mentioned above, the sequences described herein are believed to have particular utility in regards to colon cancer. However, they may also be useful with other types of cancers and other disease states.

- The present invention will now be illustrated by reference to the following examples which set forth particularly advantageous embodiments. However, it should be noted that these embodiments are illustrative and are not to be construed as restricting the invention in any way.

XI. Examples

A. Identification of differentially expressed sequences.

Description of the Libraries

- SEQ ID Nos: 1-4470 were derived from libraries designated as 101, 102, 103, 104, 109, 110, 111, and 112 as described below briefly and in the accompanying table (Table 1). For example, the 101 library is a normalized, colon cancer specific, subtracted cDNA library. It is specific for sequences expressed in colon cancer [proximal and distal Dukes' B, microsatellite instability negative (MSI-)] but not expressed in normal tissues, including normal colon tissue.
- The 102 library is a normalized, colon specific, subtracted cDNA library. It is specific for sequences expressed in normal colon tissue but not expressed in other normal tissues.
- Characteristics of the remaining libraries are described in Table 1.

Table 1 Library designation and description

Library Designation	Description
101	Specific for sequences expressed in colon cancer (proximal and distal Dukes' B, MSI-) but not expressed in normal tissues ⁴ , including colon ²
102	Specific for sequences expressed in normal colon (normal tissue from proximal and distal Dukes' B, MSI-matrix patients) ³ , but not expressed in

	other normal tissues ⁴
103	Specific for sequences expressed in proximal Dukes' B, MSI- colon cancer, but not expressed in normal colon tissue ³
104	Specific for sequences expressed in distal Dukes' B, MSI- colon cancer, but not expressed in normal colon tissue ³
109	Specific for sequences expressed in proximal Dukes' B, MSI+ colon cancer, but not expressed in normal colon tissue ³
110	Specific for sequences expressed in proximal Dukes' B, MSI+ colon cancer, but not expressed in other normal tissues ⁴ , including colon ²
111	Specific for sequences expressed in distal, Dukes' D, MSI- colon cancer, but not expressed in normal colon tissue ³
112	Specific for sequences expressed in distal, Dukes' D, MSI- colon cancer, but not expressed in normal tissues ⁴ , including colon ²

¹ cDNA synthesized from SW480 poly A+ RNA obtained from Clontech, Palo Alto, CA

² cDNA synthesized from normal colon tissue total RNA obtained from OriGene Technologies, Inc.; Rockville, MD

³ Corresponding normal colon epithelium from colon cancer patients.

- 5 ⁴ A pool of cDNAs synthesized from the following normal tissue RNAs (poly A+ or total) obtained from OriGene Technologies, Inc.: heart, kidney, spleen, liver, peripheral blood lymphocytes, small intestine, skeletal muscle, lung and prostate.

Construction of the normalized and subtracted cDNA libraries

10 The normalized and subtracted cDNA libraries were constructed according to published procedures (Daitchenko et al., 1996 PNAS 93:6025-6030, Gurskaya et al., 1996 Analytical Biochemistry 240:90-97). Commercially available kits from Clontech Laboratories, Inc., Palo Alto, California were utilized (Clontech SMART cDNA synthesis kit, catalog number K1052-1, and Clontech PCR-Select cDNA Subtraction kit, catalog number K1804-1). For each subtracted library, the specific or "tester" cDNA was comprised of amplified cDNA from four similar
15 sample types that were pooled together. Likewise, the reference or "driver" cDNA was comprised of a pool of sample types as illustrated in Table 1. During the subtraction process, the genes or transcripts unique to the tester are retained, and the genes or transcripts common to both the tester and driver are removed. Thus, in principle, the clones present in the subtracted libraries indicate those genes or transcripts that are expressed (or overexpressed) in the tester, but

not expressed (or underexpressed) in the driver. Reverse-subtracted libraries were also constructed in which the tester and driver materials were reversed. These libraries were only utilized to prepare labeled targets (see below).

To construct the libraries, one microgram of total RNA from each sample was
5 representatively amplified using the Clontech SMART cDNA synthesis kit. The amplified cDNA was purified and pooled to create the individual tester and driver samples that were used for the subsequent library construction. To construct the normalized and subtracted libraries, the Clontech PCR-Select cDNA Subtraction kit was utilized. A forty-five fold mass excess of driver cDNA (450 nanograms) was used for each subtraction experiment. Subtractive hybridization of
10 tester with driver cDNAs was performed twice, each time for about 8-12 hours. Subtracted cancer specific cDNA was ligated into the pCR2.1-TOPO plasmid vector (Invitrogen Corporation, Carlsbad CA) and chemically transformed into ultracompetent Epicurian E. coli XL10-Gold cells (Stratagene, La Jolla, CA). The transformed cells were plated onto LB-ampicillin plates containing IPTG and X-gal. Individual white colonies, representing those with
15 cloned inserts, were picked and grown overnight in LB-ampicillin broth. Plasmid DNA was purified using QIAprep 96 Turbo kits from Qiagen (Valencia, CA).

Sequencing of the clones

The nucleotide sequence of the inserts from clones was determined by single-pass sequencing from either the T7 or M13 promoter sites using fluorescently labeled
20 dideoxynucleotides via the Sanger sequencing method. The nucleotide sequences of the individual clones were compared to those in public databases (GenBank, dbEST, Geneseq) via Blast 2 homology searches according to methods described in the text.

The sequences derived from individual clones from the libraries described above represents a sequence from a partial mRNA transcript, since the cDNA used for making the
25 subtracted library was restricted with *RsaI*, a four base cutter restriction endonuclease that generates fragments with an average size of about 600 base pairs.

The nucleic acids of the invention were assigned a sequence identification number (see Figure 1). The nucleic acid sequences are provided in the attached Sequence Listing.

Validation of differential expression in colon cancer

30 To validate that the differentially expressed sequences found in this library were specific to colon cancer, the inserts from the plasmid DNA were amplified by PCR using vector-specific

primers. The amplification products were arrayed onto nylon membranes and hybridized with ³³P-labeled cDNAs prepared from both the subtracted library cDNA as well as the corresponding reverse-subtracted cDNA library. Each membrane array comprises approximately 3,456 clones. Four such membranes were generated comprising the clone libraries shown in Table 1 as indicated below in Table 3.

Membrane ID Number	Library Clones
101-1	Clones from subtracted library 101
101-2	Clones from subtracted library 101 and 102
103104109	Clones from subtracted libraries 103, 104, and 109
110111112	Clones from subtracted libraries 110, 111, and 112

The set of four membranes is hybridized, using techniques known to those of skill in the art and further described above, with ³²P-labeled target nucleic acid molecules obtained from human colon cancer tissue. A second, identical set of membranes is hybridized with ³²P-labeled target nucleic acid molecules obtained from normal human colon tissue. The signals of the hybridization products on the cancer membrane are subsequently compared to those on the normal membrane. A difference in hybridization, indicative of a difference in expression of the sequence in colon cancer vs. normal, of at least 3 fold is considered to be indicative of differential expression.

Using this validation technique, the full length cDNA sequences of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 have been identified as significantly differentially expressed in colon cancer relative to normal colon tissue.

Those skilled in the art will recognize, or be able to ascertain, using not more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such specific embodiments and equivalents are intended to be encompassed by the following claims.

All patents, published patent applications, and publications cited herein are incorporated by reference as if set forth fully herein.

What is claimed is:

CLAIMS

1. A method for detecting cancer in which one or more of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 are used as probes,
5 said method comprising:
 - (a) collecting a sample of cells from a patient,
 - (b) isolating nucleic acid from the cells of the sample,
 - (c) contacting the nucleic acid sample with one or more primers which specifically hybridize to a nucleic acid sequence of SEQ ID Nos. 1-4470, 4472, 4474, 4476,
10 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 under conditions such that hybridization and amplification of the nucleic acid occurs, and
 - (d) comparing the presence, absence, or size of an amplification product to the amplification product of a normal cell.
2. A method of claim 1 in which said cancer is colon cancer.
- 15 3. A method for detecting cancer in a patient sample in which an antibody to a protein encoded by SEQ ID Nos. 1-4470 is used to react with proteins in said sample.
4. A method for detecting cancer in a patient sample in which an antibody to a protein encoded by one or more of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, or 4494 is used to react with proteins in said sample.
- 20 5. A method for detecting cancer in a patient sample in which an antibody to a protein having the sequence of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, or 4493 is used to react with proteins in said sample.
6. A method for identifying an agent which alters the level of expression in a cell of a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470 or a
25 sequence complementary thereto, comprising
 - (a) providing a cell;
 - (b) treating the cell with a test agent;

(c) determining the level of expression in the cell of a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470 or a sequence complementary thereto; and

(d) comparing the level of expression of the nucleic acid in the treated cell with the level of expression of the nucleic acid in an untreated cell, wherein a change in the level of expression of the nucleic acid in the treated cell relative to the level of expression of the nucleic acid in the untreated cell is indicative of an agent which alters the level of expression of the nucleic acid in a cell.

7. A method for identifying an agent which alters the level of expression in a cell of a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, or 4494 or a sequence complementary thereto, comprising

(a) providing a cell;

(b) treating the cell with a test agent;

(c) determining the level of expression in the cell of a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, or 4494 or a sequence complementary thereto; and

(d) comparing the level of expression of the nucleic acid in the treated cell with the level of expression of the nucleic acid in an untreated cell, wherein a change in the level of expression of the nucleic acid in the treated cell relative to the level of expression of the nucleic acid in the untreated cell is indicative of an agent which alters the level of expression of the nucleic acid in a cell.

8. A method for identifying an agent which alters the level of expression in a cell of a polypeptide of one or more of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, or 4493 comprising

(a) providing a cell;

(b) treating the cell with a test agent;

(c) determining the level of expression of one or more polypeptides of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, or 4493 in said cell

by reacting said cell with an antibody specific for one or more of the polypeptides of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, or 4493; and

- (d) comparing the level of expression of said one or more polypeptides in the treated cell with the level of expression of said one or more polypeptides in an untreated cell, wherein a change in the level of expression of the nucleic acid in the treated cell relative to the level of expression of the nucleic acid in the untreated cell is indicative of an agent which alters the level of expression of the polypeptide in a cell.

9. A pharmaceutical composition comprising an agent identified by the method of claim 29, 30, or 31.

10. A pharmaceutical composition comprising a nucleic acid which includes a nucleotide sequence which hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470 or a sequence complementary thereto.

11. A pharmaceutical composition comprising a polypeptide encoded by a nucleic acid which includes a nucleotide sequence that hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470 or a sequence complementary thereto.

12. A pharmaceutical composition comprising a polypeptide having the sequence of one of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, or 4493.

13. A pharmaceutical composition comprising an antibody which binds to one or more polypeptides having the sequence of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, or 4493.

14. A method of determining the phenotype of a cell, comprising detecting the differential expression, relative to a normal cell, of at least one nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, wherein the nucleic acid is differentially expressed by at least a factor of two.

15. A method for determining the phenotype of cells in a sample of cells from a patient, comprising:

(a) providing a nucleic acid probe comprising a nucleotide sequence having at least 12 consecutive nucleotides of any of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494;

(b) obtaining a sample of cells from a patient;

5 (c) providing a second sample of cells substantially all of which are non-cancerous;

(d) contacting the nucleic acid probe under stringent conditions with mRNA of each of said first and second cell samples; and comparing (a) the amount of hybridization of the probe with mRNA of the first cell sample, with (b) the amount of hybridization of the probe
10 with mRNA of the second cell sample, wherein a difference of at least a factor of two in the amount of hybridization with the mRNA of the first cell sample as compared to the amount of hybridization with the mRNA of the second cell sample is indicative of the phenotype of cells in the first cell sample.

16. A method of determining the phenotype of cell, comprising detecting the
15 differential expression, relative to a normal cell, of at least one polypeptide encoded by a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470, wherein the polypeptide is differentially expressed by at least a factor of two.

17. A method of determining the phenotype of cell, comprising detecting the
differential expression, relative to a normal cell, of at least one polypeptide encoded by a nucleic
20 acid which hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, wherein the polypeptide is differentially expressed by at least a factor of two.

18. A method of determining the phenotype of cell, comprising detecting the
differential expression, relative to a normal cell, of at least one polypeptide selected from the
25 group of polypeptides of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493, wherein the polypeptide is differentially expressed by at least a factor of two.

19. The method of claim 16, 17, or 18, wherein the level of said polypeptide is detected in an immunoassay.

20. A method for detecting a mutation in a test nucleic acid which hybridizes under stringent conditions to a nucleic acid of SEQ ID Nos. 1-4470 or a sequence complementary thereto, comprising

- (a) collecting a sample of cells from a patient,
- 5 (b) isolating nucleic acid from the cells of the sample,
- (c) contacting the nucleic acid sample with one or more primers which specifically hybridize to a nucleic acid sequence of SEQ ID Nos. 1-4470 under conditions such that hybridization and amplification of the nucleic acid occurs, and
- (d) comparing the presence, absence, or size of an amplification product to the
10 amplification product of a normal cell.

21. An isolated nucleic acid comprising a portion of a nucleotide sequence of SEQ ID Nos. 504-1103 or a sequence complementary thereto.

22. A gene which hybridizes to one of SEQ ID Nos. 1-503.

23. An isolated nucleic acid comprising a nucleotide sequence which hybridizes
15 under stringent conditions to a sequence of SEQ ID Nos. 1-503 or a sequence complementary thereto.

24. An isolated nucleic acid comprising a nucleotide sequence at least 80% identical to a sequence corresponding to at least about 15 consecutive nucleotides of one of SEQ ID Nos. 1-503 or a sequence complementary thereto.

20 25. An isolated nucleic acid comprising a nucleotide sequence of SEQ ID Nos. 1-503 or a sequence complementary thereto.

26. A nucleic acid according to claim 25, further comprising a transcriptional regulatory sequence operably linked to said nucleotide sequence so as to render said nucleotide sequence suitable for use as an expression vector.

25 27. An expression vector, capable of replicating in at least one of a prokaryotic cell and eukaryotic cell, comprising the nucleic acid of claim 26.

28. A host cell transfected with the expression vector of claim 27.

29. A transgenic animal having a transgene of the nucleic acid of claim 25 incorporated in cells thereof, which transgene modifies the level of expression of the nucleic acid, the stability of an mRNA transcript of the nucleic acid, or the activity of the encoded product of the nucleic acid.,
- 5 30. A substantially pure nucleic acid which hybridizes under stringent conditions to a nucleic acid probe corresponding to at least 12 consecutive nucleotides of one of SEQ ID Nos. 1-1103 or a sequence complementary thereto.
31. A polypeptide including an amino acid sequence encoded by a nucleic acid of claim 25 or a fragment comprising at least 25 amino acids thereof.
- 10 32. A probe/primer comprising a substantially purified oligonucleotide, said oligonucleotide containing a region of nucleotide sequence which hybridizes under stringent conditions to at least 12 consecutive nucleotides of sense or antisense sequence selected from SEQ ID Nos. 1-1103.
- 15 33. An array including at least 10 different probes of claim 32 attached to a solid support.
34. The probe/primer of claim 32, further comprising a label group attached thereto and able to be detected.
35. The probe/primer of claim 34, wherein said label group being selected from radioisotopes, fluorescent compounds, enzymes, and enzyme co-factors.
- 20 36. An antibody immunoreactive with a polypeptide of claim 31.
37. A method for determining the presence or absence of a nucleic acid which hybridizes under stringent conditions to one of SEQ ED Nos. 1-1103 in a cell, comprising contacting the cell with a probe of claim 32.
- 25 38. A method for determining the presence of absence of a polypeptide encoded by a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-503 in a cell, comprising contacting the cell with an antibody of claim 36.
39. An antisense oligonucleotide analog which hybridizes under stringent conditions to at least 12 consecutive nucleotides of one of SEQ ID Nos. 1-503 or a sequence complementary thereto, and which ~ resistant to cleavage by a nuclease.

40. A test kit for determining the phenotype of transformed cells, comprising the probe/primer of claim 34, for measuring a level of a nucleic acid which hybridizes under stringent conditions to a nucleic acid of SEQ ID Nos. 1-4470 in a sample of cells isolated from a patient.
- 5 41. A test kit for determining the phenotype of transformed cells, comprising an antibody specific for a protein encoded by a nucleic acid which hybridizes under stringent conditions to any one of SEQ Nos. 1-4470.

Figure 1

SEQ ID NO: 1 GGTACATTGAATTACAAAAGGATCCAAGAATATTGAAATAGTTACCAAAAAA
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SEQ ID NO: 36 ACCATTNTATTTAGTGTGTAGGAAATGTTGGGTACTTCTTAAAAACGAAAC
CAAAGAAATCAAAGTCCCAAAGAGAAAGAGGAAATAATAATTCTATAATCCAAAAACGT
TGGGCGATCCTTCAATNGGAGGAANANGGCGTCANTTAANTAGCTCACACTGTANATNTGGANAC
ACCATATGGANATACGGAGTTAAGNTNGGTTGGATACTAGGAATTAANTTCTCCCCCTAANGCN
TAAATNTTTCAGNCTTGANAGATNANTNGTAGTTCTAGAAAAANANATAAAGTTTACTGNAGAA
NGTGGGAGGGAAGGACGGCNTGGC

SEQ ID NO: 37 ACTTTTTTTTTTTTTTTTTTTTTTTTNGANACANAGTCTTGCTCAGTTGCT
CGGTTGCCAGGCTGGAATGTCAGNNGGCAATCGCAGCTCACTGCAGCCTTAACCTNTGCGGCTC
AAACGATCCTCCCATCTGTTTTTATTCTGTAAANATGGTGTCTCACCATGTTGCCTGGGCTGATCTC
AAACTCCNNGGCTCAAGTAATCCTTCTCCTTGGCTTCCCTAAATGGTTGGATTACAGGTGGGAGT
CACTCTGCCTGCCCTGNCAAGTCTTTNCCATNAAAAACTTTTTATGTTTTTTTTTAAAT

SEQ ID NO: 38 TGAGAGGAAGTTCCATCGCCTAGGTTCTGGGAGAAGCAATACGTCACAATCC
CCACTAAGGAGAGGGCTCAGGCAAAAGAGGAGAGTGACATTGCCTAGGGCATGGGCCAGAGTT
ATATCACAATGAACATGTGGACAGGGCCAACGCAGAAAGTGTAAATGACCTGTGTGCTGGGCCCA
GAGATATGTACAGTTACTTTAATGGGCAAAGCCACATCAGATAAAAGAGGCATCTCAAATATG
TTGTAAGTTGATGAGCCCTGAGATATGTACAATGTCCCCCCCAGACAGATTCAAGGCAGGAGAT
TCACATCACCTCGGTGCTGAGCCCAATGAAATGGCACAGTGTCTCCTGAGTGCAGGGCCAAGGCA
AAAGAGCAACACCAACTTGGTATTGAGGCCAACCATATGCCACAATCCACTCTGGGAGCAGTTGT
CAGGCAGGAGAAAAGAGTCACAACACCTGGGTTATGGCCCAATACATATGTTACAATCTTGCCCA
TGGGCAAAGCCAGGTTGAGACAGGAGAATCACATTNAA

SEQ ID NO: 39 ACTTCAGCCTGGTGACAGAGGGAGAGTCCATCTCAAAAAAGAAAAA
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GTGCTCATTACCATCTTCTACTCAATTTTTTTTTTCTCATCCATAGTGAAATCTTAATCTTCAAAT
ATCATAGCCTAGTTTTTCCACACTGGCCAGCCCATCTTTGGCTTTTCTCTCACGCTTTCAACTAA
TGTAACAATTAGTCTGGCTATGGTCTAGTTAAGGAAGTAATTTGAACACGAATCCTCCAAAGTG

GCTACATTGTCTTTCTACTGTACACATATAAGAGTGATGAAGTGCATTGATTTTAAAAAGCTGGTG
AAATTTGGGGGCATAGTTCCATGTCAAGTAAAAAAATCCATGACTAAGTAGATTAAATATGTA
ATAAGAAAAATAGCAACACCGTATTTTAAAAATCTACTTCCTATGCCTCATTGCTCATTAATCAGGG
AAATTATCAGTAGATATTTATAAGTGAGGNATCTTATATTGGTTACTTA

SEQ ID NO: 40 ACGCGGGCAACTACGCTAAAGAATTTTGAGAACACCAGTGTGTCTACATTCA
GTTTGCTGTGCTGGTTAGGATTCTTTTCAGCAATAATTCTGCCTTGACTAGCCAGTCTACCTTTCCT
GTGCTTGCACTCTTAATGCTTTGTTTTTTGTTTTTAAAGGAGGAAGGCTAAAAATGTCAATTACTTT
ATCCCTACCAAAGTTCATCTTATGCCTCTTCAAATCTACATAGCTTATGTCTCCAACCTTATGTTCTC
CCATTCAACTAATTAATTAATAAAGCATTTTGTTCCTTTAGCTAATTTAAGTTTTCAAATAA
GGCCACAACAACAGGTCTCTGACAATCTCCAAATATCCTTGGGTTTATCACATCATCTATATTTTC
CAACAGGGACTTGGGCTCTACCAAGTATTCAGTATAAATCTTTGTAAAGTAAAAACATGGCCGGGT
GCAGNGGCTCATGCCTTGTAATCCACAGCATTTTNGGAGGCTGATATGGGCAGATCGCTTGAGCCCA
CNGAGTCAAGACCAGCCTGGGCAAAATGGGTGAAACCCCAT

SEQ ID NO: 41 ACTAAGGTTACAGCTGTTCTGTTGGTCTAGGCTCTGAGTAGACAGAGCCAA
GATACTGCAGTCACTGGGATGGAAAGATGGAGTGCCTCCTTGGCAGTTTGTTCATGGGGTTAGA
AGTTGTAGCTGCTCAGCTGCAGAATGGTGTGCTGCCATTAGTAGGTGGTGTAGTGGCAGTGAA
GCCTAGGGTATGGGAAGATACAGTGGCTATAGACCCCAATGAGAAGGCACCCTAGCAGTGGCT
TCAGTCTCAAGATGCCATTACACAGCAGCAGCTTGGATAATAGGGCAGGAGGAGACACAATGTGG
GCTCCTTGTGGAGTAACATAGTCATGTGAACCTCCAGGCAACCCCTCAGGCTGGGCTTAAGGACC
TGTGAGGACTACAGTGATCTCCATGAGCCAAAGATGTGGGTGTCCACATTTTAATTTTGATTGTC
TGAAAGGCCTTCCTGCATACCTTTCTNTTGAAGGAGAGTCCGCTTGGCTCTTGACCTNATNCC
ACTAGGANAGACNAGATGGTNAAGCAAAATGTTTCATTCCCTTTTTAT

SEQ ID NO: 42 GAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCGCCAGTGTGATGGATATC
TAGCATAATTTCCCCTTAGCGTGGNCNCGGCCGATGTACTGAANTATACTNGTCCNATGCTACAGG
AATTCTTTGGAATTTTATTACTATGNTTNTTCTAAGAAGAGGTATGNACCAA

SEQ ID NO: 43 ACGCGGGGACTGAGAACAGGGACAGGCGACCCGACCCCGAGGGCCCGGTG
CTCAGGACAGAGTAAAAGGCCAAGCTATGATAGCAACTGGTGGAGTGATAACTGGCCTGGCCGCC
TTGAAAAGGCAAGACTCTGCCAGATCACAGCAGCATGTCAACCTCAGCCCGTCTCCTGCTACCCA
AGAGAAGAAGCCCATCAGGCGCCGCGCCCGGCGAGATGTTGTGGTTGTTCTGGCAAAATCCGGC
TTTATTTCCCATCTGGTTTTTTTCTTATTTTAGGAGTGCTCATCTCCATTATAGGAATTGCTATGGCC
GTTCTTGATATTGGCCCAAAAGAACATTTTATTGATGCTGAAACAACACTGTNAACAAATGAA
ACTCANGTCATTCGGAATGAAGCGGTGTGGTGGTNTCTTTTTANATATTTGCATTCT

SEQ ID NO: 44 ACTGGTGTGGAGTGAAGCAGGGCCACTTCTATGGAGAGACTGCAGCCGTCTA
TGTGGCAGTTGAAGAGAGGAAGGCAGCGGGTGAAGTCTCCAAGGACAGGGCCTGCACCCCTCAGA
CCCAGAGGCAGGACTTCCTGAAGGCCCTGCCTGAGAGCTTCTCAATCAGTGTGCGCCCTATGTT
TGGCTGTAAGAGGCTGAAAGTGGAGAGTGGGAAGGGAGGGGACATTTAGGTCCTATATAGCCTCG
TTGAGCCCTTCAAAGGGACATCTCATATAAACATACCAACTAATTAATAAATAGTGGGTTTGCTATT
TAACCTCGGCATTNAGACAACCTCCCACTGAATGAGTGGCTCACACCTGTATCCCATCACTTTGGGA
GGCCGANGTAGGCANATCACTTAGGCCNGGANTTCAACACATCTGNTGACATGGAGAAAAT

SEQ ID NO: 45 ACTTTTTTTTTTTTTTTTTTTTTTTTGGNTAGTTTCTATGACTATGTCTAACAG
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TGTGTGTGATAGTAAAAAN

SEQ ID NO: 46 ACGCGGGATATGCTTGCAAATTCATTTAGTTAAATTAACACAGTCTTTAAAA
TCTCTAAATATTGATCTCCAGTTTGAAGAACTTTCTCTAAATAATATTATGCCAGAAATTTGGGCA
GCCAATTCATAGTCATGATATCTTCAAATATCCTAACCTTATCANCAAAATCTTTGTTCTTCCAAA
TTTAGCTACTTATTTAAACTACATAATGTCTTTTTTTCCTTTTTCTTTGCAAGNTNACATAATGT
NTTTTTTNTCTTNGCTACNAAGATGTTTNCCTATNTATGAAAGGNNCTANATTATTGCCAGTTGC
GGGTGGNTTA

SEQ ID NO: 47 ATGNGGATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGA
TATCTGNTGGAATATCCGCCTTTTCGAGCGGNCGCCCGGGCAGGTACAAAAGGAACTTGCACATTT
CNCAAAAAGCAATTTCACTTGAACCTCTGCTTAAAAAACTGNTTCCNANCANCGTNATGAANACA
AACCANTAAATGTTAATNAAANCTACAAGATTTATGGCTCTGAGAGAAATATACTGANTGATGCA
TCNTAANTATCCACAAATACCNATTAAATGNAATGTTTAATACTATATNAT

SEQ ID NO: 48 ACAAGTAGAGAATGCTTTACTTTTTTCCAACCACTGCCATCTCTTACTCTGAT
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GGAGCTGTAGACCGGAGCTGTTCTGTTCGGCCATCTTGGCTCCTCCTGCCAGATAGCTCTTATTT
TGAGCTCTGAAGGCTGAGAACTTCAAGATCAAGGCACCAGTAGACTCAGTGTCTTATGAGTGCTA
CTATTTGCTTCAAAGACGATGCCTTCTTGTCTAAATCCTCTGCAGAGAGTAACAGTGCAATTTGACA
TAAACAGCTCCTTGCCTATCTGGCTGCCAGCCAAGCTGGGTCTACACAAGTTGCTATAAGAGCT
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TATTAGTGGATAGCGTTGTTGGAATTCAAAAACAACATATTGCATAGAAATGNGTGAAGATTGCA
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SEQ ID NO: 49 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGCAATATTTAAAAATATAATTG
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ANATTTTAGGGGATTTCTATGCAAAACAATCATGTTGTCTGTGAATANACATGGCTTCATTTATTT
TCAATCTGTATGTCTTTATTTCTTTTGTCTTACTGCAANGGCTAGGACCTGTAGTGCAATTTTGAA
TATGAGNNGGGAAAGNNGGACATCCTCAGTTTGTCTTAATCTTACAAGGGGAGCATTTAGTCATTC
ACCTTTGAATATAAAGTTAGCTGCAGCTTTTTGNGGATCCCATTATGAGGTTGAGGAAATTCCT
TCTAAATNGTAAGAGTTTGTATCATCAACAAATGTAAATCTATCAAAATGGTTTCTGATCTATTG
ANAGANCAAAATGCTTTTCTTCTATCTGN

SEQ ID NO: 50 ACATTTACATTCTGTAAGAGATTGAGCCTGAACTCTCTTAGTCATAAAAAACAT
CAAAATGGCCACATGTCCACTACCAAGCTTCTCTATGTTAAAAAAATAATAAAGCAGTTTAA
CCTGAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 51 ACGCGGGGTATGGGGTTTCTTTTTGAGGTGATGGAAATGTTCTGGAATTAGAT
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ATTGTATACTTTAAAAATGTTGAATTTTATGCTATGTGAATTATATCTCAACTTTTTTAAAAAGAGG
CAACATCAGAATCCTAGAAATTGGAAGAGNCCCCTGAGAATTGTGTGGCCCAAACTTCAAGTCTTG
GCAGTTGAGAAATTTTAAAGGTTATGCAAGAAATNTGTCTTTAAAAATAAATTTGAAGCAGGTTT
CTCTCTTGCTTAGAACCCAAAGAGACTTGAGAAGGACAGCTGGCNTTAAAAACCTTTATGATCCCC
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SEQ ID NO: 52 ACGCGGACACAGGCAGTCACTAAAGGGATGGCAAAGACAGAAAGAAATCTT
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SEQ ID NO: 53 ACTNTGTGATCTTGCTGAAGACTACAGGCAGCCAANTGGTTCCAGATACTTC
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SEQ ID NO: 54 ACGCGGGGAGGCTAGCCAGGTGTGGTGGCTCATGCCTGTAATCCCAGCACTT
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TAACCCCATGTCTACAAAAAAAAAAAAAATTAGCCAGGTGTGGTGGTGGNACCTGTAATCCNAGN
TACTGANAAAGCTGAGGCAAGAGAATTGTNNGAACTGGGGAGGNGGCTNNACCAGGNGAGGCA
NANGTTGAA

SEQ ID NO: 55 ACCACTTTGGAATGCACTGACTCTTTAAAGCCACATAAATGTTTCAAGCCATT
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TTTTATCTTCATTCTTGGTNGGAAAAAATAAATCTATTATTGAATCTTTTACACACTNNCNTAA
ACNNTTTNGATTTTCTTATCCCTTACTTTCAANAATTTTATTAACNGGGTTATCCCTACATTGG
GATNATACCAACCCCTTGGGAAGGGGGGGNGCNTTGGCCANCCNAANCAACCNCATGGGGNANG
GGCAGNCTA

- SEQ ID NO: 56 ACCAGCGGATCGCANCGTTGCCATGAAATCTGTGCATTCAAGGCCCGTTTGGATGTGGGTAACTCAGTGGTTCTCAGGTGGGGAGGTATCATGATTACCTCCAGGGAATACTTGGCCATGTTTGGAGACCTTTTTGGTTGTACAGCTAGGGGAGGGGTGCTATTGGCATCTGGTGGTCAAGGCTAGGGATGCCGNTGAATATTCTACANTCCACAGGACCACCCGCCNCAAGAAGGNTCCCANCTGATATGTNAGGCTTGCCACNGGNGGGAAACCCCTNATTAAAGTATTAATAATTTGAANTACATNTNTNTTANTNCCNCGGGCTTTGTTTTTA
- SEQ ID NO: 57 ACAACCACTATGGGGAATAGTTTGGAGGTTTCTCAAAAACTAAAAATAGAGCTACCATAAGATCCAGCAATCCCACTGCTGGGTATACACCCAAAAGAAAGGAAATCAGTTTATCTAAGAGATATCTGCACTCCCATGTTTATTGCCAACACTATTACAATAGCCAAGATATGGAAGCAACCTAAGTGCCATCAACACATGAACAGATAAAGGATATGTGGTATATATACGCAATGAAGTATTATCAACCATAAAAAAGAATGAGATCCTGACATGAGGTCATTATGTTAAGCAAAATAAGCCAGGCACAGAAAGACAAACATCACATGCTCTCACTTATCTGTGGGAGCTAAAATTAACAATTGAAATCATGAAAATAGAGAGTAGAAGGATAGTTCTAGAGGTTAAAAGTNCCTCGGCCGACCCNTTAAGGCNATCCACNCCTGCGCCGTACTATGGTCCACTCGGACAANTGGGNATATGGATACTGTTCTCTGGGAATGTNTCCGTC
- SEQ ID NO: 58 ACGGCCAGGGCTATTNTTGAATGAGTAGGCTGATGGTTTCGATAATAACTAGTATGGGGATAAGGGGTGTAGGTGTCCTTGTGGNAAAAGTGGNCTAGGGCATTTTAAATCTTNANCGGAAAGCNTATANTCACTGNCNCCGCTCATAAGGGNTTGNCTTGGCNNGGTTTATATATAGTNGGGGGTTCGCTGTAATTNAATGA
- SEQ ID NO: 59 ACCTAGAAGAGAGGCGNTTCAAAGAAGTAGTGAAGAAGCATTCTCAGNNCA TANGCTATCCCATCNCCTTNTTNGGAGAAGGAACGAGANAAGGAAATTANNGATGATGAGGCTGAGGAANAGAAAGGTGAGAAAAATGAGGTAAATCNTTATTGATTGATGAAAANCCAAAAATC
- SEQ ID NO: 60 CGCGGCGAGCTATCNTTTGAATANTGAGACAGAAATNAATCAATATAGAGGCTGTGCACGGTGGATCACGCCTGTAATCCAGCACTTTTGGGAGGCCANAGGCAGGTGGATCGGACCATNCTGGCTAACATGGTNAAACCCGGTCTTTACTAAAAATACAAAATTTNCTGCNTGNGGGTACCGGNCACNGTAT
- SEQ ID NO: 61 ACGCGGGATCAATAATGGGTCTGATATAGACTGAGGATTCAATTAACCTCACATGCCTCCAAAAAGGCAACCTAGAGTCATGACTAATACATGGAAATTGGTGCCTCCACCCGAGCTGACCCCTTTGGTCTCTTAAGAAAAGAACTAGAACTTTTAAAGGTCTGAGATCAAGATCTTACTTTTTTTGTTTAGTAAGTATTTAGCAAATATTTTGAATAATTTTCCATGAGAAGCATGAACATGAGCTACATGTTTGAAGTAAAGGATGTAATTGTAGCTTCCACTTGCCTNTCAACATGGAAATGCTAGAAGTTTACTTACAGGGTTCAAAAACATGTATACAGTCATCCCTCTGTATCTGNGAAGGATTGATFCCAGGACCTTTCACGGATACCAAAATCTGNANATGCTNAAAGTCTTTGACATAAAATTGGCATNTNNTTNNCATATNNACTTATGCNNNTCTCCTATATTACNNNTANNATTTNTCTACATTACTTATTTTACC AAANNCAATGTAATAAGTTCTTTAACTGGCATTGGNTTAAGGGGAACNAC
- SEQ ID NO: 62 ACGGGGGAGACTGTGGAGCANTTATTCAAAACTCGGAGGGAGTGGCATGGGAGGATCCATATAATTTACGCTAAATTGTGCNCGTCTGTTTGTGAAATGTGAAGNGCACATTGT TTTTCTGGAAGGCAAATTTCAATTNTTATACCACCTTGCCAGAAAGATCTGTGATCCCAANGAAC TGCTGTGTTANAAACAANGACAATCATTTTGANGCAANAAATGATGGTTCCAACNAGGGAGGGAGTAACCATGGATATTGCTGAAATGCAGTTGGTGCCAGGGATTATTANGACATGATTAGTTCTGNAATCATCCCTAANGTAGCGATGAAGTCTCNCTATGTTGCCAGNCTGATCTCAAACCTCCGGCTCTAAGTGATCTCCACCTCATCACTCCCAAANGTGCTGGGAATTAAGGCCCTGANCCATTGTGNGCCAAACCTNAC
- SEQ ID NO: 63 GGGGACTGAGAACAGGGACAGGCGACCCGACCCCAAGGGCCCGGTGCTCAGGACAGAGTAAAAGGCCAAGCTATGATAGCAACTGGTGGAGTGATAACTGGCCTGGCCGCTTGAA AAGGCAAGACTCTGCCAGATCACAGCAGCATGTCAACCTCAGCCCGTCTCCTGCTACCCAAGAGAAGAAAGCCCATCAGGCGCGGCCCGGGCAGATGTTGTGGTTGTCGTGGCAAAATCCGGCTTTATT CCCCATCTGGTTTTTTTCTTATTTTAGGAGTGCTCATCTCCATTATAGGAATTGCTATGGCCGTTCTT GGATATTGGCCCCAAAAGAACATTTTATTGATGCTGAAACAACACTGTCAACAAATGAAACTCA GGTCAATCGGAATGAANGCGGTGTGGTGGGTTGCTTCTTTGAGCACATTTGCATTCTGATAAGATGAAAATGCTTGCCCATTCACCATGGGGATTGGCATTTTCAATTTTCAATTTGTGCTAATGCCATCTTCA TGAAAACCGTGACAAAGAGACAAAATCATACCATGAGGGATATCTTTCCAGTCATTGACATTCACACGCTAAGAATAAGGAGCAAAGCAAATG

SEQ ID NO: 64 ACGCGGGGCGGTCGAAAAAGAGATAAAGTTGAAGGAAATAAAATTGGCAGC
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TCAGAGCGTGTGGACCCCAACAANTCTGCGCAAAATTTGTCGAGGAGGTTTGGCNCGGCAGAAA
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TGAACANTTCANGAACCNATGCTTGAGAAAAAGAAAAANTCTNTCGAGCAGCTTTCNGATCTANAA
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SEQ ID NO: 65 ACGCGGGCACCACGATGAAAGGGCACTGGCAATGGGAATGGCATCTATAGT
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GAGATCTGCACTCCAGCCTGGGCAACAAGAGCAAACTCTGTCTCCAAAAAAGGAGGAGGAGGAGG
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SEQ ID NO: 66 GGGACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGANACANAGTCTCACTNTGTT
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GNGATCTGCCCNCCTNANCTCCCAATGNGCTGGGATTATAGGCGTGAGCCACCGCAGCTGGCCC
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SEQ ID NO: 67 ACTGAAGTCAAAAACAGCACATGGGCCTTGACGATCTGGGGTGACGCAAGC
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GAGATAAAAAGCAGGCGGTTTCATGATAACGAGCTTCTTTTTTGTGTAGGATGATGATGCAAGT
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GCTCATCCGGATGAGGGACTCACAGAGACAACTGGCACATTAACAGATTGCACTGTCTCTTCCT
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SEQ ID NO: 68 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGGGACGGAGTCTCACCGTGTGCCCA
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ATTACANGCTCAATGCCNCCACCCCAAGNTAACTTTTGTNTTNTCCNCCANNTTTNGNTCAAGG
CTGGTNTTTNACTCTNGCCCTGGAANTNCCCCACCTTTGGC

SEQ ID NO: 69 ACTTAAAGTAATGGTGATCCTTATTCCAGGGCTTCGCCGCCAGGATTTCTTGC
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CCCANGGTTANTCTGGGCCATACCGNTNCACNGACGCCGCTCTCGATCGAGGAAACNGA

SEQ ID NO: 70 ACCACCTTCTTAACACAAATGATTTAATTTAACCATTAAGTCAAGTCTGCAAT
ATCAATATCATCTTGCTCATTTTACAAGTCACAAAAATGAAGTTCAAGCAACCTTAGTTTGGAGCT
GGTATTAACAACTGAGGCTCGTCAACGTTAAGTCTGTGTTCTGCCCCAACAGGCAGTATAGTCTTA
CAAAGACATTCTTTCTTCCAGTCTCTGAATATTCTGAATTATCACAAGTTAAGTGACTTTGATGT
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SEQ ID NO: 71 GGCATGCTCNAGCGGCCGCCANAGTGATGGATATCTGCANAATTCGCCCTTT
CNAGCGGCCGCCGCCGNCAGGTACGCGGGGCCAGGTCTCTNACTTCTGGCTTGTTCGCTGGTGGCG
GTCNNANCCGAGCCGGACTGGTCANAGATGATCACGGACGTTTCAGTTCGCCATCTTNNCCANCAN
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SEQ ID NO: 72 ACTTTTTTTTTTTTTTTTTTTTTTGAANAATGAGGTTTTGCCATATTGCCCAGG
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GAATGACCATGGCACCCAGCGTAAATGTTTCTTTTCANACTTTTAAAGGTGTCAAACCTGGCTGG
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CTTNTCTTCCAAGTTTTT

SEQ ID NO: 73 ATCTTTATATTATTTNCTTAAATTGATTGGGCCCTCTAGATGCATGCTCGAGC
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GGGTAGGGAGGGGGACCAAGTGGCAGAGGGACCTTAGGTGATCCTTANAAATAAAGGCTAGTTTTCT
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TAAAGCAAGAAGTTGGAGAATATGAGATACATCTCATCTCTTTAAATACTTAAATGACTTCCCT
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ACTTACANACTAAACTTG

SEQ ID NO: 74 ACCAGCCCAGAGAGGCTCTCTGCTACCTGACTTTCCTACTCTATGGTAATGT
GCAATTTCTCCCGCAACTGAACTACAACAGAAGTTTAAATGTCTAGCCTACAGATAGATGTTTCCA
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TTGCTCTATTCTGCATTAGGTACGCCAAACGCTTCTGTCAAGACTCAGTAACCTCACCATACAT
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ACCTNCTTTAAATNTGGTTTTTTCATTGGTTAGG

SEQ ID NO: 75 ACTNTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGGGTGTTGTTTCACTTCTTGGN
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CTTGNGCTTTTGGNGTCATATCTAAAAAACCATGTCTATTCCAAGGNCATGAANATTTATACTCA
TGTTTTCTTCGGAGTTTATACCTTTAGCTTACATTTAAGTTTTTGATGCNTTTANAGTTAATTTT
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ATATATCTATGGGGTAATTTCTTGAGCTTTTGCTTTATTCCANTGATCTACNNGGCTATTCTTTNCA
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SEQ ID NO: 76 TTTCATTTTGTANGCATTTGGGCCCTCTAAAGCATGCTCGAGCGGCCGCCAGC
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CTNTGNTATCCTGNGGAACACACAACATTACAGTGAANCCTCTGTGAAAGATGCCAATGGTNTA
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GCCNTAAACAANTTTGNNATTTTNTATGGAAATAAGGTTTANAGTTTACA

SEQ ID NO: 77 ACTTAAATGTAGTAGATTCTATGCCTATGCATATTTCCCAAATTTGTAAGTG
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AGAGGAGACTAAAGCACCCCTCCAGGCACAAATTAACCAAGTTCCCAAATAAACCTTTTACCAAC
TCACTATGACAAAAGCATAGATGAGAGAAATAACAGCATGCCAGTTCAACCGAGTCCATAGGTGA
GTGTAGCTGCTCANTAAGTGTGGTTGATTAAATTAAGGGTGACTNAAATCCATGCCCAAACCTGAG
TCCTTACNAAATGCCCCATAAAATTTAAATTTAGAAGAGTTAGTAAAGACTTCTTGAATACTAA
CTGCATGGAGATACTACACAAAACAGTCATNTTAATTCCTACANCCTTCANAACAAAAGAGTCC
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SEQ ID NO: 78 ACCTTTTTTTTCTTATTTAAAGCACAAAGAGGCCCATAAATCTTGAGTTACTTTA
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SEQ ID NO: 79 ACTTTTTTTTTTTTTTTTTTTTTTTTNGANACATGGTCCCGTTCTGTCAACCCAGG
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SEQ ID NO: 80 ACGCGGGGATTCTGAAGCTGGCAGCATTCCGGCCGAGATGTCTCGTCCGT
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NTTCCATTCTATTCCGAACCTCGGCGCGACCAAGCTAAG

SEQ ID NO: 81 ACAGTTCCCATCACGTATGTCAGTTTTGTGTATGCAGCAGAAATGATACCTA
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SEQ ID NO: 82 ACGCGGGGACATAAAATNTNCTTTAACGCATTAAATAAACAGAAATCATAC
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CAAAATTTGGAAATAAATATATCTAAATAACTCATGGGCCAAAGAGGGAGCTAGTGTAAAAAC
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SEQ ID NO: 83 ACAAGGAAAACTACAAAATATGTATGAAAGAAATTGGAGATGACACAAACA
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CGTGGTTTGATTAAAAACAGACNCTTCCCATGGAACAGAATAGATACCCAGAAATNATCCCTT
ATTTAGCCAAACTGATTTTACAAAGGCATGAAGACATACATTAGGGAAAAGACCCCTTCAA
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SEQ ID NO: 84 ACCGCCGGGCANGTACNCGGGACCATACCATATCCACCAGAGAGTGACTCC
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GCTGCTTC

SEQ ID NO: 85 ACGCGGGAAGCGTGAGCCACCGAGCCCGGCCACAATGTGTTTATATACACAA
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CACCGTAGAATCTAAAAATAGTCAAAATCATAGANAAGTANCATGGTGATTTCCTGCGTGTTA
ATTACCAATCTTCCCATATAGGTAAATCCATATGGCACAACTGCCCTTACTTGNAGAGCCACCNCA
CCCTGTGNCATGAACTGNAGGTGTNCTTCCATGGTTGCTTGCCTANTCAGGGCCTGTATCTCTTC
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AAANG

SEQ ID NO: 86 ACGCGGGGAAAAATGGGGAGCAGGAGGCTGACAATGAGGTAGACGAAGAA
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ATGTCGATACCAATAAGCAGANNACGNCGAGGATGACTAGACAGCAAAAAAGGAAAAAGTTANA
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CCAANCTTGATATTCNCAGGGGANGAANANACCAAANTTTCAGGNCNTNTTTTTTAAANNCTT
GNCNNANNCNTNTGCNATTTCTNCNTTGGCNCNTNTTTTGGTTCCNACTTNTCCANCTTGNNTTAT
TGTTATTTTNTTTTTT

SEQ ID NO: 87 ACTCTGTATACACACATGAGAATGACAGTGACAAAAGGCAAATAATGTCTTAG
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AGGGTAAGGCAGAGTAGGTAGTTGCTCTATTATGACTTTTCTTGGTTCAAGCAAAATAAAACCGC
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SEQ ID NO: 88 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGTGTTTTGANACANAGTCTCA
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SEQ ID NO: 89 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTNAGAANANATGGGGTTNTCCATGTT
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SEQ ID NO: 90 ACGCGGAAAGGGACATTTCAAAGCCTATTGATGCTTGTAGTAAAAACCTTA
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CACAGAGTTTACTTCTTCTTTGATTCAANAATGTTGGAAATACTTCTTTTTGTAGAATCTATGTGG
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CATGCGATCTGTGAAGATACATCTTCACAGATTCATCTGTGGATTCATCTACAGAGTAAAAAGCTTT
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SEQ ID NO: 91 GAGTCTAGCTCCACCAAGCAGTCGGGCCTGCCTCCTGCAAAAGAGGGGAAAG
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TGGAANAANAAAAGGANAAGAATCTNTTTGNA

SEQ ID NO: 92 CGTGGCGCGGCCGAGGTACTTTGACCAAAAAATTGACCAAAAGTAAGAAAAAT
GCAAGTTCTAAAAATAGACTAAGGATGCCTTTGCAGAACACCAAAGCTTCCCAAAGGAAGTGTA
GGGAAAGTGGCCCCCTGTCTCCTGGAAGTGGNAANAAGCCTGCTCCCTGGCCTTTGGGTTGCTT
GGGGGCCACAATAAAATAANTNTTTGGCCCCCNNTTCCAGGGNCAAAAAA

SEQ ID NO: 93 ACTTTTTTTTTTTTTTTTTTTTTTTCAANATGGAGTCTTGCTCTGTACCTAGG
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CCACCCGCTCGGCCTCCCAAAGTGTGGGATTACAGGCATGAGCCACCATGCCTGGCCAAAGTT
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TCTGTATANATNAAAAAATGGAAACTGANACCCGNGTACCTTGGNCGGGACCAACC

SEQ ID NO: 94 ACTCCGAGGCTTTANATTNATTTTGGGTCTTTGGGGGGGACCTNTATCATTAC
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GGCTTTATAAGCGGCCCGCTTCTTTGAATNNAATNATCCTTGCAAANACCCATTGGCAANTGNTT
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AATCCNATCCC

SEQ ID NO: 95 GCCGTGGCGCGGCCGAGGTACTTTTGATATTAAGGCTAATTTTTAAAAACCC
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SEQ ID NO: 96 ACTTNTTTTTTTTTTTTTTTTNGGACAATTGTTATTTAGTTTTTATTTCTATAA
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SEQ ID NO: 97 ACAATCTTACTATCTTTCTTTTCAGTTTGTGCCTTTAATTTCTCTGCATACTCC
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SEQ ID NO: 98 ACTTNTTTTTTTTTTTTTTTTNGCGGTGCCTCTAATACTGGGTGATGCTA
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SEQ ID NO: 99 ACGTGTCTAAGTTCTAGAGCCTCCTGACGTGAGCATGGCTGAGAGTGAGGGA
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CANGGGTTTTGAAACCAAGGGAAACCTGGANACCACCTTGAAGGAAATTAAGCGGTTNATTATN
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ANAAAACCGGTGCATTGATCAAGGGTNTNTTGGGAANTNANTCATGAACCATGGTCAATTTGGTC
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SEQ ID NO: 100 ACTACCTGGGGGGGTTGCTTTCTGCCTTTTCTCTGTTGGTCAACATCTTCT
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CNNTGGGNACCCANTGAACAACCTTTCTTACATACTGGGGGCCCTTNTTATTCCNCCAANGANA
ATCNTCT

SEQ ID NO: 101 ACGAGTGGTGGAACAACAGTGCCCTGGGGAAACAGCCCATACCATCGGGCTCCT
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SEQ ID NO: 102 ACACCCGCACGAGGAGCGGGGACGGCGGGCGCAGAAGTGGGCCACCATATC
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TGANCGTCAGCTGTGTGAAGTCTCCAAATTAAGTTGGGNTGTTTCTCTACCTTGTCTTTCAANTT
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AGCAACNAGTTTGTGCCANATTTGGNAAAGNGTCACTTGTGAAANTANCTNTCCNGGANCAAGG
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GGTT

SEQ ID NO: 103 TNGATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATAT
CTGCAGAATTCCTCCCTTGAANCNGGCGCGGGCAGGTACAGGAAGCATGGCTGGGGAGGCCTCAG
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GAAATTCTTTATGGTGACANGTAGCCGTAAAAAATAACTGCTTCACACTGACTTGTATNCCTTT
TGGGTGGGGGTANGGGT

SEQ ID NO: 104 ACNCGGGCACTCACAGACATGACACACTCACAGACATGACACGCTCACAGAC
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ACGCTCACAGACATGATGCACTCACAGACAGGACACGCCCANATGCTACGCACTCACAGACGTGA
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SEQ ID NO: 105 ACTTTNNTTTTNTNTTTTTTTCTTTTAAAAATTTGAACACATATTTNATAATTT
GNGATAATGGTTTTGNGGCTAACTCNAAAAANGAACGGCCCAATCTTNAAGTCTACNCTGA
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SEQ ID NO: 106 ACTTTCTATGANAAGCGTATGGCCACAGAANTTGCTGCTGACTCTCTGGGTGA
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NAGGTGNTCTTGCCCATGGCCGAGTCTCCTGTACTGATTAAGGGNACT

SEQ ID NO: 107 ACAAACAATGNTTATTTGTTGTAAAGTGCCAGGTTTATATTTANNTAAACAT
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TAATCTN

SEQ ID NO: 108 ACGCGGGGCTCTTTTCCGGCTGGAACCATGGAGGGTGTAGAAGAGAAGAN
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SEQ ID NO: 109 GCGTTGGGCCCTCTATNGCATNAATCGAGCGGCCGCCAGTGTGATGGATATC
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NCCAGCCTCAACCACAATTCTTCCATGCTGGGGCTGATGTGGGCTAGTAANACTCCAGTTCTTANA
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SEQ ID NO: 110 TGGGCCCTCTANAGCATGNTCGAGCGGCCGCCAGNGTGATGGATATCTGNNN
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SEQ ID NO: 111 ACCCTCCAGAAAATTGGTGACTTINCTTTTGTGACTGACAACACTTATACTAAG
CACCAAAATCAGACAGATGGAAATGAAGATTCTTAAGAGCTTTAACTTTGGTCTGGGGTGGCCT
CTACCTTTGANNITCCTTCGGAGAAGCTTCTTAANATTGGAGAAGGTTGGATGTCAACCAACANTA
NTTNGGCCAATTACTTGANGGACCTANTTATGTNGGANCTTTAACAANGGNCNTTNTCTTTT
TAANATNGNACAAAGGACCTTTTNNCTAACNTTNAAAATTNNGGNTANTGGGGGAT

SEQ ID NO: 112 ACITTTTGGGTTTTTTTTTTTTTTTGTATAATCTATTCATGGATCTCCACTTT
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SEQ ID NO: 113 ACTTGCCCTTCCCCAGAAAAGCGGGACTTGCTGCTAAGGGTGAAAGGACCA
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TTNGTTCNACGATTAAAANCNGTTTTNTTTGGCCTTTCCANAANATNAAATGGANTTTGTNATTA
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SEQ ID NO: 114 ACGCGGGCAGTCAAGCTGGTTGCTCTGAAAGTAACCCAGCTTGTTGCTCTAA
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SEQ ID NO: 115 ACTTTTTTTTTTTTTTTTTTAAAGCAACCACATTTTAATCAATAAATATGAA
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SEQ ID NO: 116 ACTTCTTGTGTTAAGTATTCAGCCACTGTTTTAGATCTAGTTAATAGGTTCT
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NANGTTGGG

SEQ ID NO: 117 ACTTTTTTTTTTTTTTTTTTNNTTTTTTTTTNGCATCAAAAAGCTTTATTTCCATT
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SEQ ID NO: 118 ACCACTTGAAGCCAGAATAGTTNGNTTATGTGAAACCACGGGACCGGAA
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GCTACGGTCTTTATCCNCAGAGCCGGTGCTAAAAATAANAC

SEQ ID NO: 119 ACACTTGATTGAGATTCCACCTGGGATTCGACAAATTTTTCTTTTTTGT
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GAAATTCCTTTCTTTGTCCTTAAATCAAAAACCTTTCCAAAGGAGCTTCCAGGCTGGTTTGG
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TGCCTCAATTTTCTTTTCTTTTNGGGGAAGATCTTCTTTTGTCTCACTTTGCTGATCCGCTATC
ANAGTTCCGCTAAAATATGTCGATTTAAGGATANGCCTCTGAATATCCTTCTGACTGCTTGGC
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GGGCTCCAAGGCCNCGCTCTGGGCCCGGACACNCTTAAGG

SEQ ID NO: 120 GTACCTCAAGGTTCTCAGGACCTCCTTTCCCAGATCTTAGGGTCTGCCCTG
TGGGTCTCCTGTGTCCAGGGGAGAGGATCTGGGAGTAAAAATTGTGAAGTGGCAAATCCCTGTA
CCCGTTTNTTGGATTTTCCAATGAAGGGCTGTCTCACATCCCACCTNCCACTAGGGTNAATGAG
AGGA

SEQ ID NO: 121 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAATTTTTTTTTTTTTTTTTTAAAC
CTTCTCCAGTTTCTGTATTTTTTAAGGNNTNAAATACATTTATTTAANATTTTCTAATNTATAC
ATTTGCTACGGAAAAATTGAAATCCGCNCACTGAAATATCCTTTTATTGCAACTNAAATTTCAAAA
ACCAAAAAATCAAATTATTTATGCTCTANCCAAATTATGNAANGGTTCTTTTCTTTTNTGTCC
CCAAGCTGGANTGTANTGGAACAATCANANTTCACTGGANCATNNGCCTCCNNGGCTCAANNAN
NTTANTTGTCTAACCCCCCGAGTNGCTTGAANTANCNGGTGAACAAAAACCACANCCAAGNTTA
TTTTTTATGTTTTTGNAAAAACGGGGCTTTGCT

SEQ ID NO: 122 ACGCGGGTGCCATCCCTCCTCTTCTGGATTTTTTTCTTTGACCATATCAAGC
TGAAGAGATGAACCTGTTTTCTCAAACCTTTGCATCAAAATTAAGAGTAAAAACAATAAAGTAAT
ATCAAATGAGGCAGGCCAACTAAAAACAAGAAATAGGTAGAGAATATTGACTCTCCGCCGGGCAT
GGTGGCTCATGCTGTAAATCCCAACAGTTTAGGAGGCTGAGATGGGCAGATCACTTGGAGNCAGG
AGTTCAAGACCATGCCTGGCCAAACANTGGTTGAAACCTTGTCTCTACTAAAAAATACAAAAATT
AGCCAGGCGTGGTANTGGGCCCTGNAATCCNAGCTACTTNGGANGCTGANGCAGGA

SEQ ID NO: 123 GTACTCTTNTTATACNTAATCTGGNGGATANCTATTTAATTTATGTTATTC
AATTCATATCTTCNGTTGNTTCNAAAAAAGTANTTTACTACNANGTATATATTTAATAAACNT
ATTAATTATAANTTTTTNGNATTTAA

SEQ ID NO: 124 ACTTTTTTTTTTTTTTTTTTNTGGGGAAAAATCCTTTTCTTTACAACTTCCAT
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GCCCGGNTTACNAATGAGCCATANTATGNNGGACTGAATACCNACCCACGTGAAAGANNATCA
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NNTANTCC

SEQ ID NO: 125 ACTTTTTTTTTTTTTTTTTTGTATTNNGGCTNCCTTAAACAGTTGGACCTTC
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CAATTGAATATGGGTTNGGNTTAAACGTTACTATTTGGTTTNTTGAATCCGTGTTTTNTTCNAN
CATTTTCCTTTTTTTAAAGCCTTATTTGGAATTGNNTNTTCTTNNAAATTCNCTTINANCCTCNCCN
NAGGGTTNGGTACCAAAAAAT

SEQ ID NO: 126 ACCCTTGCTTTCTCACATCATNAGATCAAGTCACTCTTGTGCATCCCTTCCT
GGCTGAGCGCATCATTTCCATGTTGAACTACTTCTGCAACACCTGGTTGGCCCCAAGATGGGNGC
CTAAAAAGTANAANGACTTCAGCATATNTGANNTCAACCNAATCTGTANGTATCAGATATCTGNA
CTTA

SEQ ID NO: 127 ACAGTGTGGCTCATGCCTGTAATCCCAGCACTTCGGGAGGCTGAGGTGGGAC
AATTACTTGAGTCCAGGAGTTTGAGACCAGGTTGGGCAATGTGATGAAACCTGTCTCTACAAAA
AATACAAGAATTAGCTGAGTGTGGTGGCACATGCCTGTANTAGCCACAGCTACTTGGGAGGCTAA
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CCAGCCTGNGTGACAGAGCAAGACCCTGTCTTAAATACANTNAAAAATNAAAAAANATNNTT

SEQ ID NO: 128 ACACGGCAGTCTTAGAGAAGCAAATGGCTCAGATGATGATAATTAAGAGTAG
CCAACATTAAGTTAATTTTAAAAATACAGTTAGGTGTTTATATTATTAGTTATTATAATTCTGC
AATCCTCTTGCTCAGGAAGTGATACAACTTTTTTAAAAATTATACCTGTTATTATTCTACTTCTCT
CTTCTATGACAACTCTAGTGCAATATTAGAGTTTCATTTATCCACAAATATATTTTACTGTTTTTT
CTATTTATCTGGCTTACTAGTAAGTCTTTTAGATTAACATCCAGTTCATTTCTGGAATATACC
TGGAATTTAGTCCATTTCTAATGAAAAACAGCTCAAATTTTAGGGTAACTAATTTGTAAAGAGTT
AACATTATATTGGATCCAATTTCTGANATATTGAAATAGTGAAATCCCAATAAATGATNTGA
ATTATTTTACTTTCAAATGTATANTTAATTGCTAACATGTTTTATTTTCATATATTGNTG

SEQ ID NO: 129 ACAGTAGAAACAAGCAGAGCTACTGATACTCTCACAGCTCATTTCAGTTTGTG
TTCCTTATCTGTATGAAAGGGGACCATAGAGAGAGGTTGAATTAGTTTCAATACAGCCCTAAGCAC
TTCTTATGGTGTTTTTTGAATTACTGCTCAACAGTTTCAGTCCAGTTAAAGTAAATAAGCAAATTA
ACGTAAGAGAATGAACTTGGCAACACCTTAGATTATAATTCTGATTTTAACAAATCCATTCTATT

AATGCACATAATATTGATACTGCGTTGTAAACATTTAGGCCCGTAAAAATTACTGAAGGACTGTAGA
ATGAAAGAGAATCNCANAATAAACTTAAGGTTANAGAACACTTAATGTTTCCTGCCTNAAAGTGNG
ATGCTATACTTGCAAAATNTTATTGNGAGGNAGAAATATTATNNTTNAGCATATAACCATTTGTTN
TCATT

SEQ ID NO: 130 ACTTTTTTTTTTTTTTTTTTTTTTTTGGGANANACAGGGTCTTGCCACTTTGCC
AGGTGGTCTCAAACCTCTGGCTCAANANATTCTGCCTTGTAATCACTGANCAAAACCCAGC
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ANANATTCTTTTTTTTTTTTTTTTTTTTTTTTNGGGAATGGAGNTTACTNNTTGGCCAGGCT
GGAATGCAGNGGCAAAATCTCGGCTCACTGCAATNTTGCCTCCCGGGTTNAAAACATTNTCTGTC
CTAAGCCTCTGANTAGCTGGGATTACAGGNGNGCNCACCAACCCAGCGAATTTTTGTNTTTT
TTTAGTAAAGTCAGGGTTTCCCAATNTTGACAGGCTGGTCTCAAACCTCTGACCTTNGATNTGC
CCCCCTTATTNTCCCAAAGTCTGGGATTACAGGCGTNAGCCACCGNCTGGCCAATATTNCCGC
NCCCTNCCGGGCGGNCGTTTAAAAGGGCAANTCCANCACTGGGNGGNCNTTNTNGTGGATN
CNANCINGGTNCCAACTTGNGGTAANNATGGGGNATANCTNGTCTCTGTGNGAAATGTTTCCC
C

SEQ ID NO: 131 ACTTTTTTTTTTTTTTTTTTTTTTTTGGGAATGCAACAACCTTTATTGAAAGGAAAGTG
CAATGAAATTTGTTGAAACCTTAAAGGGGAAACCTTAAACACCCCNCTCANGCNCANGACCAAG
TGCAAAATGGACTCTTTNTGGATGTTGTANNANACNTGGTGCANTCNTTTCTAATCTGATTCTTA
AAATTAATCAACCTNTGCTGATNAAGAGGGATNCNTTCATATATTTANNATNTTTAGTNTTGANT
TTTTAAATGGTNATNATT

SEQ ID NO: 132 ACCTACATCAGATCTAACCTTGATCCCAGCAATGTGGATTCCCTCTTCTACGC
TGCCAGGCCAGCCAGGCCCTCTCAGGATGTAGAGATCTCTATTNCAATGAGACCAANGATCTG
CTTCTGGCAGCTNGTCANTGAANGACTCATNCTGTTNCCNGATCTACCATCCANTANNNGCTNTT
AAGGGGCTTNGGCCCTTTNNNANCTATCTCANTAANCNCTCATGTGNCNTANTCTGATCATGTTAT
CTANGA

SEQ ID NO: 133 ACAAATGTTTTTTTATTCAAANGTNCAAAATAAAATTATCTGTAGGCATGGACA
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AGCCGCCTTTTCTTTATTTNTCCAACCTGACTTCTCTGAAAGTTATTGGTGAAGGAACACTGCCTT
GGCCTTCTGCANANNTCATTAAANTAAAGNAAANCCTAGCNANGAGNTTAAACATGCCACNTC
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NNAC

SEQ ID NO: 134 ACTTTTTTTTTTTTTTTTTTTTTTTTGGGGATTANTAAAAATAAATGTAT
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TTAAGTTCTATATAGGCTCCCTCTCTGTGCTTCTGTTTTTGCAAAAACCTTGATTAAATTTATTTCCCT
CAGCACCTGATCCTTGCCCTTGACCCACTGGCCATTTTGGATNGGACCACTGATACANGTTGGA
CCAAGTTGGTTGCATTAATCNATTAATCTCTGAACTCTGGCAATCANCAACCATCANTCTTTTTN
TTTTTACAAAAAATACCAACCCATTTCNCCAAATTTCTTNTTGAANCCTTAAAAGGCATATTTTCC
ACCGTTTATNCTATTTCTTAATAGGCCTTCTTGATGAAACCTTGAAATAATCTTGNGGAATCNTG
NCTCAAACCTNGGGCAAAAAACAAAAATTGAGGGCANTNAACATGCCCTGNGCNTGNTTATACATA
NTCCTAAAAAATTTCTCCNTAAAAANANTNGGNGGCCAAAAATTTNCNCCCTTTTTTTGGGAA
ATTAATTCNGTTATAT

SEQ ID NO: 135 ACATAGTAACTGTGGGTATTCAGGGAGATAAAAGTTTTTTGTTTGTGTTT
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AACTCCATTTGATTCTGACAACCTTCAGAAGCCTTAGGAACTAGACAGTGAATTATGGGATTT
GCTCTTAGCCAGTTGCATTTTATTTGAACTGGCTTTAGCAATGAGCACTAATGAAAATTAGCCAC
TGCTGTGGGTGAGTGGCTCATGCCTATGATCCACACTTTGGATCACCTGAGTCAGGATTTCAA
CCACCTGCCACATGGNAAACCCCNCTCTACTAAAAATAAAAAATTACCCGGCATGGGNGGTGGAC
CCTATAATAGCCACTACTGG

SEQ ID NO: 136 ACCTTTTTTTTTTTTTTTTTTTTNGGTAAACANGGCGGGGTAAAGATTGCCGA
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ATGACTTGTGTTGATTGGAAATATNGGGCTGNAATTGNCAATCCAGTGTTTATAATCTGACCC
CANNCTTATCCGNAGGANAATTCTNNNATTGNTACTTNTACACAAACACAATTNANNTTATNAG

CATCATAAAATCGNCCCA

SEQ ID NO: 137 ACTTGACCCACAGCCGTCNGGGATGAGCCGCTTCTCAGCCACCATGTCTTCA
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TGAANACTTGTG

SEQ ID NO: 138 ACACAGCTGTCAGGGAAAGTCCTGATGGCCACAGTGAAAAANGTCATGGTTN
GACAAAANATTTCATNGCANCITAGCATGGNTCANACCAAGTNTCNTACNTAAATNNCTAGNTCNCA
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SEQ ID NO: 139 ACGCGGGGGCGAAGGCGGGGTCGGCGCTGCCGGGTGAAATCGTAGGACAGT
GAAGATGCTGCTGGAATTGTCCGAGGAGCATAAGGAACACCTGGCCTTCCTGCCTCAANTGGACA
GCOCGGTGGCTCCAANTTTGGCGGATTGCGTGGANATTTNTGAACTCTGGCNNAACNCAAA
ANTNTANTGAAGGNNCNTCCTGAAAATC

SEQ ID NO: 140 ACTTTTTTTTTTTTTTTTTTTTTTCCGGTTTTTTTTTTTTTTTTTTTTTAAA
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AACNTGAGGGNGTTTTCTCGNGTNAATGAGGGTTTTATGTTGTAATGNGGGGGGTGAGGGACCC
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SEQ ID NO: 141 ACTTTTTTTTTTTTTTTTTTTTTTGGANAAGGAANAGGTTTTTATTCGGCCG
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CTTGGGTTT

SEQ ID NO: 142 ACTTTTTTTTTTTTTTTTTTTTTTGGCTGGATTGCCTTTATAGGANAG
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GAAAGCNGGATTTTNTCCNACTCCCNNTTANCTCNTAAGNNAGCTGGTNAANTGGGATNTTGN
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AATACTT

SEQ ID NO: 143 ACCGAGTGTGGCACCTAGGACAGCAGGCAGTAGTGACAGATAAGGTGTGACTC
TTTCTAGCATAGCCAGGGGGCATGGCTACCCCTCATATATCCCCAGGCCTTCCCTAGACTCTAATGG
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CCAAATGTTTAAATTTTGAAGACATTTTATTTTACCAATAATCTTTAAACTATCTTTATCTCCCA
AAGATTAAAGTCATGGGAACATAAAGGCATTAATAATTTCTACTTCTCTGAGAAATTTTAAAGTGCT
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CCGTCCCTAGGCTGGAGNGGGAGTGCCATGATCTTGGCTCATAACAGCCTNAACCTTCCANGGTTCA
AGCAATTTCTTGNNTTNAACCTCCCGANTAGCTTGGGACTACAGGCCCCCGCCCCACGTTACAGN
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SEQ ID NO: 144 CTGAAGNAACTANCNTCAANAAGTAGCCTCTGTATGGGAATAGAGCTAAGGA
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AACACATTTGTCAACTTGACAGGGAGCTTGGGCTGCAGATTCTGCCCTTGTGAGACTCTGAGGCC
CGGCAGAAAGAGCCAGGCATGGGAGTCAGACTCATGGGAGGGTGTGGGGTAAATCCTGGCCA
TGCAAACTTCTGCACTAGGATCTTTACTTCCCCTGGCTAGAAATNCTATNACTATAAAANTGGGGG
GAATAAATGACTGGNTCANGGGGGTTTTAAAAAGAAATTNAAANGGGTTAAATTTATGCAANAA
ACAGGGATTGTGGNGAATNAAACNGANGGAATTCAAGCCAAAAACCATGGGGGAAAAAAAACC
CCCTT

SEQ ID NO: 145 ACTGTTCAATAAAATTTAATCACTATAAATCAATTTTTTAAAAATTAATTATA
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SEQ ID NO: 146 ACTTTTTTTTTTTTTTTTTTTTTTTTATTGGCTTTTAAAAAACCCTTTATTTTTT
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ACAANNATTTNANANTTTGACATATTCTCNAAATCCTGTGTGTAGGCACAACATCCAATTTTATG
GGA CTGAAACTG

SEQ ID NO: 147 ACTTTTTTTTTTTTTTTTTTTTAAATNACAAAATNAAAACTTANACACTTTAG
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ACCGAAAAANTANTAAAGGCTGCCTTTNCCTTTTNAAGTCTTATTAGCTTTATATACAAAATA
CAATGNTNTNACTAATACATTANTACTNAAAGGTGCTTAAAAAT

SEQ ID NO: 148 ACTTCCGGTGCTAAGGGNTNTCCGATTTGTAGAAGGCACAAATATTAATAGG
ATCACTTTTAGCTCTTGGGAATGTCATCAATGCCTTAGCANATTCAAAGAGAANGAATCANCATAT
CCCTTACAGGAAATAGTAAGCTTACTCGCTTGTAAAGGATTCTCTTGGAGGAACTGTCAAACCTA
TAATNATAGCTGCTGTTANTCCTTCTGTATTCTACTATNACACATNTAACACTCTTAATTNGCT
AACCGNCAAAAAGNANATTAANTCTCTTTGAAATTGNA

SEQ ID NO: 149 ACGCGGGGCCATACCAGCCTAGGTGTGGAGCAAGAGGTAGGGAGGCCCTCG
TGGATATACACAAACCCCANATACAAATGGAGCATTGTGGTAGTGGTTAGGGTGTATTATGN
AAACANITTAATTAATNANTTCTATTCAITGA

SEQ ID NO: 150 GTACGCNGGGACGACGAAGATGATGAANATGATGATGATGAAGATGATGAG
GAGGAGGAAGAAGAGGAGGAGGAAGAGGTGGGGTGGGACGACAGTGAAATCTAGAGTAAACC
AAGCTGGCCCAAGGTGTCCTGCAGGCTGTAATGCAGTTTAATCANAGTGCCATTTTTTTTTGTTT
AAATGATTTTAATTATTGNAATGCACAATTTTTTAATNTGCAAAATAAAAAGTTTAAAAACTTANA
ACNCAAAAATTNAAANAATTNTAAANTTTNAAATNTNCTTGCTGGGCTGGNNATTNGAAAGGANA
TTTCCATCANNCTGCTTTNTTTNTTTGTATCTNAACTCNGCNNTATTTGNTNNTGATNTTNTCTT
AG

SEQ ID NO: 151 ACTTTTTTTTTTNTTANTTTGTTTTTGACATANATNTANTCTNTGGTNANGGTGG
CTGGAATATACCTGACCCACCATTTTANAANGACCCATNTNANGTCTGACCATTTGGGAGCAAG
CCATGTTNACACTGACCTAATGCAAANTATGGAACCATTTGGGCTGGTTATACATTTCTGTTTCTTA
AATTATNTTCCAACNTNGA

SEQ ID NO: 152 ACGCGGGGAGACTGAAAACTGCCTCATGCATGTGTTCTATTTATTGATATATG
CACATATGGCTGTGATTACGTAAATTCATTTTTAAATGTTACTGAATTCACAGTATCTTTCTCAA
CCATGTATTTTCTCAATAAATGAATACTAAGATGCANTTTTGAAGTATAAAAAATAAGGAGCTGCT
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NAATATGGTTNNAACANCTTATTGCTTTTGTATCA

SEQ ID NO: 153 ACTTTTTTTTTTTTTTTTTTTTTTTTGGAGACAGNCTCACTCTATTGCTGAGGCT
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CTCAACCT

SEQ ID NO: 154 ACGCGGGGAGAAAGGAACACAGTAACTGAATTGATCCGTTTGAAGTTTAC
AATGAAGTTTCTTCTAATACTGCTCCTGCAGGCCACTGCTTTGGAGCTCTTNCNTGAACAGCTNT
ACATGCCTGGAAAAATAAATTTGTCTATTNGGTGAAAGATACTTANAANAAATTTNTTGCCTTTNN
TANANTCATTTNTATNAANAGANATNTTNAATATTNGTATATNTT

SEQ ID NO: 155 ACTTATGTCCATTTTCAGTTTCCCCACCTATAAACAAGAGCCAATTTCTCTTATT
TCCCTGCTCTCCCAGGTTGAAAAGGTGCTGGCCCTTGGAAGATTGTATTGACTGTGTGGGGA
TCTGGTGCCACCTGNTGNATGCCACAAGAAAGGCCTCTCCTGACTCCCAAGTTGTAACCGTTTCC
ACCAATCGACTTCCAAATAATTTTATCAAATCATCATCTGTGCTTTTCTTCTGTTTCAGACCAC
TTTTAAGGTGGAAGGCAAGGCTTATATGTATTTCTTCCATAATGAGTCCNTCANAAAA

AAGTTNCTTCGGTGAAATTNTTGACCACNTTATGTTTNGGGGGACTCCCTATNGGATCA

SEQ ID NO: 156 ACCACTGNATTGATTAGNGGTGTATNTAAACANGGCTCCCTTCATTGCATCTG
AGGACTTGTTCCTTTCTTTTAAATCCTCTTAGTTTAAATATATTGCCTAGAGACTCATT
ACTACCCAGTTTGNNGTTCCTGGGANAATGTAAGTGNACAGTTACCTTTCAATTAAGACA
CTTACCCCAAAANAAAAAATTAAAAANAANTNCCGTCCNCTTTTGTGT

SEQ ID NO: 157 ACCTGGAGGCTCAACGGTTTAAGCTTCACCACAAAAGCNAAATGGGCACACC
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TNCNAT

SEQ ID NO: 158 ACTGTAAAAGTTCTGACACAAGACAGTGGCAGTGGTTACTTTTCATCGACTTT
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TCTACACNTNTTACTTTACCAAAGAANTAACNTTANTINGAAGGGGTTAANTTTTNTTTNATT
AAAAAATTCACACTTANCTTTT

SEQ ID NO: 159 ACAACTATGATACATAAAATTAATAACAAAAAAGGAGGGGGCAGGC
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GGAGTTGAGACCACCTGGCANCATATTAANACTCCTTCTCTACAAAANTTTAAAAAATATNTC
CAGGINTGGNGGNTCAACTCNTTTANCCCTANNTATTTNTNATACCTTATTCNNTAATTTTCN
TTAANGNTTNTATNATTAATATC

SEQ ID NO: 160 ACCCCCTCTCCCACGTAGCCACGGCTCCCTACTATCAACATCCTGCACTA
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AANGATNNATNNGGGGGGNCAGGTGGGGGAATTAACNNAANTTTNTTTTCANGGGGGAGTC
CTNACCTGGCNTNATGCCATGAATGAGTNGCACAC

SEQ ID NO: 161 ACGCGGGAGTGAAGAAAAAGAAATTCTGATACGGGACAAAAATGCTCTTCA
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TTACTAACCATTTTAAAGACCACCACCAAGGGAAACCAATCTTTCTTGAAAGAAAGTAAAAAT
GAATACCTTTTGGGTNAATGGAATTGAAATNCAAAANAATCTGNNCTTTATTGACAACNAATGG
NTGTAATTNATGTTGTAGATAAACCTCCTNTTATNCANCNAAACCCCTGTTGGGAAATGAATC
AACTNCTTGAAATACTTTATTAANTAATCCAATTNCTTCCNAANTTTAAGTTTGTGCGTGGTACNCCC

SEQ ID NO: 162 ACAAATTTTGGGATTAAGCTGCTCCCAAGACAGTCTTCATCACCTTTGTGAAC
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ATAAATGTAT

SEQ ID NO: 163 ACATATTGGCATTTCATCCTCAAAGGAATCATCAAAAGAAAATTCAGT
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CTGCCCTGCTACTGGAGAGATCTCCTGAGAATTCAGTTTGGATTGGTGCTGTCTCTCCTGGGAA
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TCCCTTGACTCTGATAGTAAACCTGCCCTCTCANCAATTGACGCCTGGGTATTTTATGGATATTTA
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GCA

SEQ ID NO: 164 ACATATTGGCATTTCATCCTCAAAGGAATCATCAAAAGAAAATTCAGT
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SEQ ID NO: 165 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGANANGGAGTCTGTCTGTC
ACCAAGCTGGAGTGTCANAGGCACAATCTCGGCTATTGCAACACTCTGCCTCCCGGGTCAAGCGCA
TTCTCTGCCTCAGCGCTCTCTAAGTAGGCCAANATTATAGGTGCCCGCACCAACACCGAGTAAATT
GGCATTGTAGTAAANATGGGGTTTCACCATGTTGTCCAGGATGGTCTCGACCTCTGACCTTGTG
ATCCACTAGTCANAGTTTGTTTTAAATGACTACCCGCTACGCTTGGGAGTCTCAGACAGCGGGA
TCATTACAGTGAAGCAGACAGCAAGGTAACCTATGGGTGGTGGAAACAAAGTATCTCTACACCT
GAAAGAANACCAAACTGAGTACCTGCCCGCGGNCGTTTCAAAGGGCGAAATTCANCCACTGGC
GGCGCTTCTAATGGATCCCAACCTCGGACCAAACCTTGGNGNAACATGGCATAAAGTGTCTGTGG
GGNGNAACAA

[illegible]

SEQ ID NO: 168 GGTACATCCCTGTTTATCCCAATCCATCCACCGAGGCCAACAGCATGGATGA
TCTGTTTGACAGGAAGCCTCCCTGCTCCCGTGACAGCTATCTCACCAGCTGACACTTTACCATATC
TGGCAACAAACACTGTTTGCTCTCTCTTGGAATTTCAAATCCACCAGCTTTTACCAGGGCCAGGCCCA
GGCTCCCCCATGCAGAAAGATCTTCATTGGCTGCATTACCCACAGCATCAACAGCAATGTGTGGTGA
GGTCATCTTTCCAGACTGATAACTCTATCCTAGGAGTCAGCATTTTCTGAACACTTGCAGAGATT
GCTGNTGCTCTCTGAACTGGANAGACAGGAGTAGAGATAGCCAAACTATTCTTGAGGAGACTTN
ACACAGCTGACCTCATTAATTTTTTAAAAATTTGAAGTCNTTNGGGGTAAATGGGAAATTCGCCACTA
TAGGTTTCTTCAAGAACANCCATCTTTGANTTTCTNTGNAACTGNTGTTCCGNCNCCATGGAAAAAN
TCATCTCANNGNCCCGGGGGAGCTTNAANGGNTATNCCCTTTNGCTTNAANNNTNANNGNNTC
AAATNGGGGCCCTTTNGGNGCGNTTTNTNGGAAAAANNAANGGCCNNNNCTNNCNGGNGGNNTN
AANGGGATNNNTNANNTGGGNGTTTN

[illegible]

SEQ ID NO: 170 CGAGGTACACTTTTCAACCAAAATCAAAAAACAACCTCTAAAAGATTCTATTA
TGTAATTCAGTTTACATAAGTATATTTTTTAAAAATTGTCCCTCTAAAGCATTITGGACTCTCA
AATGGTTTATTAATAATGTTTACACAGATGAGGTTATTTCTTTAATGTTGATTCTCTATGTGAAAA
ATTGGGTTATTTGTGACACAAAGTATTCGGTTCTCCACATCTTGCCAACTATTGGGTTTCATGACTA

TTTTTTACTTTAACCATCCTGATAGGCGTGTGCTGGTATCTCACTGTGTTTTTTAAGTTTGCATTTTC
CTGACCACTGATGATGTTGAACATCTTTTCACGTGCTTATTTGCCATCTGTATAACCTCTCTAGTGA
AATGTCTGCCGCGTACCTGCCN

SEQ ID NO: 171 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGGGAAGTCTATTTATCATTTTAAAG
AACAGATTGNGCCTTTGGTGTCTATNTAAGAAATACTGTCTAACCCAAAGCCAAAATAGGTTTA
AGTTTTGTGCCTTAAATTTAGGTCTAGGATCCATTTAGACAATTACATACNGNGCAAACTGAAA
TGTGTTTTTAAAAAATATGAATAACCAATTATTTAAGCACTATTTGTTGAAAAAATATCATITTTGA
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TTACTATATTTCTTTGATTATTGCAGGGTTTTTAAAAAGCCTTGAAATCAGGAAAAGTTATGATTC
CTAACTTTGTCTTTACCAAGGGTTAGACTATCTNGNCCCTTAGTATTTAATTATATNANCTTGTTA
NTTCTACAAAAAAGGTATNTTGGAAATTTGATGGACATTTGGCTGAATCTNTTTCAACCTTTNCC
NAACTGGTATTNAANATCTGGAATTCTTTTCTCGCAATCCGGTTNNTTTGGCCGGACCACCTTNG
GGNAATTNACCCCTGNNGGCGNTANTNATNGGATNCANCNNGGACCNACTTGNGNNTTATGNNA
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SEQ ID NO: 172 CGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGGTTTGATTCTCTCTCATTCTC
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CACCCGCGT

SEQ ID NO: 173 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGTAGAGACAATGTTTCACTATGT
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GATTACAGGCATGAGCCACCATGCCTGGCCCACTACTGAGATCTTATCCGGAAGTTGCTGATTAC
CAGCTTCAGGTGTTTCTGTTTATTGGGAGACTGTTCTGCTGCTGGCTGTGACCAATTAATTTTA
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CNITGAAAAAATAATTTCTNATAGGTAGGGTTTCATNTCCAAATACCTGCACATTTGGTCAAAAAAC
ATTTCAATTTTCTAACCCCTGNTAT

SEQ ID NO: 174 ACCCGGGGGCANNCCNNGTGGTCCCATAGCACAAAGCTGTGAGGGGATTCACTT
GTGTGCGNAACTCCTCGGAACNTGGTGTCCCTAAACATNTTCTGGGAACAGCCNTNCTAAGA
CCCTGATGACTANNGAGCTANCTAAGATCAGCTGANTTA

SEQ ID NO: 175 ACTTTTTTTTTTTTTTTTTTTTTTTTTTNTGAGTGAGGCAGGAGTCCAANGAGGNTAT
TTGNGGCANTAAATTTGATTAAGGATNCINGTTTANGANATCAGGTACGTCTTTAGNGTNGCGT
ATGGNTATCANTCGAATTGAGGTTA

SEQ ID NO: 176 ACTGGGATTACAGGCATGAGCCACTGCGCCTGGCCCANAAATCTCTTTGAA
CANTNTTCAAAAAATACAGCTAGCCTCAGTGGTTTCATGCCTGTAATCCTAGCACTTTGGGAGACCA
AGGCAGGCTGATGTTTGGAGGCGAGGTTTGAGACCAGCCTGGGCAACATGGCAAAACCCCAT
TCTATTANAAAAAANAAAAAACCCTTGGCATGGTTGCACGTGTCTGTAGTTCCANCA
CTTGGGAGGCTGAGGTGAGAGGATCACCTGANCCAGGAGGTGGAGGCTGAACTGANCTGTGATT
CCGCACTGCGCTCCAGCCTGGGCAATANACAAGACCCTGCCTACCAACCCCCCAAAATACCATT
TATAATAACTTTAAAAAAGANTCGCTTAGGTGAAATCTAAGGACTCATATAGTGAAAGCTATA
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GGAAGACTGGACGGAGTAAAGACCTCNTTCTCTCCATATTGATATGTAAACTTANTGCAATTCCTA
TTCAANCTCCAGCAAGACTTTTCAGATATAGACAAGATTNTTCTACANTTNACTGAACGCTAAGG
GAACTANAATAA

SEQ ID NO: 177 TATACCACTCACTATGGGCGAATTCGAGCTCGTACCCGGGGATCCTCTAAGTC
ACCTGCAGCATGCAAGCTTGAGTATTCTATATGTACCTAAATNCNCCGNGAAGAAGGCNGTTTT
GCGTTATTGGGCGCTTCTTTCCNCTTACCTCGATCAACTTGACTCANNNTTGGCGCTCGGGTCNTCN
NGCCTGCGGCNGAAGCCGTATACANGNTCACTCAAAANGCG

SEQ ID NO: 178 ACTTTNG
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NATCATGGCCAAAAAATTTGNTTAAACCCCNCCCCCCCCCAANGTTTNGCNNGTNTTGGAA
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TNAAGGNCGGGGCAATGGGTGCCAATTTTACCTNTCAGCAGGTTAGTCAACCANACAAACNCGGG
GGCTAAAGTCCAAAATTCTTTCCAGTTTTCTNTGCTTATTGGCTTGANCACATNCAAACTGNCN
TAANCCTGTAAATTTAAGGGGAGTTGGGGTGGGGCGTAANAGCAAANGGACAGCCGGANAAN
AGAAATNNCGGGTCCCCAAGTTTTTCTGGGNTAGNGGCTTNGNTTTAAATTTAAAAANNANA
GGGCCAGAGTAAATGGCACNCNCNNGTTTTTTATNAAAGAAAAATTTCCCNATATGAGGGAAC
NTNAA

SEQ ID NO: 179 ACAGGCTTGAACAGAAATTGGAGAATGCCTTGAAGACAATAGAAAGTGCC
CACCCACCAGACAGACCAACTTGAANGGAGCTTTATTGGCCAAGTGGTATNCCCGTTGGGAACCT
TTTATGAATGCTTANNCACTGGANTANAGATCTNCTCCGAAACNTCCCAANATGANTTTTGATN
AGGGGAAGGAAAAACCAACCTTTCCANNATTGNTTGGAACTNAAAAAATTTNGGAAAAANGGG
TTTCCANANAAACCTTGGGCCTCCANAAAGGGCACATTNNACCTTGGGTTCAAACTTTTTTTTTC
CCTTTNTTTGGGCCAAGGCCCTTTAACCNGCCCN

SEQ ID NO: 180 CCCCCGCGGGCACCTGGAGCAGAGGGGTAATGACCACTGGAAACACTTGCG
GTATTCCAGGAGAACTTCCCCACACATCGCGGGCAACAGGGCACATGCTGAAAACATATGCCCAA
AATCTCTCGAAGAGCACCTCCAAACGCTAATCAGATTCCCAAGTGATGAGGAGACATGTGATGG
CACCGAGAGAGAACTGGTCCGCTTACCTCAAGGAAGCCATCAGACTAACAGCCGATCTCTCTGG
AAGAACCCTACAACAGAAAGAGTGGGGCCAAATATTCAACTTCTTAAAAAGAAATTTCAACCCAG
AATTTTCATATCAGCCGACTAAGCTTATAGGAAGGAGATATGTCCTTTTCAACAGCAAATGCTGAGA
GATTTTGTGCCCCAGGCCTGCCCTAAAAAGAGCTCTGAAAGGAACACTCCTTGGAGGACTCCGTGT
CCTTGCCNTCACACTGGNCGGGCCGTTCCTTAGNGGNTCCNGANCTCNGTACCANGCTTGGCNGA
AATGATT

SEQ ID NO: 181 ACTNTTTTTTTTTTTTTTTTTTTTTTCTAAAAACCACTTCTGAATTTGTGAT
CTTTTGAAGGGTTTTCGNGTCTCTATCTTCTCAGTTCAGCTCTGATTTTGGTTATTGTTGNCCTCT
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TGANATCTTTCTAATTTTTCATGTGGCCATTAGTGCTATAAACTTCCCTCCTAAAACTGTGTTGG
CTGTGTTCCAAAGATTCTGGNATGTTGTATCTTTTTTCTGATTAATTTCAAANAACCTTCTGATTTT
TGCCTTAATTTTCAATTTTACCCNAAAGTCATTCAAGANCAGGTTATTCAATTTTTCATGCTTTATTA
GCATGTGGAATATTNGGAACAACTCCAAAAATGCTCCTTTTGTGTGGGGTGTTTTATTTTTCAT
TTTTATTATGAGAAAAATATACATGACATAAAATATANCATTTAAAAATTACTAAATATATATTTAA
ATGGCATTTAAGTAAAAATTCACAATGTTGNGCAACCATCACCATTATATATTTCCANACTTTTACA
TCATTTCCAAACANAACTTTTGNCT

SEQ ID NO: 182 ACGCGGGGAGAAATTAGGGGCTGCAGCGGGCGCTGGCTTTAGGTGAACGACGT
GAAAAATTACTTTTCCCACTGAAACACACCCCAAGTATATGCCAGCCTTCAAGAAAGTGAACAGAG
AAACGAAAGCGCCTTTATGTGGGTGGCCTTAGCCAGGACATTTCTGAGGCAGACCTACAAAATCAG
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CCAACCTGTTAGAAAAGACAGGAGGAGTGATTTCCATATGAAAGCTGTGCCAGGGACAGAAAGT
CCATGGCATAAGATTGGGTTTGTGAGCNAATTTGGGAAGAGTCTTACCTGTTTCTCACCTTAAA
AATCAACATANNCGTAAAAATCATCTNATATGGATCCCTCAAAATTCGCCCAACCTG

SEQ ID NO: 183 ACGCGGGTGGCCAACATGGTGAAACCTGTCTCTACTAAAAATACAAAACT
TAGCTGGGCGTGGTGGTGTATGCTGTAAATCCAGCTACTTGGGAGGCTGAGGCAGAAGAATCAG
CTGAATCCATGAAGTGGAGGTTGCAGTGAGCTAAGATCACACCACTGCACTCCAGCCTGGGTGAC
AGAGCAAGATTCCACCTCAAAAAACAAAAACAAAAACCAACCCAAAAAATAAATAAGTAA
ATAAATAAATAAAGGTGGAGTGACTATTAACACCAAAGGTCTTTCCAGGACANGTATCACCAG
ANATAAAGAGGGTNAATTTATANAGGCAAGAGGTCAGTGATCCAGAAGACACCAATCCCTAAG
TGTATAAGTAACATAATANCAGATCTTCAAAATACGTGATNTAAANGCTAATAGAACTGCAAGGAT
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GTAATCTGAATATTTANNATTTA

SEQ ID NO: 184 ACTTTTTTTTTTTTTTTTTTTTTTTTNNATTTTTTTTTTTTTTTTTTTTTTTT
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CAGCCTGNGANATCCGACCATCCCATTAACCTTGAAGNTTNTCTNGATTAATAAAAAAAGG
GGNGGGNGAAAAAAGGNGGAACATGCTAAAAACCTAAATGACAATCATCCAAATGNGAGGAAA
NAANAACCGATTNACCAACTNCTTTTTNTNTTTNAAAACTTTCTANATCTNANTNTATGATTNG

GCCTTCTGGCTNAAAAAGCCTGCAGNCCCANAGAACCCNTGAAAAANAGCCATGGNTCTNCAAAA
GAANTAGGA

SEQ ID NO: 185 ACAGTATTNTGAATGTGAGATGATTGTGTCAGGACTAACTGTCTTTTAAACAAA
ACATTTTCAGTNTTTTAAATAAAATTTTGNAAAAGNAATGTGAATTAAAAATCCTGGAACANATNTG
AATTCATTCACTATTGNGTANGAANATGCTGTTAANACATAGGAAGGG

SEQ ID NO: 186 ACTTTTTTTTTTTTTCTTTTTTGTTTTTTGGTGATGTGGCTTAAATGCAATAGTT
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GAGAANATACATTAATAAAAAATCTTCTGATGTTTTGTAGCCATAACTAAATTATGGTAAAAATGTG
CACTATTGTGAAAAGGAGCAACGNAGTTTTGGGTTTTTGTGTTNGTTTGCTTGTCTNTGTTTCAT
AAGAGATTAAAAANGTTTCTGGATAAGGGATTAGCTTCTCGAAGTGCCATCATCTGNGTAANAA
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SEQ ID NO: 187 ACTTTTTTTTTNTTTTTTTTTTTTTTTNGTAATAAACATGTGGAGNGTCNTGTAN
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AAAAACATCACTACCAAATTCNANTATCCTAANTTTCANGTNCGGGCCCGGCCCTTTCNAAAG
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SEQ ID NO: 188 ACCACTCACTCCAGCCTGGCGACAGAGTGGAACCTCCGTCTCAAAAAATAAA
ATAAANTAAANTAAAGCNAAAATNTAAANTGTTAAAAAAAACAAAAAAGGGAAAAAGGANGC
TGATTGCCCTTGGTGAGTCAACACTGGGTATTTTCTGACCACTATTTGAAAACAAAAAAGGAAACNAC
TGATATTCTATGCAAAGATCTNTTCTGGANGGCACNTTGCNGNACACCACTGNGNACTNTGAT
NANCCCTTCATTGATTTGAAT

SEQ ID NO: 189 ACCTCCAAAGTGTTTAAATAAAATTAAATTACCACTGGAAGAGAATAAAAAATT
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ATAGCATGGGTATTTCAATGCTGAATTTATTTATCTGAATACCAGAGTAGATGGGGATCTCTCAT
ACTTTTTTACATTTGGCTTCTTTTTCTGAGAATAACTTTTTTATTATCTTTGTGTCAGTTTGGTTAGG
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SEQ ID NO: 190 ACCCTACCACTGTTGGACCAGTGGAGAGCAGTGGATTGAGATCTCGCTACCG
TTCTTCACCTACCGTCTACAACCTACCTACTGACAAAGAAGACTACATGACCGACCTACGAACCTT
GGATACTTTTTCTCAGAAGTGAAAGAGGAGAAACAGCATAGGGTTAAGCTGGGGAGCCAGATTCTA
CCTCTCCTTCCAGCAGTCCTACTTTCTGGAACATAAGTCTGTTCTATGGGGGATTATGCACAACTTT
AAAGAAGTTTCAGTATCAGCTTGCCTGTAGGTCTCAGGCCCATGTGCTAACAAAGATGAAGCCG
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CTGAAAAGCTGCCTGGTAAGNNCTTTTTTCANTT

SEQ ID NO: 191 ACACAATCCTTTATAAAAGTNGTATATATTTTTTCTGTCAATACCTTCATTAC
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SEQ ID NO: 192 ACTCTGGCTGTGCTTAATACTGTGGTTAAGAGAATCACCTATATTGTTGCAT
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TTACAGATGATCATTTGGGTTATTTCTAGTTTGGGGCTATAATTTGTGCTGCTGTGAATATTCTCAA
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TCATAGAGTAGCATTTATTTCTAATTCTAATGCTCTCANAGGGAATACNNGGAAATTTTAGNAAAG
CAAAGGNCNTTTTTAAATCTGTTAAGGAAAACTGAATTTGACATTGTATTCTGNCCTTNGACA
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SEQ ID NO: 193 GGTACAAAATAAACTTTGAGGCAAAAGGCATTGCTGCAGATAAAAAACATGC
CTATATAATGACAAAAGGCTAAATTTACCAGAAAGCTATATCAATTCACACGTGATTATACCTGAT
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CATAGTTTGAAAAATTTAACTAACCTTTCTCAGAACCTTATAAAGCAAGAAACCACTAGATTATTT
CAATATCATCTCGATTTATAATCACAATAAGTTTCCCTTTTGGAAATTAATAGCAATTTATTTAGT
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SEQ ID NO: 194 GGTACTTTTTTTTTTTTTTTTTTTTTTTTGACAGGGTCTCACTCTATCACCCAG
GCTAAAGTGCAATGCGGTGATCAGGCTTACTACAGCCTCGGCCCTCTGGGCTCAAGCAATCCTCC
TGCCTCAGCCTCCCATGTAGCTGGGACCACAAGCATGCNCCACCATGCTCAGCTAATTTTTTAACT
TTTTGTAGCAACAGGGTCTCACTTTGTTGCCAGGCTGATCTCGAATTCCTAGGCTCAAGCATTNT
CCCACCTTGACCTCCCANAGNGCTGGGATTATAGGCATGAGCCATTGCACTGAGCTCACTAGCCA
NAATTTCTAAAAATCTTCTNTCAGGAGACTATANATAATGNCCTACTTCTCTCTTTCCAGTATCA
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TTCTATGTGGGAACCTAAAAANNTTATTTCTTAAATATAAAAAAGGTTATAAAATTTACCAAGCTNT
TGGGGGGGNGGGAATTTTTNTTTAAATCACCGGCTTNG

SEQ ID NO: 195 ACTTGATNNGATTCTCAGCTTGGTGTGCTGTTGGTGTATAGCANAACTACCGAG
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GAGGANTCGTTCGGGTTTTCTANATNTACNCCGAAGGAGGGAGGNAGGACAT

SEQ ID NO: 196 ACTGCGGGGTCCTTGATGGACCCTAAAAGGGGTTGGAGAGACCGATTACAG
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NCNCATTATTTCTCTGAGCCTCCAGAAAGGAGGAAAGCCTAGCCAAACNCCTTAATTTTAGCCTTGC
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SEQ ID NO: 197 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGCCAAGCATTTTTTAATAAATTAAAAAAC
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AGCCTGCGTATTTCTTTAGCAGGTTTTCTTAGAGACAATAACAACAGCTTATCAATTTCTTTACA
TCCTAATCTACAATGT

SEQ ID NO: 198 GGCTGCANAACAAATCAAGCACATCCTTGCTAATTTCAAAAACTACCAAGTTC
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NTGANCCNATTTAATNAATTATT

SEQ ID NO: 199 CTAATTTATATGTTGCTCTGCTTATTAATAATCAGCTTAAGGATAATGGGGT
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CCAAGATGANTTAATTTNTANNAGTCCTTATTACACAATAAACANTNNCTTAANNTGNCACTGT
GGCCGAACACGGNGGCTCATGCCTATAANCCAGCACTTTGGGAGGCCGTAAANGGGTGGATCAN
GANGTNAGGAGATCCNAGACCATCCNGGCCAATGGGTGAAACCTGTGCTCA

- SEQ ID NO: 200 ACTTTTTTTTTTTTTTTTTTTTTTTTACAAGGGTAGCAAAAAATATNTGTAA
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AGAAANATTTTNTAGATGAGAACANGATGACCNTGNGAATTTTAAANAATTGCATTATGNAGAG
TTTGATNTTTGCT
- SEQ ID NO: 201 CGTACCAGATCCACCTAGGGGCGCNACTTGCTTGCTAATCCTAAAAANAC
CTGGNCACCNTNNANNCNTAGGACNCTGACTNNNGCTGGNAAAGGGGNTTNATNANNTTNGNT
NNNAGAGTCAAACTATAAATTACNTNCCAAGGTTAGGTTCTACCTATGCCAGNAATGAACAAGG
ACAGCTTAATAGGTTATAANCAAGATGGAGTCNTTTNGGGTCTGATCTCTTTCAGTGCATAATTT
CCTCAGTTACAATTTTGTAAAGGTGGNTTCAAATGCTTTGCTGACCTCCCATTAACAAGGATGTG
CCGATTGGAACNTNNTTTTGC
- SEQ ID NO: 202 ACTTGCTAGGTATCCTGGGTGAGTGGCGGTGCAAACTGGTTTCCTCAGCTGCC
TGCCATGGGGCTGAGTCGTCAGGGACTGGTAGTGGCTTTGGAGCTNATAGCGGAGATTGACTGAA
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CNAATAATTACATCAGACAAATCTGCCAGNGTAATTTTGTCTGGGTGGGGTAAAGAATTCCTC
GTGCTTCTACTCCAGCAT
- SEQ ID NO: 203 ACAGTCATTTAATGATGTTGATTCTTCCAAACAATGATCATGGGATATTTT
CCACTTACTTCTGTCTAGTATTTCTTTCAGCAGTGTATTTATAGTCTGTTGTGGACATCTTTTA
CCTCATTTGGTCTCCTTTGTTAAATATATTTCTAGATATTTATTTTTTGTGTCTATTATAAATGAAAT
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CAATGCCTAGTTTGGTGAGGGTTTTATCATACAGACATATTGGATATTATTGAATGTTTTTCTGC
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TTTGC
- SEQ ID NO: 204 ACGTGACAGAGCCAGGCTTAAACGCAGATCATCTGGCTTCAGACTTTCATCA
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CTTGTTTCTTCCACTGTTGAGTTTTTCAAAAGCATTTTCTAGAAATTCGACTTCTCAAGTCATGAA
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- SEQ ID NO: 205 ACTTTTTTTTTTTTTTTTTTTTTTTTGGGATGGAGGGCCGCTCTGTTGTCCAGG
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GGTTGNAATGCAANCTTTAAACTTAAACCCAAATAANGAATT
- SEQ ID NO: 206 ACCGNATGCTGGCNGGAGGTGGCATATAGCTCACTGGNACTGANGGGCTGG
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- SEQ ID NO: 207 ACAGAGAAACCCCTTAGGCCAAACTTAAAAATATGTAAGGAGGCAGCTTTAGGC
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SEQ ID NO: 208 ACTGNNTGCAACAACTCATGGANTTTGATGGGGAAGACCTGGTCTCAAATAC
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SEQ ID NO: 209 ACGCGGGGAAACGGAAGTGAGCGGCGGGGTGACTGACGGTAACGGGGGA
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SEQ ID NO: 210 ACTCGGGGAAACGGAGGTGNNCNCGGCGGGGTCNACTGACGGTNACGGGGC
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SEQ ID NO: 212 ACGCGGGCAGGGGTAGAATGGAAGGAGAGCGGCTGGAGAGGACAGGTGGT
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SEQ ID NO: 213 ACTTTTAGGAGAGATGGGATTTACCATGTTGGCTAGGATGGTCTCGATCTCT
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SEQ ID NO: 220 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGAAATGTTTATGGTTTTTTT
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SEQ ID NO: 228 GCGTGGTCCGCGCGGAGGTACTACTTCTCAAGGAGGATTATGGTCTGTCTCT
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SEQ ID NO: 229 GCGAGCGGNCGCCGGGCANGTACAGNGGCCCGGTGAAAGACAGAATTG
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SEQ ID NO: 230 CNCNGGACACTGCGCCATTTCCTGTCCAAAGCTGGGCGAATCAGGGATNCCG
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SEQ ID NO: 233 GGTACAACCTTCAAACATTCCAGTTTTTATAAAAAAGGGGCACACAATCGT
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SEQ ID NO: 241 CGAGGTACCTGGGGGCCAGAACGTAAGTTTGAATCCTCTGCTAGGAGTGAG
CTCAAAAATGGATATGATTCAAATACATAGATGCCTGTGGCCAAATATTCCGGATCTTACAGTCCT
CGGAATGCCCTGGCAGGGCTAAACTCCTTTTGTCCAGTCCCTCAAGCTCAGACCTGCAAACTC
TTCATTTCTTACTGTGATTGAGGGTTCCCTGAACTGAAGGAAGAAAGTGTCTGGAGGGTGGGAGA
GACCGTGTGTGGCAGAGTTAGAAACATCAGTCTATCTCAGGGTCTAGACAAGTGATCTCCACAT
AATCAGCAACAGATGGTCAGGCAGCACCTCCAAATATTTGTATCCTTATCAATCATATTTATGTGT
GACTGCCAATCCATATGTATGTGATTAAGCTTTATTTTAGGTTTTTTATTTTTTTTGGCGG

SEQ ID NO: 242 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGNTTTTTTTTTTTTTTTTTTTTC
CAAACTGCAAAATGCCCCAANTTTTATTGTAGTCCNTACAAAANGGAAAAAANTTAAGGTTTTN
TAAACNCCACCTACTTGGGGANATGGGGAAATGGNACTGTCCCCCTCACCATCANCTAAACNTTA
TNGGTGACGAGGACTTGNATACATACCAACTGACTGTCCCAANAGGANCTCAGTCT

SEQ ID NO: 243 ACTAGCATTTTCAATTACCAAAAACTATTAGCAGTAACATTGCCATTGGTAG
TATTTTCAGTCAGTCCACTATCACTAAGCTAATGGGAAATCAATAGTAATAAGTGGTAGATTATAA
TGTAGCCATGAAAAATGTTGTTTAAATCAAGTCCACAGTCTTTCAGAAGAGAGGGAGATTGTTT

SEQ ID NO: 244 CGTACATNAAANACACGTCCACATCACANTTGGCCCCAACTGCCTGTGCTC
CTCGATGGTGTCTCTCCCTNCATAAAACGCATGCTTATTGACCTTGGTTTTGATNTGCTTGGCCNTG
TCNGTGANGATGAT

SEQ ID NO: 246 ACTTNTTTTTTTTTTTTTTTTTTTTTTCCGACCCATGTGGACCAGGCTGGCC
TNAAACTCNTGCCCTGGAACCCCGCTCCNNGAGGGCCNAGGGCAGGCNAACCGGCCTGAGCC
ACANTGGCTCCCGCTTACCTNGGCCGANACCANNCTAANGGCGANTTCCTCACACTGGCGGGC
GGTANCTANTG

SEQ ID NO: 248 ACGCAGGGGAATGGAATGGAATGGAATGCAATGGAATGGATTCATCCGGAA
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GGATTGGAATGGAATGGAATGGAATCAACCCGAATACAGGGGAATGGAATGGAATGGAATGCAA
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AGGAATGGAATGGAATGGAATGGAA

SEQ ID NO: 250 ACTCAGGGGAGGCCAGGANGCCTTGANCTGGGGCCGGGCACTGAGGCGCC
CCACATATGCTGAGAGCAGGGGGAACGCATCCAGNCTGCCANGGGCTAGGACCTNTGGATCANC
ANCNANTNCAGCAGGTTGTAATTCAGCATAAGGATATNTGGTTTCCACNATTNAAGGINTTGCCTCA
CCTGNTCTGGGACACAGNGGTCTAAAAAGGCTTAATATTNCCCGGACAGGNCCTTCACATANTC
ATTNCTTGGCCACCTCTTTNTT

32

NACCTTNCAAGANGGCNTANCCCCATTGNAAGAGCTCCCANTGCCAAATATA

SEQ ID NO: 252 ACTTTTTTTTTTTTTTTTTTTTNTTTCGCGNAGATGTTCTTTCTTTCTTTCTTTCC
TTTTNCGNANANACAGGGTTTNCNCNTGCTGCCAGGCTGGTCTCAAAGTCTCGGCTTAAGCNAT
CCACCCACCTTGGCCTCCCAAANNCTGGGATTACNGGCATGAGCCACCNCCTCTGACCANAGTN
ACTTTTGNAANGGGCACTAATNCCACACNTGAGGCTCCACCTTNACNACCTTTTCATTTCCTCAAAG
GCTNAACNTCTGCCCNCTCCCAATGAGNCCAGTGGCTTAACCTTTCTNTNATTNTTTTNGNAA
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SEQ ID NO: 253 ACCCAACAGGAGGTTTTTTCAACTTTTGCTCTTCTCCCTTCTCCACCTCTCA
CATCCCCAGAGCAAATTCAATGTAANTATACANTTTCTTCTTTCTTTTACAAAATATTNTGTTAAN
ACTTACATGAGGTCTTGAAAAATTGGTCTAATATTTCGCTTNTAAAANCTAGATACANAGCCGGGG
TGTGGGTGGCTCACGCTTTGNAATCACAGCACTTTTGGGAGGCCAANACTGGTGGATCACNAGGT
CAGGAGATCGANACCATNCTGCCTAATACCGGNGAAANACTGTCTATACTAATAATTCAAAAATA
TTANC

SEQ ID NO: 254 AGCGGCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGAAAAANAAAA
AGGAGCATTAACTTGACTATGCTTTTANCTNCAGCCACCTTTTAAAGANTAAATTGCTGGGCAGG
NGGGGGAGGGCTANTCANGNAACGAAACTGTAAGCCGGACNATNTGTGAGGAGGGGAGGTTAT

SEQ ID NO: 255 ACTTACATGTGTGAACACATATAAAGTGTCAGGTTTACAGACCTTGGCTCAA
GGACAGTCTANGATGGGAAAGGAGGTANGGCGAGAAGAATCACATATTANACTCCCNNGGTGCTT
NAGCCTCACCTATNCAAGGGACATGACNTATGGGGTNTNNTTANTCCATNCCAGGTNCTATNCT
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GNT

SEQ ID NO: 256 ACGCGGGGAGGCCCCAGCCATCTCAGGCTACNCTATCCCAGGATCAGCATGG
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AGGCNTCANGAAAGCTCCCTTTNTCATGAATGCCANTNNGTGANCAC

SEQ ID NO: 257 CGCGGGTTTGAAAGTCTTTGGCAATGANATTAAACTANAGAAACCAAAAGGA
ANAGACAGTNANANAGANCGAGATGCGANAACACTTTTGGCTAAAAATCTCCCTTTCAAAGTCAC
TCGCGATGAATCGAAAGAAGTGTGGAAGATGCTGCGGAGATCANATTAGCANNAAGGATGGNA
AAAGTNATAGGGATTGCAT

SEQ ID NO: 258 TCGCGGCGAGGTACACCAAGCTTCATTTTTGTTTTTGCNNGCTGAAGTCATG
GCATGCAATTTTTGCATTTACGATTCTCTTGGGCATGCCCTGTGATCCACCCNCNCNGATTGAGTG
CNTAGCCANTTGTGATCNTACTNTCCANATTGACTTCTTCCNTGGNCTTTCNAAATTTTACAGAA
GTTGACTG

SEQ ID NO: 259 ACGCCNTTCCGGCCAACANATGATATGCAAACCATTGTTGCTGTGGCCGAA
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TTCTGACCTCACCTANTNTNTGCAANAGTGCAANAANCCCCACAATNTCTNTGCTGGGCATCTCAC
TGGAANATGGGGAANTGGTNGNCCCTGATTCCACANCCACCCATNTNATGTCTGGGTTTNTGAG
CNAAGGATCAAGCTNNGNCTTAGNGGCCNTNTAANCAGCCTGTTTCAAANTGCCATATGGACNAG
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SEQ ID NO: 260 ACTTATTTGNNAATNG
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CAGGGACAAACTTCTAGGNAATTCAACCCGAAAAAATTNTTATNTTCCAANATTNTTACNCTN
TGAAANATCCAGCCTTCTNATNTCCTNAAAATCTTNTATGACNTCGGTANTTTCTGAAAAAAT

SEQ ID NO: 261 CGCGGCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGANAGAAGGANCCA
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GGTGCTCANTGTGCCAGCTGNTGGGGCACCCTTGTGAATGGGCTCCACANAGGGGGCATCNCT
GGGCCTCGCCTTTGNGCACCAAAACCATACAACGCTGGTTTTGTCTCTTANAGAT

SEQ ID NO: 262 ACCCTGGCATTGCTGACAGGATGCAGAAGGAGATCACAGCCCTGGTCCCCAG
CACCATGAAGATCAAGATTATGCTCCCCAGAGCGGANGTACTTTATTTTTTTTTTTTATTTTNTCA
AGGGTATAANCATTTAATTNAATTGANGGTAGNACCAATNCAAANTANGTTTGGNTNTTTATAA
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GATGGGTTTTATTAAGNGGAATTTNCTTGACACCNTCTTTGGGAATTCANNTTTTGAATGCT
NGATTACCCNATACCTNTNTAAATNNTCTNTTTGTTTTAAAGGNTTTTCCAAAAAAATTGNAT
AATACG

SEQ ID NO: 263 ACNCGGATGTGGAACATCTTTGCATGTTCTGTCCAGCAAGTTCTCTCTCCA
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CCAAGACTGGAAGTGAAGTGCATTAGGAAGCTGTATGTTTNGGGAATTTAAATTTCAATA
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SEQ ID NO: 264 ACAACCTTCTCACCTGTGGGTTGGAGCCGAGTCAGGCCACTATGGGGAAG
CAGTTGCCCCACAAAAATGTGGGTTTGCTGACCTATTCTAACTGTTGAATATGCTGCCCATTTGCTG
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CCCTTTNGGCNTTCCNAAATGAAANGGGGNTTCTTCTTAACTTTCTTTTCTTTTGGGTTAN
AANGCNCATCCNGAAAGGGGCTNNGGCTGTTAAAAACNNGGCTGGCCTTNNGTTTAAANGGAG
CCCA

SEQ ID NO: 265 ACTGTTAAAAATGTTTCCATTGTTTATTCATCCACTGGCATTAGGTATACCTCT
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CACTGTCTTCACTCCATACCTACTCCCCATTGGCAGTTTCCATGCAATGTTTCTCTCAAGTTCA
GACCACTGTACTTTNTTTTNTTTTNTTTTTCGGGGACATTTCCACATGCTTTATCCCNCGCAATC
AAAAATAANAAAAANCCATCTCAATTATTATNCACTNCAAAAAATAGGGTACCTNNGNCGGNACC
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SEQ ID NO: 266 ACGAAGAAGTCTGGCAAAAAATCAGCTCCACATCCACAGATCGGCTCACAGT
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NTCNACTAAAAAACTTGGGCCNAAAGTGAAGACTGNAAAAATTTGACATTCCTTGACNTNCAG
ATGGACCTNCAANCAATTTCTTTAATTTTCGAAACACTCTCGTGGGGNAACNAAANGGGTCNT
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TATTTNTTCTCTNAAT

SEQ ID NO: 267 GTACGCGGGGGGATACGCCGNGCGCACGGCANTTAGTGGGTAGGCCTGA
ATAGCCGAGGAAAACTGAGCCGTGGGCCTCANAAAGAAAGTTAANGCACCCGCAAGCCGGGCAAC
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CCTATCAAGGAAAAATATTCNAGTTGGCAACTGCNATGCCACCTTGGGACAGGCAAGACCAAGGT
TCTCNTGGGTINGNCCCATAGGGGACTGGTGGGANTTCTGCCTTCTNAAAAATNNAAGNTGCCCC
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GGCANAATTTAGANAATCTTTACTTATCTNNGGGCTTTTAAAAAGTAAAAA

SEQ ID NO: 268 ACGCGGGGCTATTGCCTAAGGACTGCTTCCCTCTTCAACAGTGAAGCTGCA
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ACAGAGCAAGAAATCCATCTCAAAAAAANGNNAAAAANNNCANTCCTAAAAAATTTGTACA
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SEQ ID NO: 269 ACTTTTTTTTTTTTTTTTTTTTGGGATGTTNGNGGTTTAACTTTGTTATGTC
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GAANAGTACGGNACCACAGTTTATTACCAATTCTGACGGAAGTCCNCCTTC

SEQ ID NO: 270 ACTTTTTTTTTTTTTTTTTTTTTTTTNTCCCAAAATGTGTTTNTTGANATGGTTT
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CCTTGCTTTTCCNCCTGTANGCTGNCNNANGACANTGGANCANCCAAACNCAAAAANTACCGNTT
GTGCATGGNTAAAAACNNGGGTGATTTTATACNTCCCTGGGCATTTACAT

SEQ ID NO: 271 ACTTGCACAGGAAGTGTGGCCGCTTGTGCATTCCGTTGCTGCTCCAAATTA
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CTNAAAGC

SEQ ID NO: 272 ACATTTGGCATGATCTGGGCCTATGCGGTCTTACAATCCCTGTATAAACTAG
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SEQ ID NO: 273 ACATGAAGTCCTATACGGTATAATGAGGCAATCAGAGATATAAGGATTGGAA
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GAAACACACCATTTTAAATTTCTTTTCCAATCCCGATTAACTAGACCACAGAGCCAAAAANTTCA
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SEQ ID NO: 274 ACCTTAGTGAGGCTCAAAAGGATTCTTTTGTAGTCTATTTACGCCTTATCTTTG
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SEQ ID NO: 275 ACGCGNNGGATAACTACCGATTGACATACGAATGTTGAGTCTCTGGTCTGA
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TGAGGACNAGACTGGGGCTTAT

SEQ ID NO: 276 ACTTTNTTTTTTTTTTTTTTTTTTTTTTTTNGGCCATTCAATTAATATTTATNGAN
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ATCACCTGAAAGTCANGANGTCGAGTCAATTNTGGCCAACATGGTGNAACCCCATNTTNCATAAAA
AAATTTAAAGATTANCCGGAGNGNGGCACATGCCCGTATCTACTACTTNGGCAGCTTAGTCAG
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SEQ ID NO: 285 GGTACAGTGGCGTGATCTTGGCTCACTGTAGCTTCTGCCTCCTGGGTTC AAGC
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ATTTTAATATTGAGAGATAATGTTACCAACATGCTCATCCACAATAATTACCAAAATTCATATAA
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SEQ ID NO: 286 TGTACTGAGGAAGACACCATTCCTTGACGGTGCTAAGAAGCCAGGTGGATG
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AGCCCTGTGAAAGACCATGACCAACGAGGCCCTTCAGATCCCCCACTGTCCATCGGAAGATG
CTCCAGATGGCTAGAGGGCATTAAGGGCTCCAGCATGGCATATCCATGCCACGGTGCTGTGT
CCATGATCTGAGTGATAGCTGCACTGCTGCCTGGGAATTGCAGCTAAGGGTGGAGTGGAAAATGG
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SEQ ID NO: 287 ACCGCGGGAAACTATATGCTATCTACAAGAAATTTACTTCACTGTGAAGGAC
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SEQ ID NO: 288 GGTACAATAAGTGCCTTGCACATAAGAGTCCAATAAAATTCTTGAATGATGA
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SEQ ID NO: 289 GGTACCGAGTGCACCTATGTCTAATCATGTGTGCATGTGAGGAGGTGCTGGC
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SEQ ID NO: 290 CCAGCGTTTCCCTGGAACTCCTTGGGCGCTCTCTGTTCCACCCTTGNCGTT
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GT

SEQ ID NO: 291 CCGGGCAGGACGCATACAATGACAAAGCCATTTTGGAGCAGAGGAACATGCT
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SEQ ID NO: 292 ACTATAAGTAGATCCACGTATAGAGAGAAAAATTGATTTTGGACCAATTTTCAGT
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TCACTGAAAGAAGAAATAAGAATTCATCAGGTAGAGACACCAATTCTATATTGGTATGCACCTAA
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SEQ ID NO: 293 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCNGAAATGAACAAATATTTA
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SEQ ID NO: 295 ACGCGGGGCTCCTGTCTTGTCTCAGCGGCTGCCAACAGATCATGAGCCATC
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SEQ ID NO: 296 CGAGGTACATCATTGAAATCTTTTGGTCTTGTATTGGAATATTCTTCACGTA
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SEQ ID NO: 297 GGTACTTTNTTTTTTTTTTTTTTTTTTTTTTTTTCACCAANAAGTATTTATTAAGC
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SEQ ID NO: 298 GGTACAACCTTCAAACATTCAGTTTTTATAAAAAAAGGGGCACACAATCGT
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SEQ ID NO: 299 ACTGTTGAATTTGGTTCGCNAATATTTGTTGAAAATTTTACACCTACAATCA
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SEQ ID NO: 302 ACTTTTTNTTTTTTTTTTTTTTTTTTINAACAAGCACNTNCACITTTATTGAATGAC
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SEQ ID NO: 307 ACCATCTCACTCAACTCTTGCAAGAACTCTAACGAGACTGGTATTATTATCC
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- SEQ ID NO: 312 ACGCGGGGAGGCTTGAGGGAAGCATGGAGGTCCATGGCAAGCCCCAGGCTA
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- SEQ ID NO: 313 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTCGGAGGCAGGATCGCCTTATATTGCT
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- SEQ ID NO: 326 ACTTTCTTTTTTTTTTTTTTCCAAATTTACCTTCTTTAAAAATAGGTTGTTGGAG
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SEQ ID NO: 331 ACTTAAATGAAGCATATTCATGTAATGTGCTTTTTTTTTTTTTTTTTTGCAGC
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GCAACTACCTTTCTTTTTNATATATTTTAAGGTATTAGTTATCTTCTTAACTGGTGCAGNCA
CTTAATGTTTTTATTAATCT

SEQ ID NO: 332 ACAAGATATAATTGATAAACTGAAAAATTAAGACACTCCGAGTGAAGAAA
ACTGAAGTTTATTTGGTCAATGGAGACAAACAAAAATGCTATTACAAATTCAGAAAGGTCCCAAG
AGTCACATAAGATTATTTTGTGAAAAACAGGTATACAGCAATGAGAAAAACAATTAATACATNT
TTCCCTCAAAATGAGATCCCTCCAACTCCCTGCATCACTATTTTCTAATTAATCAAACTAAANAC
TTGTGAGAGAAGATTGAAAAATANAACCTTCAGTTNAAAGCTCTTAAAGAANCACA

SEQ ID NO: 333 GTACAACACTAGTTGGAAAAATGACTTGGTAAAGCAATTAATGTNACTTTCA
CTAATAAAAGAAAGAAATTTCTTATAAATAAAACATNGCAAANAATAAAGGAAATTAATACAGCTGT
CATTCTGGCTATCTTACAGCTTTTTCCAGTCNTATATTTACACCCACTTTATTANGAAAGCTTCTT
T

SEQ ID NO: 334 ACATATTACTGAGACCTTATCTAACATGTAATTGTATCTAATTACCAGACACA
ACCAACCCCAACTGTAGAACTTGGGCAAAACAATTAAGCACACAACCTCTTCTATATATAAATA
CTTTTTACGTTCTTTTTATAAAGAAAAACCTGGTTAGAAATTAGGACATCTAGAGCCAGACTT
AAAAATTTATGAAACCAATGGGCTGACTGATTTAATGTCTCTCATAAATATCANGAATTTTTA
TGTTCTCACAAATTAGATTGTATATTTGTAGTTAAACTCGGTCTACCTTCAATTTCTGATCATT
TGTCTAGGAAATAATACTGGGAATCAACAATAATTTAAAAAGGTCAAATAATGGTCTTATCAA
AAAAATACTGAGCCCAATTCAAATCACTGGCTAACCTACCTACCCCAATGGGTAGATACTTN
CAAAATTTGGNATATTTAATTTNCAAGATCATTTTAGATGTTT

SEQ ID NO: 335 ACCGATCCTGAGACCTTCGTGCAGGCAATCTCTGATGCCCGCTGTGTTTTGA
CATGGGGCTGAGGTTGGTTTCAGCATGTATNTGCTTGATATTGGCGGTGGCTTTCNTGGATCATN
ANGATGTTA

SEQ ID NO: 336 ACAAATGAGACAAAGGCACAGAGGTTAGTTCATAGCTATGAGGCACAGG
CAGAATTCAAACACAGGCAGTTGGCTTCAGAGACCATGATCTTAACTGCTATGCTCTGATGTCTC
TCCAAAAAGTATAAACATGAGCAGGGTTAATTGTAGCAGCTACTTGGTTTTTACGTCAAGAATCA

TAAACCACAAGAGGAAACATGAAGTTTTTGTCTTTTACTTTTCAAGATGGAGTCTCGCTCTGTAC
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TCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGTGTGTGTACACCTGGCTAATTTTTGTATTT
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CTC

SEQ ID NO: 337 ACTTTTTTTTTTTTTTTTTTTTTTTTGGNCAATCAACAAGTGTATTGATCACC
TACTGTGTGCCTGGCACTGTACANATAGTCTGGGGGATACAGANAGGTCTAGGATATGGCCCCC
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AAAATTGTGAATGCTAAGCATCAAAAAGCAATTTATACATTGAGGGTTGGGGAGGGAGGGGT

SEQ ID NO: 338 ACCTAGGGAGTGGCAGAGTAGTGATGTAACTCAGGTCTCTATTACTCCTCG
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CATTTTTCTTCTGGGACAGAGTCTGGGAAACCTTTCTTCACTCTGTTTCTCTCCCTTTTTATACA
ATTATTCAGGACTCAGCTCAGACTTTGCTGGGGTTGCTGTGTCACTACTCTCANTGTAACTTGG
GAAAGTCATTATACTCATGCTGTATGGAAATGTCTGTAAATGTCCAATCCTGCATTAACTCTGG
GCTTTCTAAGGCGGGAAAATACCTTCATAGCCTCAGTANCTGGCATGTGGTAGGTGCTTCGNTCTT
GGTTTTTGNITGGTTGGTTGGTTTCTGGTTTTTCATTGGCTAGTTTTATACAGGGATTGNAAAACC
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SEQ ID NO: 339 ACATTTGGCATGATCTGGGCCTATGCGGTCTTACAATCCCTGTATAAACTAG
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SEQ ID NO: 340 ACACAGAAAGGGAGGTGTCAACAAAAGAAGATAAGCCCATACAGTGCACAC
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TTACATGAAGACAAAAAGAAACAAAAACAACATATTTTGTAGTCCCCAGTCAGGTAGCCTTTC
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GAAAATGCAGCACTCTAAATGGCCACTCAGGCGTTCTTACTCGGAAAAATTAGGTTCAATTTC
CAGGACACAGCAGTGATGATCAGGCTTCAACTTAACATTTAAGGGAAATGTGAGATTTTTTTTAA
TTAATGAAATGTGAATGAGGAAAAATTTTTAATATAGTCTTATCTACCAACATCCCCATAGATT
AAGGATTTTAATA

SEQ ID NO: 341 TCATACAGACCATGGAATACTNTGCAGCCATGAAAAGGAACANGATCACGTT
CTTTGCANAGAGATGGATGGAGCTGGAGGCCATTATCCTTAGCAAACATAATGCANGAAAAAGAAA
CCAAATTCCACATGTNCTCACTTATAAGTGGGAGCTAAATGATGANAACACNTTGACACATGTTGC

SEQ ID NO: 342 ACTTTTTTTTTTTTTTTTTTTTTTGGTAGANACAGGGTCTCACTATGCTGCC
CAGTCTGGTCTTGAGCCTCTGGACTCAAGCAAACTCCTGCTTTGGCTTTCCAAAGTGCTGGAATC
ATAGACATGAGCCCCATCCTTGCCAAATTTTAAATATCATATATAAAAAATTCGGACTTTTGTGTT
AGCTTTCTGTTTTTAAATTTCTCTCAAATTAAGGAGCAGTTGAGTTTGTGACTAAGAGCTTGGG
GTTGGGACATGGAAGCCAACCTTCCATCCTCAAATTTGTGCTCATATAGTTTATGAAACTACCAC
AGACTCAACATNATAATATGAAAAATGTAAATACAAATACATACTATCTATAAAATNATTAGCCA
TATAAAGAAAACTTCCACTCCCTCTCCTTCTCTGCTCAAA

SEQ ID NO: 343 ACCTGGNGGGTCTGTTTCAATNTNCCAACCTGTGTGCCATCCACGCTAAGAG
AGTCACCATCATGCCAAAGACATCCANTTGGCTCGCCGGATACGGGGAGAGAGAGCTTAAGTGA
AGGCAGTTTTATGGCGTTTTGTA

SEQ ID NO: 344 ACTTTTTTTTTTTTTTNGGGNTTTTTTAAAGTANNGGGNGTNGAGCCCCGACG
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NTNTNTCTANAGCCCAAAGAGCTNTNTTCTTAGGACTANCAATTTAAATNTACAANGGGATCCT
AAAGGGNTATGTGGNCAATNTATAGTTCANCGTANTTATCTATNTTNGNTNAACCANCNTNT
NANCAAAACACTGGTATNGTTATGNAGCCATCTACCTTAAAAATNTTCTCTCNTNTNTNTCTACA

TATTACAGATTGNGCTTTNTNTANGNCTGGGCCCTTTNAANAAANNTTNTCTANGNGTTTAAATNGNG
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AAANTGANGNTNATNNNTTANTNTTATNAATNNATGGGNAAAAAATNCTCTCAAAACTATNCTA
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SEQ ID NO: 345 CGAGGNCNCGGGGGGACCTGGGCTGCAGTCTTTCTATTGTCAATGGCCTAT
ATGACCTATGAGGTTAGTTAATCNTTTAGAATCTTAGTTTCTTCACTTGTAAAAATTAGGTAATTGAA
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AGGAAATACACATTAGAATATGAATGTCTTCTCCACATTATTCTGTAAATCCTATTACNTCCCAT
TATCCANAGTAAATATGGGATTNCAATGAAGTNTATTAGTTACCTAACACTTTAAGCCTAATGGT
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TCTCGCTNGATTAGCNCCTNTGTGCACTNGATTNTNCTGTATTGGCCATTTNNATGCGCTNNNTGCT
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SEQ ID NO: 346 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTACGNGGNTTTTTTTTTTTTTT
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TCNTAATAACNTANATTTNAAANNANAACCTAANCTAACNCGCTNATTTTCTTTTAAACNGGCTAA
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NNTNNTANCTACTTTNACNTATANTTCNNTNAANTTTTCNGTACNTTTATNNTGTTCCNTTTATAAA
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SEQ ID NO: 347 ACCGGGGGTAGTGNCCTATTGTCAGATAATTTNAGCNTAGGGNCTGGGGGNT
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AGGCCATGAAGCTTCCCAACTTNTTCNCCNTTTNTANTTTATTGAAACTGGGNCNANTCGNAGCA
ANNNTGCATNTCTTGCTTGCNTTGNCATNTGATTACTCCAGATNTATTAC

SEQ ID NO: 348 AATNCGCCCTTAGCNCGGNCCNGGCCGACGNACANCGGTACCGCANCATGG
GCCANAATGTGTCATATTACATGCTCTACTNAGTGGAAGAAGATGAANATGCCNACAAGAAACAG
NTCGCTNAAAGTCTNTGTGCAACANNANGAGCCCCGAACGTGACTGN

SEQ ID NO: 349 ACTNTTTTTTTTTTTTATTAGANTTNTNAGACACACTGTCTNNGNTNCCAA
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TATANNCNACNTGNCNCAACCAAAGNGANGGAGNNTACNGGCATTTAACCAANTGCCNCGNCC
TGAANANCNGTTTTNTGATTTCAANNCTTTNNTNGGCCCTGGCGANTTCTCCTTACCCGNATNNAT
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SEQ ID NO: 350 TCGAGNGGCCGNCNGGCANGTACATTCAAAAANCNTNAGGAAATATTNTG
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SEQ ID NO: 351 ACTGCATAGATTAAGAAATCNACTGCNGNANNCCNCTCGTANGGAANGA
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NAACAGGTNATAACCANCTGATAAACACCATANANNNGCATGCCAAGCATGTNNCNCATNTGG
TGTGACCAANNACTATTCATANTGAACAAAAGTTGTGTATANATNCATNCNAAAGGGCAAACTCCC
TCCNATGATAATACCAGGCTAAGGGCTTCTTAGAACNGNTGTTATGGAATNTNACNGNGAGAAN
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CA

SEQ ID NO: 352 ACGGTTCTTCTGTGTGCTGCTGCTTTTAAAGAACCAAGAAG
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TCTANTCCACCTCCGAGCATNGGCTC

SEQ ID NO: 353 ACGCGGGGGCTCAAAGNNGGCGCCATCCGGGACCGGCGGTGTCTGTGGCCG
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TGNTNCANCAAAAAATCAAATNCTAAAAATNCCCTTCCAGGTINGTTNACAANTNCTNGTTGTATNC
ATCCNTTAACCAANCCACCCGCTTGAGGAAAGTNACCCCTTGNANTGAGCAANCAAAAAA
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SEQ ID NO: 354 ACAGAAATTTACAAGATGTCAAACACAGTGATGCCATTTGCTATGTTTNAAT
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AAAAATATTCTANAAAAAGTTTCACTAGGTAAAGTNTGCAATCNTTATNTAAAAACCTTCTTTAAG
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NTTTGANNGTNTNANANAATTTGNGGCCAAGAAANTACATCCCNNTNGINTTAAATCCANGTTT
GAGGAACNTTANATTTTAGGGTTTATAAACTTNGGCTGATTTCCCGCCACCAGNANAGGGTTNC
CATCTTTGCCAGTAAAAATAAANNANCTNNTTNCATAANCTTTGANTGGNGGCTNNCNGGATC
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SEQ ID NO: 355 ACTTTCCTACGGCAGCAACCTGCTGACAAAGAGGATCCACCTCCGAAACCC
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SEQ ID NO: 356 ACTCTTTGTTTTGGCACACTTTTCTGACAAACAGCCGGTGTCTNAAACACNT
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SEQ ID NO: 357 ATTCGCCCTTACCGNGGGCCNGNCCGNGCGGCNCCTTGGGTNTGAAGGGGT
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SEQ ID NO: 358 GCGAGGTACTTNTCTTCNCTTTCTTTTTTTTGTTCANGTNGCNCNATAC
TTTNNCCACTNTGNAANNNGTACCAGTTAATTNCTTTGANTGTNGCTAAAAAGGACNTTATGTGT
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ACTNNNGCNGNTCACTGTGTCTNTATGCTCNATTGAGNCNTGTNAAGTAGATGTGGGTTTATNANN
GGCANGTTTNNCCNANCATGTNCTNNTTGTACATAATANGCCNGNTCNTCANTGNTGGANAT
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SEQ ID NO: 359 ACTTNTTTTTTTTTTTTTTTTTTTTTTTTNTTGTAGCTGGANACTNNCTNTGTTG
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GNTTGGGATA

SEQ ID NO: 360 ACTTTTTTTTTTTTTTTTTTTTTTGGNGCNTTTTTNTTAAAAAGAACNAAATNT
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SEQ ID NO: 361 TCATTTCTACCGAAGACTTNCNCCGAACNTGTCTGCCAATGAGATAAANTTG
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NGANATAAGGCCTTTTTCTTNAATCTTATCCNNGTNCATACNTTNTCAATGATCTTGCAATCN
GCCCTTTTGGGCNNCNTAAATATGGGAAATTAANTTTTCTTCCANTCCANAGATCTCNCNTNATTTG
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SEQ ID NO: 362 CCCTTNNCGTAACGGCGCCCGGGCAGGTACTATTANCCATGGNCAACCCCAAC
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SEQ ID NO: 363 ACTCTTGGTTTGTCAATGGGACTTACCAGCNNTCCACCCANNANNTTTTINATC
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SEQ ID NO: 364 TNCGNATGCTACTTGNNCANTGATGGTAAAAGGGTAGCTTNTGTTGATCT
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SEQ ID NO: 365 ACGCGGGACAGNCCNGNCCACAGANNANGGCGATANTAACTTATTCATTNC
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SEQ ID NO: 366 ACTTTTTTTTTTTTTTTTTTTTTTGTCTGGTGTTCAAATATTTATTTTAAAGTA
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CNATTTCCAAANACTTTTTTATTTCTTNCCTAAATTT

SEQ ID NO: 367 ACATCACAACATGCTTTTAAANNTCATTATGCATTGTGCTCACATTCCTTAA
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SEQ ID NO: 368 ACGCGGGGCGAGTTCGGCCATGGCCCTCCTTGAAGTCAAGTCGTAGTCTCGC
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SEQ ID NO: 369 ACGCGGGTGGGAATGACAACCTTCGGTCGTGGAGGAACTTCAGTGGGTCGTG
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 GCCCTATNGCGGNGGANGGCCATACCTTNNCAAACCAACNAAACCAANGNGGTTNTGCGGTCC
 ACAACACCATTTNNCTTTGGCAATTGCAAAANATTTTNNATTNNGAAACCAAACTTAACAAGAAAA
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SEQ ID NO: 370 ACTGCTGGGCGGCTTCTTCGCGCTCGTGGGGTTGGCCAACTCTCGGAANGA
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 AAAGGGNTNANACCCTTTTNAAAAAAATTTTAAATNCCCTNCCCGGNGGCCCTTANAAAGG
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SEQ ID NO: 371 ACAATTCATCTAACTTCCGGAAAGCACTTTCAGTCCAAATGCATAAACCGTCC
 CACATGCCCNCCAGAACCACTTNAAAANGTCAANTTNGCTAACTTTAACCAAGNANTTCNAGG
 GNTGTTTNTNAAGGCCTNNNTNATNCNNTNNTCTNNTTNTAANTNATNCNCGGCCCTTGCCTG
 NNTNCGGNAACGGTTTTTANTTTNGCNTT

SEQ ID NO: 372 ACGTCGACCACTACAGATCCCTGGAGGAGGACCANGAACCCATTGTTTCACA
 CCANAAACCTGGGAAAGGCCACANCAATTCCTTCAAGANAACTTCGGGGCCAACCAANAACN
 ACNCTNNGNGAAACCCCATNGGAAAGGGGTTNGGANTCAAAANAAGGANCACNAATTTTCCAN
 NANGGCAACCCCCCGNGGATNCCNANAATGATNAAAAGGCCNTTNNGGTGANCNANAANAAT
 NCNCNANGGCCTTTTCAANANGNAAANCNAAGGCCCTTAAGGGANAATGNAGGGAAAAAC
 CGCCCTTTTGGCNTNAAANAAAGANAAGGGCCGAAAGGGCCCNCTNAAAAAANTNTTT
 CCTNCTTAAAGGCGNTTTNNNAACCCCTNTAAANCCCTAGCCCNAGACCCCTNATAAGCCN
 AATTTGGCAAAANCNATCCANGGTTNTGAAAAANCTTTACNANNGNNAANGNCCNGNACCTNT
 TGNCCNAAANGNTAAAAANAAGGTTTTACCCCTNTAACTCCNAAAGGGAAAGGCAAACTTTTG
 GNTATAAAA

SEQ ID NO: 373 ACCTTGGCCAGGTCTCCACCAGGCACCACAGTGGGAGGCTGGTAGTTGATGC
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 CATNGNGANGGTCAATTTTCANCAATTTNGTGGNTNGCTNAAANCAAGCNTTGGTGANNTTTNNT
 TNNANAAGCTNNTCGTGGAAGNTTTNTNAACAAAAAANNANCNGGGCNTTTTNGGCCAAAGGA
 AATGGATTCCGGGGTNAAGGTACCAAGTTTGTCTNGAATTNTNGNAAGGNAACATTTAAGGNTTCA
 TTNAATNTTAAAGGNACNATGNTNGGAGAACAATTTGGTAATAANGGGGTAAAGGTTATGTNNGG
 TGGCCCTTNTATTAGNGGTTTATAAANAATGNTATAANGGGCNTTTNTGTNACNNNNAAGGCAN
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SEQ ID NO: 374 CCGCGGCGAGGTACTTTTTTTTTTTTTTTTTTNTGGGAGTTTGAAGCAAACA
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 AAAATTNTNCAACAANCATNGAAANNTGGGCTTTTTTTTTTTTAAACNCAATTTGTTGGGTTTACCC
 CCCTANNGATAAAACNTNTNCANTTTTACNCGCAGGNGGANTAACTTGGCANCAAAAAATNGCA
 CCCCCATTCAAAANCTTNAAGNANTACCTNTCCCCCTNTAACNAAAAAACCATTNTTTTNGAA
 TTCNAAANATTTNATTTTNGGCTNAGNTTNTAGCCNNGTTTTTGGGATTCTNAAAGGGTTTACCC

AAAAAANGGAAAAATAAANCCTTTTGGGAACCTTTTCNNTTTTTTTTNGATTAAANCCANGGGAAC
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ANCCNCACTTTTNCNCCCAACCTNTTTANNCCCTTNNATTTGAAATTNCCNTAAGGATTAACANC
CNAAAATGGGGGCGGNTNCTT

SEQ ID NO: 375 ACTTTGGCTCTCTGGGATAGAAGTTATTCAGCAGGCACACAACAGAANGCA
GTTCCAGATTTCAACTGCTCATCAGATGGCGGGGAAGATGAAAGACAGNTGGTGNNACCACANTT
TCGTTTGATTTCCACNNTTGGTCCCTTGGCCGAACGGTCCACGGGAACACTNTNATNTTGGNTGA
CTNTAATAAACTGCCCACAATCTTNAGCCTGCATGCTGTTTGATGGTNAAAANTNAAANTNTTTT
CCAAAACCCGNTTGGCACTGGAANTCGGTCAAGGGGACCCNCGNATTTCCGGGTAAGATTGCC
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CNTCTTGACCANAACCAAGTCAGGGGGTTTTNGGA

SEQ ID NO: 376 CGCGGAGGTAAGTGCCTCATGTGCAACATTAAGATCCACGAGACACAGCCNC
TGCTCAACCTCAAACTGGACCGGGTCAATGCGNNGGAAACATCGTGTAAGCTGGGNCCTNGNC
TTGGAAAGACAGTGAAANAGAAACCGGGTTTCGGGGAATTTTACCCAANTCCCGNNNGTTNGG
AACCGGGTNNACCAACCCNNTTGGGGAANGANCCNANTACTTGNCCAACCTTCNGGCTTNC
TTTCANNAAGNTTGTGACACTNNTAAGGCCANTACTTTTGGCTTATGATGANCAAGTTNANCT
GTNCCNTTGAACCGG

SEQ ID NO: 377 CGTNCCTAAANTGAGTATCAACTGNTNNTGCCATANCACTGTGNNAAANTGCA
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AANNTGTGCGCNATATTANTCACNANGTTANTGGCTGCTNCAANCTTATNACANTANCTTGNNTA
ANCTTNGACTGCTTCTNANGAAANNCCTGCNNNGCATNTCTNTAAAANGTNTANTNACAN
TCGACTTTATCTCTG

SEQ ID NO: 378 ACAGNTGGACCTNNTGNNATTAGAGGCNNTNNNGGTACCAAGGCCCTNCTG
GCCCCACTGGTCTATTTGGNCCTCCTGGACCTCCAGGTGTAATNCGGTNAACTNCTNGACTNAAAGC
AATCATGGACNTTATNCTGGNTGTTACAGGGGAATANCCAACTCTTTACTGTATGCANANNTGT
ATGAAAAAATAATTAATNCTTTNATGACTGNNAAAGGNTTAAANNTGTATCNTCTGAAANG
NAANGNTTANNTAGGNGGNTTNACTNATTCAAATANTTTAA

SEQ ID NO: 379 CATGCCTCGAGCGGCCCGCCATTGTGCGATTGATTTTNGCATTNTTCNNACTT
TCTTCAGCTTCANCCCTAACAATGTACNTATTCTNCAATNTAAAANTTCNCGGCNTCCNCTNCT
NNCNTCTNNGCTCTCNGGTCCGCTCTCCTCTCTTTTCGATN

SEQ ID NO: 380 GTACTCTTGGTTTGTAATGGGACTTTCCAGCAATCCACCCAAGANCTCTTTA
TCCCCAACATCACTGTNAAATAAATAGNGNGATCCTATACCGTGCCAAAGCCCANCTCCAGAC
ACTGGGCTCANTANGACCACAGTCCNATACNATCACAATNTCTATTCAANTAGCCCNCCCTAAA
CCACTTNCNTCATCATNCAAAACANCTTNNAAACCCNNTGTGAGANATNGANGATGCTNTANCCNT
TAACTGGTAANCTTGANATTNAAATAACACAACCCNACCTGTGGGNGGNTNAAATNANANNT
NTCCCANNTAANTNCCAANNTTCTATNTNCCANATTGANNANNGGAGCCTTTATTATANATNA
ATTGACTNAAAGNTCGGANTATTGACCTNCGTANATTTNANTNTA

SEQ ID NO: 381 ACTCCTTGGCGCCTCACTAGCACTCTCCGCCTGCTTTTTAAAGGCTTCATTG
GAGCCAGCAGCGTGGCCTGCTGCNAAATGAGAGTCACCAGNCGTTTAAACAGGAAGGACAGC
CANGGAAANCCACANTGTAAANNTNCTTTGGGCCGGGAAACCTTATTNNGAAATTTNCTNT
TGCCCCGGGATTGNTCTNGAAGNTNAACTTTTTCGGNAAAAATTATTNNTTTCCAAATTTTCNCC
CCGGATTGATTANCAACCTCCCNANGGTTTANCATTNANAACCAACNAAAAAGGNGTTTGCCA
TTNGANACTTANAAAACTTCANCANCCCGGACTTGAAAAATTTTNGCCNTTTTTTNGGGAAAAA
ATGAANGGGAATTNCCGAAAGGCCACNCAAAAAACCTTTCCCATNAAAGAAAGGTNCAACTTC
ANATCCAATNCAAAAAAT

SEQ ID NO: 382 ACCGTTGCACTCCAGCCTGNNCTAGATANTNAGATNCTGTCTCAAANNAATT
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TNTNTANANNAATATTAAATTAATTNATCTNTGNTACNANTTCTATAATTAATTAANAAATTTNTN
TAATTAATCTCTATNTNTNTTTNATAATTNCAATNTNACCTNNAANCTANNAAAATTTNATNTA
TATNAATTTCTNTAAATNTAANATNTAATATTNTATANCNAAANTAANAAATNTNAACTNATATA
TANTC

- SEQ ID NO: 383 CGTACTACCGANATGCCCGTTCTTACAACCGGTNTCAAATCGNACACTGTCA
CCGAAAAAGGTGTTGAAATNGAGGGACCATTGTCTACNTNAAACCACTGGGATNTCGNCCANAT
NAACANTGGNCTNTNNAATGAAATACAGATGCNTCTTTCAGAACTGANAGTNGCCCTACTNNTAA
CTATNAACTNGGCT
- SEQ ID NO: 384 ACGCGGGGAATGTCTGAAAGTCCATGAGCTGTCTTTAATAGCGGATTATNAA
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TGCANATTGNAACATTATATCANAGTTGTGNTTNNNTAATTATANATATATTTCNTTATNAAATT
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- SEQ ID NO: 385 ACGCGGGGGACTGGAGACACTGAAGAAGGCAGAGGCCCTTATAGTCTTGGTT
GCCAAACAGATTGCAANATCAANGANAACCCANTGAGTTTCANANAACCGCTAANTANGTTATA
GANATTCTAGTNTATCATACATATTTAAGTAINNANTAATTNNTTNTAATATANACNT
- SEQ ID NO: 386 ACTTTTTTTTTTTTTTTTTTTTTTGNCTCTTATTTTCAANNNTTGGCTTANTA
ANATTTTTCTTATTTTATAANGCNATTACNACAATTTANGNAACNAAACNATTINAACNAAAAAT
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AACNCNAAAAACCTTCCGCTTTAATNANNTNAAATNCNNTTAACTTNTATNGGATGCNTAAAC
AAANCNAACTTTNATNCNATTNAAATNAACTTCATTNATTGGACNAAATNCC
- SEQ ID NO: 387 ACTGCNNGGACTTCTCCTTGCTGCTGCCATGTGAAGAAGGATGTGTTTGCTTC
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NACTTATANNCCANTNTTTAANACANNAGTNTTTTAAGTA
- SEQ ID NO: 388 TCCNCGAACCNGCCCGCCAGTGTGATGGATATCCTGCANAATTCAGTCTCT
ACTGGCNGCCGTTACTACTNGATCCNAGNGGGNTNNCATTTTTTCCACTNATATATGGNNATACT
TANCTATTCNNNCTATNNTATTTNGANCNNCNTAATTAATTTTCANATNATTATTAACCCANANTN
CNATGTAATTTNTAGTTANATTTTACCTTTAATAATTTNTNNTANNTTATAAANAATAAATTCANTCNA
NNTNAAATTTNAACTCTNTNATTTATNTTATAATNTAATGANNNTATTTNATNNNTNATATTATNA
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CTNTGAAT
- SEQ ID NO: 389 ACTTTGTGGATAAGAAAATGGAGGAACACATCTNATGGANAGTGGGCATTGG
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- SEQ ID NO: 390 ACCNNGGNCCNCTATATCGCNAGNCTNTTCTNCCNAAAGAAGCACACTTTG
TGANANCCAATGGGAAGGAGCCTNANCTGCTGNAACCTATNCCNTATNAAATTCATGGCATAATAG
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NTG
- SEQ ID NO: 391 CAANTNTAAAGACCCTNAGGAGTTCATGGANCACATATATGTTCCCANAGGA
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GCTGNTGNTNACATCNTNGTGCTTTTNCCTNAGGGACCANATGAAACTCCAAATGCTTGGATGT

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SEQ ID NO: 392 TTTTCCGAAGCCGGNCCGCCCGGGGCAAGGGTACACCTTGGTTGGGTGTTT
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CCCAANCATTANATNANTCCATAAACTACCNANTTANAANNCTCCCCCTACTCACACTATCCT
CCTNCTCGGNTGCNAGCCATTCCACACCNCTACCANTCCACAANCTCNCCATNACTCCCCCTTN
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SEQ ID NO: 393 ACGCGGGGAGTTCGTCGACGCGGGATTGGGTGCGCAAGTTCTTGGTTGTG
GATTGCTGGGAATCGTACTTTGACAAATGCCAACTTTCGGTGAAAACTCTTGACTGGGTAAAG
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SEQ ID NO: 394 CGTGCACTCTGNTTGTCAATGGGNCCTTNCANCAATCCACCCCTNGANCTCT
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ACATCTCCAAACCCCTTGGNGGATG

SEQ ID NO: 395 ACGCGGGTTGAAAAAGAAACAAAGGAATACTTTGAGAGTTGGGGAGAAAGT
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SEQ ID NO: 396 ATNCNACCCTTCAANTTCATANGGTGGGGGAAAAACCGCNGGACTTTTANAT
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SEQ ID NO: 397 ACTTTTTTTTTTTTTTTTTTTTTTTTNTAGCACTTTTTTTTAACTCGGTAANAA
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TTTTATNTNATGAT

SEQ ID NO: 398 ACGGGGTCCCTCACCAGACATTGAATCTGCCAGTTCCTTGATCTTGAACCTCT
CAGGCTCCANNACTGTGAGAAATATGTTNTATGATATTTGAAANCCNCCCAATATATNATCNGTG
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SEQ ID NO: 399 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGGGGACAGTGCAANAANANA
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SEQ ID NO: 400 ACTTCACACANGATCCCAACCCCCACNNANNTTCAATGTGACCNCTGATC
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SEQ ID NO: 401 ACGCGGGGAGCACGGTTCGTTTTTCTTTTANTCAGGAAGGACNTTGGTNTTTA
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- SEQ ID NO: 402 ACTGCATTTTTTTTTTTTTTTNATAAGGCTTATAACTATGGCTGGATCTTTTG
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- SEQ ID NO: 403 ACGGATGCTACTTGTCCTCAATGATGGTAAAAGGGTAGCTTACTGGTTGCTCTCC
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- SEQ ID NO: 404 ACTTCAAGATTAGGANNGTGGGTTTNACATAAATGTATTCTCTGGTNANGGT
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- SEQ ID NO: 405 ACNCGGGGGGTGAAGNGTACAAGCTCCTCCTGTTCCACCCCTGAATTAACCC
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- SEQ ID NO: 406 ACNCGGGTGATCCTAATGTGGNTANTACTNNTNTGGANANNACTCCCTATAN
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- SEQ ID NO: 407 GCNTTIGAAAGATTGGGGCCCTTCTANGATTGCATTTCTTCGANGCCGGCC
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- SEQ ID NO: 408 CGTACCCATCTCAGATGAATGGNTACGGATCATCACCTACCTTTTCCAGACG
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CTTTT
- SEQ ID NO: 409 ACCCGNNGGGTNGCTCNTATNAAAACCTCATNACAAGNCATTTATTCTGT
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- SEQ ID NO: 410 GNNCGNCCGGGCACGAACCNCNGGGGANAGATNNANAATNATTGCCAGNC
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SEQ ID NO: 411 ACCTAACAAACCCACAGGTCCTAAACTACCAAACCTGCATTAAAAATTCGG
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NTTGTGNGTCCCCAANCTCTTGGGAGGNNTTTCGTGGCG

SEQ ID NO: 412 NTGTACTTTTTTTTTTTTTTTTTTTTTTTTNGAGAGGAAAAACCCGGTAATGA
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SEQ ID NO: 413 GGTACTTTTTTTTTTTTTTTTTTTTTTCCCTCCCCACANAACCCATCTCAAAT
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AACNCTGACNNNACCTTNGTNTAAATTNNNTGNNNN

SEQ ID NO: 414 TCNAGCGGCCGCNCNGCGGCCNCTTTANANATTGGCNCCTATTGGNTGANC
GCGAGACNCTTAGNGCCATGAATNATTACACAGTAGGAACAGGTTCTTTATNGAGACTGGACTG
CATNGCTCTNAGATGATGINTGNGGGGTAATCNCAGACTCTAACACTTACTGTATTACTTTATATG
CGTTAGTTAACNNCTAAGNNCTAAAANACGTATAATGTNNNTAGGACGCTCTCCATNTANTCT
TGGAATACCCANNTNNTGGNNTACTATNGATNCTAAGGGGTCAGGCTTATGGCATGCCTATNGC
TAGNGCTNAANGAGCGTAAAAATGGCATCTNTTAAAAATCTCTATGCATAATCTATGCTATCCAATG
NNAGCACAAATTCNTTCAAGAAAGCCNTTCAACATGAAGNGNACTGCNTGGANGGGAAAAGAAC
ATTGGTACTTTTACTTTAAGANANCGTTAATTTTTCNCAANGNACATGGNANAAATTGATTTNT
TGNAACATAATATTGCGCTTTCNAAGNTTATCAAGNGGCANNNAATTTGTTTTANGTCCCTCGGN
CNNGGCACCCCTANGGNGANNCCNCCNTNNGGGCGTACNNGGGACCANNTTGGTCCAATTTG
GGNAAATGGCCNGGTGGNCCCGGGGAAANNTTCGGTCNGTTCNNAATCTTCGNCNGGACNTNA
GNTANG

SEQ ID NO: 415 GGTACTTT
TTTCTTCTTCCCGNGTNCCTGGGTNTCATTTGNAATATAGNGACCTGAGTCCAAAGCAAACCCAC
NTNNTTTANAANAGGNGGGCNTGANTTAAATGTNTCTTNGGAAAAAATACCCAGGCCTTTAT
GGGGNTNCAAAANTNTCTAACTCCNGGGGCATAATNTGGANAAATATNTTATGTTTCCATGCT
GGNCCCNAAAATAAAGGAAAGTGAACCCNAGGCTNANAANCTGTTNTNATTTNAAAAAATTTGA
CTGNCATTTTTNTAGGAAACNNGGANTNCTTTTTTGGCCCCNAAAAAAGGNTATTGAANGAN
ANNNTCCNGGGCNGGCTTTNAAANGGNGNATTCANCACANTGGNGGGCGTTANTTTNGANTCC
NATCNTTGTCCAATCTTNGNGNAAAAATGGNAAAAATTTTCTTNGGGAAAAATGTTTTNCNNTNN
ANTTCCCNATAATTTNANNCGAANTTNAAATGTAAACCGNGGGNCCAATATGTNANNNTNTNT

TTANTGGNNNNNTNNATGTCNCTTTTNAATGAAANCTTNNNNCCNNNTTTAAAAANNCCACTN
CCGNANANNNGNTTNTANTNGGCNTTCTCTCCCTC

SEQ ID NO: 416 TCGCGGGTCTCGTGAGATCTGGTNGTTTAAACGTTTTTGGCACCTCCCCACA
CTGCTTGGATCTGCTCCTGTCACTGTAAGGCACCTGCTCCAGTTTGCCTTCTGCCATGNGGAAAAG
TTACCTGAGGCCTCTTCAGANGCAGAAGCCGTCATGCTCCCTGTACAGCCTGCTTAACATGAGCC
AATTNAGCCTCTTTCCCGTATAAATTACCCNGTCTCANGTATTTCTTTATTCAATGCNTGANCAGAC
NACTACTAAGACTTTATTGAANAAATTATAGTTGCAAAGACAATATTGCTTGTGNNCANGGATAC
AAAATTGAGCCNTTTGAGAANAAACCGAACTTCAGNCATTANACTNGNGTTANTTTGNGGAATC
NACTGATGTTTNTTATAAANNCTANTGGTGGAAAGTCATACNNNNTCNAAGTAGNTNNGTTTNGG
GGTGANATTTAACTGNATCNCNTTGGGGTANAAAANGGTTTTTANNGGACAAAANGCATTATAT
NNTTAGGNGTNGGANANNANNGCCTACNTAAAAATCCGGAAGCCTTGNCNNCTNTNNTN
TTANGGNAANTTTGGNGNATCGNGNGNGNNTTTTTTGTGTCNCGAATTNTANNAANTTTNTG

SEQ ID NO: 417 TTGAANCTTCCTTTTGGGCCCTTTCTTTCCNACCTTGCCGTTTACCGGATACCT
GCCGNTTTTCTTTNGGAANGNGGGCTTTNTATAACTAACCTNNAGGNTTAAATTNNGGGGG
NGNCTTCTCCAAACNNG

SEQ ID NO: 418 ACACTAANATTTTATTAGNNATCGCTCNGCTTACACACTCCANGCAGGAAG
TTATTTAAATCACCTCANANAAAACCTGNGTGACCTAACCNANTACNTNATATGCAGATCATGAN
TACTTCCANANTANANTCACCNAAGNTNNNANGGNCNTAGGCCCTACGTGNANGANATGTNGCT
TANNTGTCTCANTGTAGGGANANTAAANAGCGTGTCTAGCTCNCNTNTCTACTNNGACAACNCTT
ACTNNCATGATGANTCGTACATANTANTCCGTGCGNCACAAACATNGCTGANGNANGTGGCTTTA
CATTTCTTNTCACACGATNTCTGCGACCCGCGCGGATTAACTCCNGTATGCTTANNNTAAAG
CTCCACAGCTANATTAACAAAATTGCNNGGNAGANCANTACAANNCTCNGNTTACAANTTAAAG
GACCTNGGCGGGGCTTNTATCTCTACAGGNANCNNGNCNTNTATTAATAAAACCNCGATNC
ACCTTACCNCTTTGTTTNNCTTTTCCGGCTTNTTGTGTCNAANCTGNTGAANGCTCCAAGTTTA
CNCCTTNTCTTCCNGGGCGGGCGGTGAAAGGCGANTTTAAACNNTTGGNGGNGGTTTTTGGGTC
CCNNTGNTCNACCTGGGAGAAANAAANTNNAANTGNTTCNNNGGAATGTTTNC

SEQ ID NO: 419 GCGTGGACGCGCGCGAGGTACTAGAACGGGACTCATCCAGAAGTACTATGCC
CTCCTNNGTTAANGCTCAATCATTTAAGAGTAAACNCAAGGAGAAAGCCNTTCTGTAATCATACCCN
TCTATGTGGATTAAANGANCNNNANTGAGANTGGNCTATGATCTNCCNNGGCTGTGCTNCTCTT
CTACNANTCTGCTGATCCGGAACANTACTATGNCNATAAAAGNNTGNGAGAAAGNCCNCGNC
TAGNCAATCTATAANGCGGNNAACANCTGCATACNNNAATGCTGGCACNNATNAANTGGCACT
NAGTNGGTGACCTATGCTTATNTATGTCATGATTGNGTAGATTGGATTNNGACGNNAATCAANG
AAGAAATNTAGNATCTNCCGTATCTNATATTNAGAAAGAAAAATGGTGTCTCAACNTAACAATT
AATGAGTNCCTTCGGCCGCGGACNACCCTAAATNGGCGATTTCCAGGNCACCTGGCCGGCCNGTGCCT
ANTNGATTCCCAACCTTGGGNCNACCTTGGNGGAATCATGGCNNNAGCCNGTTTNCCTGGGTGA
AATTGGTATTCGGNCNNNTTCCNCAANAATANNANNCCNGTACCATTAGGGTAAACCTGNGGG
NCCAAAGAAGGNCCTAACNCNATTATTNGGTTGGTTCNNNCCCTTTAATTGGGAACNTTTNGCCC
NTTTTTANTAANCCC

SEQ ID NO: 420 ACTTTTTTTTTTTTTTTTTTTTTTAAAGGAAGGGGGNGTNNACCTNNANCCCTT
TTTNAATGGGGGGNNGNTTTAAGNCCNACNNNGGGGTAAATTTTANCTNTNTANANGGTT
TTTNCNNAGGGCCNAAAAACCTGTNCNTTTTNGGACNAACAGTAAANTTTANANGGGNTTNA
GGGTTNTGGGNCAAATTNAAAGTTAANNNTAAATTTTNTTTNGNANAACCANTTNTNACCAGCN
TNGGANGGTTNGCCCCCTTNTNCTATAAATNTTCCNANTNTTNGNTANANAAACGGGGGGGCTN
TTTNAACTGTTNTAAGGAACCTCGNNNGNTTTCGGGGGTTTAAANNITGGNTNTCNTTGCAAAGTT
TTTNTAGTTAATTCTTTNTNCAAAAGGGATAGGGGTAAACCTNNCTANATTAGGCTNGGTTAAAA
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GGCCNTTTAGNGAACCNAACTCGGGACCAAATTTGGNGAAAAAAGGCAANANTNTNCTTGG
NGAAATTGNTNCCNTNAAAAATCCNAAAAAANAACCGGAACCTTAAATGTAAACCNNGGGGGC
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SEQ ID NO: 421 ACTTTTTTTTTTTTTTTTTTTTTTNGGTTTTTTTTTTTTTTTTTTTTTTTTT
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGGGGGGNTTTTAAANNAATTTNTAGGGGGGAAAAA
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GCCNCCANANGGGNNGGTTAANAANAAAAATTTNTTTNNNTTTTNGGNAATTAANNTCA
AAAAACAAGGGNNGGGANTTTGTTTNTTTTNAACCNNTTTTGTGNTTGCAAAAAACNGCCN
TCTNACTGGGGCCNCCCTGGCTTGGCNGTGCNNACATTGNTGGGATTTNTATGCCAAAGGAN
CCATTTTGGATTAAAAACACCTCCTTGAATTAANNCCCTTTTNAAGGGCTTATTTTCNAANA

GNCCATTAAAAAATNGGGGGTTGGACCCNCCAAAGAAATGGGGGAACACAGTNACCCANC
CAAGGNCCNTTTTAGGGTTTGGTTAAAACTTGGCCAAACCTCCCCTANGGNAAAAATTTTTTTA
GNAANTNAAATTTTTAAAGGAAACCNCCCCATTGAAAAAAAAAAAAATTTTCCTTGNGAA

SEQ ID NO: 422 ACANTATGTNTAATNNTTAAATGTTTTATTATTGGAAAAATAANGCGTGAA
TANNATGCCAGGGACTGNCAAANGACTTGATACAGGATGGNTANNCTTGTCAGCTAAGGNACAT
TGNGCCNTTNTGACCTTATCTTCTGGACTATTGAAANCNAGCTNANTGNATNNAGNATATTACT
ATANCGATTGANNNGGCANTAGTTAAAGTNATNAGCATGATNAGAGTNTCTGNCAATCATGTATT
ANAACTGATTNTNAGNNTNACANAAATGTCAGANTTGCAGCTATTGCNGGAATCCAAAGTNATG
GCCNGCTAGCTAGGTTAAAGATTGGTTTAAATCTGGGATNTTGTCTTTNCCTGTNGACATTGCTT
GANGACATTATCTGANAGACAAGTTTGTNGCNCAGTTGCCTGNTANAAAAACCTTTGNNANACT
TNNTTNTNCAANAGCCATTGGNAAAAATCCGAGGAGNTTGGANNGAAAAANCNNNGCTTTAA
ACTNGTTGCCATTTTAAANANNNTAATGTATCGTNAANTTTAAGCCTCNANTTTACAANTCCC
GCTTNGATAANAGACCTATCAANTNTTTGCTCAAANGCTTNTTACNCTATTA

SEQ ID NO: 423 GGTACTGTNGNNTCATCNNTGGGANNGCCACACCNACANNCCNGCTTTC
TATGCNCNACATNANTGCCNATCNATGGNNANCNNAGANCNNNGCTCNGCNGCNGCNGC
NTTANNNCCNCCNANGANGATCNACANTATGGACNTGCTCCTGCTTNAACGTGGCCAN
CGTCNNGCATCAGATTTGGAGTTGTCTGGCCAAAGGTGGCTCTGATAANCAGCCNTGGTGTNTANA
NGATATTTACGAAGACTGGCNTTANNGGACCATACCTGNANTNTTCTANCTACNGNAANCCCA
TTTTATNOCATGGANNTNTTNAATCAANGTNTGCTNTGGTCTGAAGCCCTATATGCTGGAGATGG
ACNCCNATNAATNATTAAAGGGGAANNCCCTATNCTGANGTGGGGTGCCTTTTACNAGACTT
TACNTAANTATAGACGGGCTAACCTGCAACCATNNTGAGAAATGACTCTTNCNCTNTTGNCAN
GGTTTTCCAAGATGTCNNTACCANACNCTTTTNTTGAAGGNTNTTCCCCCTTAATANNNCC
TGTATCTTCCCTTTTNCNTTGAAGGNGAGATCTGCNTNAGGGTTCNTAAAAAGG

SEQ ID NO: 424 GGTACTTTTTTTTTTNTNTTTTTCTTTGGGAGACTAAAAANTTTATTGCAT
CTTTAAAGCCTTAGGCCGTATGACTAAATGANTAGACTGNANTGACNGCGGGGAGGAAGAANCA
NANGAAAGATNTTAAATGAGGNGGTCNGGTTGGGGGAAATAANNCGAANATTCNCTNCCAGGGTG
AGTCTCACATGGCCTNATGCCCTTGTGANTTGNCCNCCAAACACAGGCTNGNTACTTNCNTT
CTGCACTAGCAGAGAACTTGCNANATTAGGGNNACCTNACATNCCNGTGTAAANTCCTTTCCCC
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NNTTGGGCTNNGGTGNCCTTNTGTGGGTATTGGNACCCAAATTCATACNNAGTTNGNGTAAATTT
ANCCAATGNNACTNTNATCNNGGGAGNAAACNANAAGGATACCTTCATNTCNCAANTTACNTNN
NNCTGGTTTCCAAGAGGCTTTTNTGNTGGNNAATNANTGTTTACNCCNNTATNTNCGGNGG
ATCACATNCTGGGNTNNTGNTGNGNNTCTAACNCCNTT

SEQ ID NO: 425 TCNAGCGGCCGNNCGGGCGGGNTCTTTTTATGAGAAGCGTATGGCCACANAA
GNTGCTGCTGACGCTATGGGTGAANAATGGAAGGTTATGNGGTCCGAATCAGNGGTGGGAACCA
CAAACATGGGTCCCCATGATGCAANGGTNTCTTGACCCATGGNGCGTGTCCGTCTGNTTCCGNGC
AAGGGGCTTTCNTGTNNAGACCACGCGANAAACGGNTNAANAGANTNNATAATATCTCCCTAGGT
TNCCTTGANAGNTNCATATNAGATCGTNCCTTATNNTTNNITNNNGNTAAAAATGGTNAAGTNN
ATTNTCCTGNACTGACTGATACGGANNTTGCCTTTGCCNGTCTGGGCCCNAAACNAGCTTGCANA
ATCCNNNGGATTTTCAATTCNTCTTTAAANAATATNANTGTGTCNGCCNNTANGNTTGNACNAATNC
CCTTACANTTAAGATNGGGNATTAATTCNTGACCNATGCNNTCNATCATTTNGANGTTTATTC
ANTTNNNNNNCTNGAACTCATACCNGCTCGGTNATTTTCGNGGANANANTGCNNGAATTTNGTNN
CNNCACNACATATGGCANNANTNCTTCCANCTGGTGNCCNACNTAATTGAANCINACCTCGGAA
NCNTNNTNGGTNAAAGTNNAGTNGTANNTNCTTCTNTGGG

SEQ ID NO: 426 CACTTCAGCAGCGNGGCGGGAACCTGGGGGTATTGAANAACNGGCAACCN
AAANTANNAATTATNACAGGGGNCAGAACGNCANGCTAGACTTNNCTTCCACTGGTCACAGNATAA
NGGCAACCTGCAAGACTNAAAAGNAGGAGANGANGNNGAATNGGAAGNATCANCGGACCGACG
GACTGGGAAACCCANGGCNGNNAACGGGNGAAGANNAAAAAGAAATCCNCCCTGAAGAACCC
GAANGANGGGGACAAGAAGGGGNNACCTGACNACACCCCGGAAGANGNCGAAGGGANGCNC
AGCNGGAAACCGGAGGANNANANAACCTGGGGAACNGANAACAANAACATACGGGGGCCG
NAANGNCGCCGCAACANNATGGGGGGNAAAAGAAACACGCGCCGNGGGCGGGGAGNAG

SEQ ID NO: 427 ACCGATGATACTGNCNCTTGCNCTGANTATNTAAACACTNCACAGTGTNTAT
ATNGGGAANATATNGGGAAGGAAATATNTNNNTNAAANATGAACGCTGNCNTNTATGTTTTNTCT
NTTTAAACTGGCTCACTTANANTCTTTNAGGATGGGANGNNTCTTNTTGTCTGTANAGCGCTCTN
NCCTTTTCACTGTATGTTGCGGTNNCANGGACCTTAGCTACCTATCANACTTTTCCAANAGTAT

NGATTACTAATGAANANTTTNACNANNCAANACCTGANAAATNTNNNTNNCGTTTTNTACNNTGA
AGCNACANGAGNGGGATCATGGGCGNTTTNCANTAAATCTNCCTGCNNTCCCTNNCGCTGGACAT
TATTATGNCNTNGCTTAATTGNNTTNTCCCTGAGCTTTAAATCANTNANAGCTTAAATTGTCATAT
CCGNTCNTTGGCTTTNCAAGGGGATTACNAAANTTTGGTGNATACAAAAANCCTATTTTGGCTCT
CTTCTACTACTNGAGGGTCNACCATCCTNATTAAATGTNTGACACCATCAATNAATAACAGNTGCT
GTTTCATGTNTAANAAGANCCNANTATTTTATTTACANGCGGGTNACCTGGGCN

SEQ ID NO: 428 ATTTTGGAAAAAATAATTNCCCCCCCCCNCNTTACNTGTCGGNCCCTG
CCNATGGTGGNCTAATNANGAAGCNGNCAGANTTTANCGANCCTNNANAANGANGGANAAGGC
AGCTGNAGCTATNAAAAAACANCNGGGGATGATNNGATACCATCAGTTTCACANANNNGGAGAT
NTGAAGCATTACTNNAAACTGGGAAAAAGGCCNCTTCGGAANGAACTGGTGAAGTGGGGCA
CCACAAATTGCACAGNTGGGGGATCTGTGNATNCCNCGAANCACAAACNGAATTTTNGCTCCNT
GCNANGCCNGGGCNCAGACGCGCNGCGCAAAACCGGCGAANCNACCTCCNAAACAAAN
CTANAANAGNNGCAGGCAAAANACAGAAAGCCTT

SEQ ID NO: 429 AGCGGNCCGCCCCGGGCANGGACATTCCTTGNNGATCCTGCTTGTCTTCGT
AAAAAGCACCANITGGNACAACCTTACCCCGAGTGGCCNAACCAACCTTTGGTTATAAGGAAC
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ANTNNNGCCAAAAANAAAAANNCNTTNNGGGGGGGNAAAAAAANNCNCCCTTNA
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SEQ ID NO: 430 ACAGAAAGTTTATACTATAAAATTACATCCCTAAGNGATTAGGGTCCCTCAGT
AACACANGAATTAAGAAATGAAAAGGNGCATTTGCTCGGGAATCCACATAACTACAGANTAGTA
GCGCAAGCTNTTGTTCGTGATCAGAAAGAGACTTTTTNAAGAACATTTTACATNTTCCCTAA
CATTATGCCCTCNTANTTAAAGGGNNGCCTANGACNNTNCCNTTNTNATTTTNGGGAANGNC
ANCCCTTTTTTTTNCNCAAAANGGNTTTTTCTCTGCTNTAAAAAANNGNGTGGTTC
CCNANGAATGTNCCCTCANTGGANNATTTCTCANNGAAGGTNCCAACNCTTTTCAATTTTT
CANNNGTNTTNTGANNGTNCNNTAGGTGNTTGNAGNANAAATTCNTANNCTTNTTGNNG
ANNNNCCCTTNAAGGANGAANTTNTTTTTACNCCANCNCACANANATATACGNNNTGGNA
NNGGAGCNGNCAANANACCNTTTTANANTNAGTATNTTNGGANTNTAANATATNANNNTCCCG
CNCNANANTTNTTNTTNNAAATNCTNAAANTNTNTTNTNATATGGANNNGTNTNCCNNTCNC
CNTGNTGTTAA

SEQ ID NO: 431 ANCCGTGGTCCGCGNCCCGANGTACTTTTGGCCTTTTCTTGGGGATAGNAAGT
TATTTACGCCAGGGCCACAACAAGAAGGCAAGNTTCCAANAATTTTNAACTGGGTTCATTC
AANAATTGGCCGGGNAANAATTAATAAANCAAAATTTGGNCCNACCCCCAAGNTTNGNTTGA
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GCNAAAAATGGAAACCCCTTTAATTTTGGGGTTTGGGGGCTTCCCTGGGGCTTTTGTGATA
NCCNATTTNCAAACTTNNNGAATAGGGCCNTAACTTTNCCGGCNAAAAAAAGGGNAATCCCN
TTNCCCCAAAAANCCAAAAAGGGGGGGTNGGGAANTTGGGNCACCCNNNTNTTAAATTTT
NGGCCCCNGANAAAAAANGNAAAAANNGACCCCCCAAAANTTTNAGGGGGGGGGCCCCC
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SEQ ID NO: 432 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGGTTTTTTTTTTTTTTTTTTTTT
TTTTTTTTTTTTTGNANAAATTTTTTTTTTTTNTTNAATAGCANINTGANNANNCATGGNCCAA
ACNCTCAAAATAATAAATNAATNTAAATNTAAAAATTTGGTNTTAAACATNATAACCAAT
GATNCCCCGTTTGCCTNTAATNTTCCNACANAAAAACNANTTAAANCCNAGGGGCCANCAAN
NTTNAANAAAAATTTNTTAANTGGNAGNTGTTAAAAANTACCANTNTGANCACTNTTGACTNTTT
TTTNAAGGCTNTNAATANCTTATAGGGATCTNANNAGGGGNGGGANNAACANNTNAACCTTGGNG
AATACCTNGGCCGGNACCACTTAAGGGNAAATTCANCANANTGGNGGCCGTTANNANGGGAT
CCTAAGCTTGTACCAANCTNGGGGAAATAANGGNCANAGTGTTCCTGGGNAAAATGTTNTCN
GCTNAAAAATTNCAANAANATACNANCCGGAAANCANAAAGTNTAAANCTGGGGNGCCNAAAGA
GNGNANCTAACCCNNTAATTTGGGGTGGGNCANANTGGCCGNTTAAANNGNGNAAAAACNTN

GTN

SEQ ID NO: 433 CATATATACCCAAGNGTGCATCTTGATCTGTATGCTCTTANATGCGCTTTA
TNTACAGCTACNGCACATANNGCNACATANCATNTTACNCACAANGGTTGAAAACTGTGCAT
GATTNNATATCATCANCNAGCACGNNTGCTGG

SEQ ID NO: 434 GGCCGAAGTACGCGGGCCTGAACCCAAGAGACAGAGGTTGCGNGTGAGCCGA
GATCGCACCAATTGCNCTCCANCCTGGGCANCNAGCANAAAACTNTGNCTCAAAGAAAAANNAAA
NANTAGANCNAGACGANAATGGCTTNCNGGACAGGAGCATTGCTCATTGTGCGGGACNGTTC
NANAATCANNCCNTGGTNTGGTCCTTCTNCTTACCTGGCTNGTTTTNTNCAANCCACGTANNNTN
NTAANACTTTNTTGAAGCNAAATAA

SEQ ID NO: 435 ACTTTTTTTTTTTTTTTTTTTTTTNTGNTTATTTTTTTTTTTTTTTTTTTT
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AAATATCATTCCGNNTTGATNNNGGAANGGGTNTTAAACGGGTTNGGCTAAGGGTTAAAAATTGG
TNTGGGNCCCCNNAGAAAGNCNNGGNANAANATCGNTAATGNCATTANAGGNGAAAAATNAACAN
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TAGGGCTTNTANTANTINAANGGCACATNAAATTGAAAGGTAAAAAANNNTGNGAGGGGGGANT
GTCTNCTGANTAACTNCTNAAAANTAGTTAAANNAANGNTGACCCAANTTTTTGGGATNGCAGA
NAAATTAATAATNCTAATTACTNNGGCCCANANAATNANATTTTNGCCTNCCGGCGAGNANAA
NNCCTTTA

SEQ ID NO: 436 ACCTTGATACACATAATCAGCCTTTTCAAAAAATGCCTGACAAGAATTAGTCTT
TCCTTTGTGTAAAAAGTCTTCCACCCATGGATGGAAACAGGCTGACTCCTGGAGGGTCAAGCAA
GGGGTGGGGAAAGGGGAACACANTNCTTTTGGGAAGGCNAAAGCAAAAAAGGGTNTTTTGNC
CAAAACCAACNTTGGGCCAGCTCAAANGGGGNCNAAGCNTNCCCNAAAAAAGGNTTCCNTTTT
TTTTTTNTAGGGCCCTGCACTTTANAAATTGAANGNTTGNANTTAANANTNNGGACCCNCTNANA
CTTTTTTCCANANGGAAAAANTTTCCGGGGCCANTCNCCTCAAGGNAANNNGGCCCTTTCCNAAN
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TTTTATTATGGGGGGGGNNACT

SEQ ID NO: 437 CNGACGGGCCNCAGGAGCANNACAGGAACACTGCGNTNCTGNNAACCTGN
GGNTGCTNATGTGCCACTGGGCACCTTATTGCNAACTGAACCAANANACCTCTGNTTACAGC
TTGGGCCTGCTGTCCAGCTTCCGAGGTGCAGCAGGTTGTGGGAACAAGAGACGACTTTNAGGAT
NAAANGACCAAGGANAAAGCTGCCTTACATGATTGATTGGGGCCTAGGANATGGAANTCANCN
TTATTNTTNAAGAGAGNTNTTNACTAATGNNGNAGGCTGAGGNGCANNCCTTNGAATATGCCTT
ANANGCCGNACGCGGTGGNTCCCCCTGCAATCCCNNTACTNNGTGAGGCNAAAGGTGGGCNNGC
CANCCTNNGGCTCGAANTCAAAGANCNTCCNTANANTANCNNNGGOTGAANCNNNTTCCNTAN
TNNNNATCCAATNATTTATCNTNNCATCTNNANCTCATNNNNCTNNTAANCNTNANNCTNGTGNA
GCATGTGGAAANATGAAATT

SEQ ID NO: 438 ACITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGATTTAATTNTNAA
CAAAAAACANCGGAAAANGGGATTAATNATNNGGTGTTANACNNGGNCANAAATAAACNCAAAA
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GGGGACCNANAGGGGANCGGCNATNAAAGGGCAATNAAANNCTAAATNCATTGAAACAAGCTTT
ANACAGTNTCNTGCANTCCACATNCTTGTACCTNNGGTCGNAACCCACNCTAAGGGCAAAATTCAN
GGCANNANTGGCGGCCNTTCTAGNGGATCCAACTGGNTCAAANCTGGGCNAAATCATGGNNAT
ANCTGNTTCTGGGTGAAATNGGTATCCANTCACAATCCCCACAACATACCACACCGGANNAT
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CCGCTTTC

SEQ ID NO: 439 ACTATGTCGATTGACAGAACANTTTTTANGATTCTCGGCCTTGCCCTTCAC
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TCAAGACCTCTTTATTTNCTATCATCTTTNCTAGACACACACAATCAAGACCTGGCAACTGNT
TTTGAACAAGAGCCATNAGGTANCCNTTANTACTTGGGCCNCTTTCTNAGTTNTGAANTATTCC
AAANCCCTTTTGGGTATNNAATAANAGTNAAAAAGGCAANCCCGCAACANNNGNANGTGACTTTG
GNCCTTTAAGATCTTTNNNAAATNAGTGGATTGNATAGTAANNNTCAACGAAANGGATATNGGAAN
GAAAAACAANANNTCCCTCNTGGGNTCATTTACNTAAANGTTTTACNTGGGGNANCGNATCTA
AAAGNGNCTNTGTANGCCCTGCAAGTTGGCTGGGNTTTGANCATTTTNGAGATTANAAAAAAA

ANTTANGTTTGNTAAACC

SEQ ID NO: 440 AGCCGTGGTCCGGCCGAGGCACTTTTTTTTTTTTTTTTTTTTTTTTCGTTTNCN
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ATAAGNCACTTTTTTGCAANCTAAAAANTAGAATCAAACCTANNNGGTGAGCTAGTCTCTAGGCAT
CCAAGGCNGATCCTTGAATCNTGANCANAANGATNGACATCCTACANGGTGCTNGCAATACGGC
TATAAACCTTCTAAANACTTNACNNCTTACATTGTTNNATTAGGAAACAGCCAANAGGCCNGCCG
NTAAAGGAATNAATNTGCAACATNTTGNNTTANNNGGGACAAAATGNTGNCAATTATTTGNTG
GCCCCCTACTNGTGAAGTGNANNCANAAATGGTCCAGGGACTGTNAANCNNAANGAAGGNTT
TACATTTTTGAAAACCTGCTCTGCAGGATAAAAAANCCNGGNTGCTGCTGNTTAAANCCNG
TGANANAANTTTNCCGGTTGANCCTCNCCTGACTNTTGNNTTGNANGGGCCNCCNCTGGACN
TGNAGGGGGGNGGGGATATNTGTACCTNCCCAGCCGCGTTTAAANGGGNAATTTCAACCCNACTG
NGGTCNNACTTNGGGGNNCCAACCCNGNNTCCANC

SEQ ID NO: 441 ACACGGGGGTGCGTGGCCGGCAGTCATNTCNGGCCGTNTCANAATTATAAG
GCTGNTGTCAGAGATTNCGAANAATGGCAACANATGAAAGCGTCANCANCTTTAGTTTCAGCATC
CTTGGCTGGGGAATATGTAGATTTTACCTTTTACNTTGANAATTCNTCTNANNGAAACAAATTTACT
ANATNGCTTGGAACTATATGNTTGNATAAATNATNCNAAAGTCCANTATTGGCAATCATTTGGG
GGATCCCCCTTANTNGTTCAANGAAGCCCTATTATNTCTTAATNCTGNTTACCTGNGNTTTTAAAT
TTNTCANNTATNCTTANTANNAAAAANTTCNANAATTCAA

SEQ ID NO: 442 CGTGGTCCGGNACNAGGNACNAGAATGNTTCATGAAATCCGNTTTTAAATGA
ACNTNTNTGNGNGCCACANTTCTANGACTGGGGCNAGGNCNCNNTGNCAAGTNTGNTTTGAGG
NTNAATCTNTNAANAACNNAATTCCTGCCNNAATGCNCNCNNAACATNAGTNANCCNAGTNGCT
CNTGCCANGGATNCTTTGACTTTTGGTTTGTCTGCTGNTGCTNNGGATATTGGGAGGGNTATNCTTTN
CANGTTNNAAGAAANGGNTGTGGGTTAANGGCTGTCNTAAAAGANCCCTGGCTGTNACNCCANCT
GANTCCNGATTGCGTTTGTACCCNTTTGNAACTGACCCGNTAATTTNAAACNNTTTTNCANCTTTT
TTNAAGCNTNTTTANGAAGCCTTCCCGGGANGNAATTTTTCCAGGTTNATNTNCTTNNCCGGGCN
GGGCCCCGTNAAAAGGGGGAATTTNACCCACTGGNGGGCNTTCTAATGGGANTCC

SEQ ID NO: 443 ACTTNTTANGGCCAN
NTTCANNCTGAANTGNCANANNNAANTNAAAAATNTNAAAAANATGCACCNTGAAGGCTTTGAG
NCGAAGAANTNAATCNTNCCNNGGGGATCTNGANCTNCAANGACTGTGACGGNAAAGGATGNTN
TTTTTTTTTACCTGGCTTNNCNAANTTATNNCAAAACAAAATGGGAANCAACCCNCAATTTTTT
GGNAANNAGAAAAACACNACTAGGGNACCCCAAAAAAACCCATTTATTTTCTTTGGAAAAAGG
GNNGGGGNCCANGNTAAAAANTGNANGGGGNAAATTAACNTNANNCAAAAGATGGAAACNT
NCCTAAAAAGNTTNCNNTNGGANGAAAGNGGGTTAAAAANNCTNAAAATCTTTTNTTGGGAAN
AGGGACTCTAATNGGTCCNTTNGGGCTNCTTAAAAANGGGAAANGGAANNAANANTTTNCTTNA
AAAGGGNGGCNTTNAAAACCCNNAANNGGAAANAAAAAANTTTCCNGTTGAGGTNNGNNNAC
ANNNTTTTGAACCCNCCAAATTTCCNTNTNGGGNAAATNTTCTTTAAAGCNANAAANANATT
TTAAAAAATAATGGNTTNGGGGGGNGNCC

SEQ ID NO: 444 ACCCGGNGCCCNACGGNGCCNACAGATGGCTGGNTNNGACATNGGGCNA
NNCTGCCAGNTGGAGCATTGNCGGCNCCGAGATTTNNTTNCATNTGGGGTGTGATGATTTGTTTCA
GAATATNTTTGCCNGAACNAGANCTGGNATTCTCATGGNTGAGNTGAGGTGACTGNATGTCA
NTGAGAGACTGAACACANATCANCATACATCTTACCCATGCTCTTCAAAGACTGTGCTAAGAGA
GAACCTGTGCNCATTCCCTTCCNTATNGGCAC

SEQ ID NO: 445 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGTTTTTTTTTTTTTTTTTTTAGGNTT
TTTTTTTTTTTTTTTTTNCANCCCTTTCANATAANTNNATTTTNTTCTTCNACCANAATAATGGNAT
ATCCAAATTTTGTCTTAACCGGGGGTNNGNAAACACAGGCTTNTCCATCCCCTTACAGGCAAG
GNAAAGGCTNNTTNTTGAANGGCCCAACCATGGACCTTNNGTAAATCCAANCNAAGCNACCCCC
TNGCCGGGNTTAAATNTAANTANACATGGGCGGCCAGTTAATNAAATCTNNACCCAAATNTTAA
NTTTTNCAGNGGNTTCCNANTATTTTGGCATGNTNTTNAANAANAAGGGGANAGACCCCTTA
ANTGNANTTNCNCCCTTTGGGGNCTTNAACNNTTTTGGACAAANCTGNAAATNACAAAGGG

SEQ ID NO: 446 ACTTNTCTTTTNTTTTTTNTNNTTTTTTNTGNTCAAGATTAATNNCTATNGACAAGG
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CACTTGTATTTACCTTNCCTAGNGNGGTGAGNAACTATCAAGAAACAAACCTGTGAAAAATCCT
GNTAACATTCACANATATTTGGTATATATANGGCTCTNGGANGCAANAATTTNTCAACACITA
ANTGGNGNANCAAGNGNGTCATNGGGANATAAACAGGATNGNTTAAANNTTGAGANTTTAATA

NA

SEQ ID NO: 447 GTANTCTTCNTNTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTT
GCAGAAATTCGCCCTTNCGAGCGGCCGCCCGGGCAGGTACNCTTAGAGGTANNTGTNNNTNANAN
AGNNNTGTNNNANTTAAAGANNCTAANGTCNTNATNTNTTATAGNCAANNTACA

SEQ ID NO: 448 GGACNTTTTTTTTTTTTTTTTTTTTGGAGTITTTATTTANTATNGGGAGCAAAT
TGNNTTNTAAAAATGNATATTGNGAATAAAACNGCNTTNNNCNTTTAANGGTNTAGGGCTGTNAA
NNGNNNCANGGGGNGNNGCCGANNNAACCATGANCTGGGCTGGGTTTNTATNTTTGATGAAAAAN
AGCCTNNNCGCTTTTGTATNGGGANANAAAAAANNNGNCATNGACCTTGACTATNNCTTTATCTC
CNGNCACCTTTNNAAACANTAAATTGCGNGNCNNGGGGGGAGGGCTNTTNNCGGAACTAAACTGT
GAGCCCTTCCATTTTTANGAGGGGANGTGANAAAAAGATTACACNGTGGNTTGAGTGNCCCTNA
GGAAANAATTNGGACCTAACNTGCCCGGAAANGAAGNNATAGGTCTGATNCGTTNGTANAANACG
ACAAANNTCACCTCCCCNTCTGGTGTGCACTGANGGGACAGGTGGAAGNANANTACGNTTA
TTGCNACCAAGTNTCTGTACCTNCTNGGGANGACCGNGTNTAAAGAAATTTGAAATAAGCTCTTTA
CNTTGCCTTTTNA

SEQ ID NO: 449 GTACTANACACATCNGGGACAACCNCCATTTCCGANATGATGCCGAAAAACNC
AAGGCCANAAGCNAAGCNAAGGGGATGGANAGTTTGNNGGAAGNTATTTCTTTACCCANNAATGA
CCTGNTGCAAGACTTGATGCNCTGGTANCTGANGAACATCNCACNGTGGACGCCANGGTCTAT
NNCTACGCTNTAGCGCTGAAACATGCNTAAGCAAAGCCATTTGANNGTGCCCTTCTTGANATTTTA
NNCCNAATATGACACTTGGCCATNTATTGTNAACGAAAAGNNCCANGCCTTGTCNTAAGACNT
TG

SEQ ID NO: 450 CGCGGCGAGGTACTTT
TTTTTTTTTTTTTGGACNCCCAAAACCATCCTTTATNGGANNATNANTTCANGGNANNCNCANNA
AAAAACATTTAGGNGGAATTNANAATTNCCGNTNAAAAAACTNGCCCNCCAACANAAACCAATT
TANNAAGNCAATTCATNAAANGGNATAAAACCNNTTGNNGGGCATGANGGCCANGGGACAAAGC
TNNAACTTGGCCCTGGNCCTTTNGAANCCNNGGNAGGNNGANCNTTTNNACCCAAAGAACCCNGAA
NCCCCGGGGCAAAAAAGAAAATCCNCTNAAAAAATTTTAGCNAGGGGGG

SEQ ID NO: 451 ACGTGCCGAGGAAATACTCCGCTAGCAATCGCATNATCGGTGCCAAGGACC
ACCCATCCTTCCAAATGANCGNGGCCNAGGTTGACATAGGTAACNGGNAGNNATAANGGCCAATT
NANANNNTGNNCNTTANGGGGGGCCNTNNCANGNATGGNGAGNNAAATNNNTNCCNTTNTCCNA
TNGGCCAAGGCCNANGGCATCNTNTNAAANAACTTTNGACNGGAAAGAATCAGAAATGTGGAAT
NTTGNNTAANTAANTAATGAAACCCAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTT

SEQ ID NO: 452 CNCCTTAACCGTGGCTTNNCCGACGTACANTCCAATCGTCTTCGNGGGGNTTN
CNCTTAGCCGANGAGTTCNCNACNNNTTCCACAAATTTTAAAGANGAGGTAGACCCACCTCCAT
CTTAANACTTT

SEQ ID NO: 453 AACTACCATCTTTCACATCAAAATNGGGGANGCTGGAGGTAGTGAAAAAGCTA
TTNGGATTNAAAGTGNNCAGAAATTCNTGTANACCAACAGCAACTGANCCNCTGTGTAATTAANGGC
NNTCCANGGGNAATCANCTANTTCGAGCNTNTTCGCTATTTAGGCT

SEQ ID NO: 454 GACGGAGCAATCGANGAGGCATAACCACACTTGGGGGTGGGCTATAGGGGC
TGGGAAAAACCTGAAAAATGAACTGGCTTTTCACTGGAGGGCCANGGGTTTGGAAATATTGGC
CAGNCTTGAAANGTNTTTAAAGNCAAANTTTCCTTTAAGTGANTCTTTCTCTNAAAAACANCA
NTCANCTTCCATTGTNCCTTNACANAAGGNCCCCCTGCGTTCTTGCTTGNATTGCTTTTGGCGACTN
CCTTGATGATNAANAANGGCCCAATTATTGATNGCCCNCAANCCNNANTCNGGGCCANGG
CACNNACCANGTCTCTGTAATCTNCTGGGANAAAGGCTTGGNACNNTAAAAATCNCCAATGCNT
TNAGAAANAANGNTNATNCAAGCCCCATGCTCCACCCTGCANTCGTAAACNTCTCAATTNANG
GCNGGAAGGGGAAATATTNGGAACCTCGGGAAAAAGGGGNTTCTTGGGCAAGGAAAAANTGTC
TCTGCACTCCTTNGNNGAANGGTTTNAATTTTAAACCNCTGACNTTNACCNTGGTNGGGNGGA
ATTTTTCTANAAACANATNAGGANANTTTGGNTCTNTTCAANTTCAAGGGTGTNTTNGAGCA
CAGTTTCNTNTNGAAGNAANTNCC

SEQ ID NO: 455 ANCNTGGCCGCGGNCGAGGTACTNCTNNACTGTGAACGGGCTCCAAAGGA
CATGGNTCTGCANTCAAAATAATNATNAAANGGACAGGCNTNGCNAAAAATGCATNGGNCNAC
TAANCNTNNNCACNATCAAGGNACCAACACTNNANNNGNTTNGGCCATTTANGTTGCNAGGT
ATNTGNGGNTGCTNCNTNTTTTTTATTCANNATCAACNNTCNAGACNTNATNGCCTATCANA

TGTGGTAATCCNNAACNCTGCTGTCTCNNTAAANTTTCATANCATGACTTACNGTTNGANNAAACC
CNGNANTTGTAGANGTCCATAAAGTGGTNNAGAACGNCGGTANACATNTCTTTTTTATAGAGGT
CGCTACGNTCTGATTTNCGCNCNAATTCNCNATNCTNNTCNANAANTNNCTTTNANCTTNATTNNA
TGNTNGACCATACTGGGGGNCGGANACCTTAGGGANATACATCTTTTGTGTTTGCANAAACAANAT
TAATTTAAATCCTTGGCCTGGGGGGGCTCTCACACTNGTGAGNTTTNNATTGNAATATNCNGCTNG
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GNAGGTCCG

SEQ ID NO: 456 ACTTTTTTTTTTTTTTNTNATTTTTGNGGGTNTTNGCATCCACAACNGTCCAAN
ATNTTTTAAACTTNTCCNGTAAAAACNAGATGAANAGGCNGCNCATCTTATNAACAAATTTGGNNC
CATNGGNCANTTCGGCAGGGCCANTGATNGNAATGCCTNTCANTTTTTTGAANACNCACAGTTT
NTTCAAATTNTCCTNAATGAATAAAATCTCATCCNCCCTCTTTCCCTTTNAAATATNTCACNNCCA
TTTTNTTNTTAAACCTTCTTTTNGCTGTTCNGNAATTCCTTTTTTTGGAAAGGAAGGCCANTG
GCCCCCTAANAGAAANGGGGGCCATTTTTCTTTNGACCCCNATTTCAATNTTTCTTTGTCTNAGTTNAA
AATGGNNTNANAAATTTNCCNGGNNANATGNANCAATTTCTTTGANTCTNTGAAAANTTAAAT
CCAANCNTCTTTTTCTTAATNTNTTNTTGTGTCNNNNNNNACTAAANCAAAGTGCTNNTTCNN
AAATTTTATCTNANNNGTNTATGGTGGTAANTCATCAGATCTCTGNANNNGNNNTCTNTANA
TNG

SEQ ID NO: 457 CGTGGTCGCGGCTCGAGGTACACTGGGAACCTCAAGAAAAAGCTTTGAANAG
AAAAATGGAGGAAGCNCGAANCCAGAAACTCTAAATCTTGAGACAAGAAAGACTNTCTATNATGAA
NGAGATCTTTTNGANCAANACCNAACNACAATGTGTGGGAGAAATCTNATGANCTAATACCAT
GGCTGCGAAANNAAAANTGCNAANNNAATNTCTNTCCGGNCGGCCGCTNGAAA

SEQ ID NO: 458 TTNGTACTGATTTNAAAACTAATCACTTAAATGTGCCACNCCGCAAAAGAG
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GANCTTNTGGGCGAAACTTGGGTGACCTTGNANNNTCCAGCTTNTCTGCTTGTCCACTNNTTT
TGATGACTTGACACAGGNATTNGCTGCTCTTTTGNACGNACNNGTNNNTTCCGCCCTAGGCGTGG
NTAGNNTTANAAAGCTTTAAACTTNGAATGGGGCTTTNTNANGGAAACCATNATNAACNATTTGGG
CGGTTTTTACGATACTNTAANATANTTAAAGGGCNCNTTNCANNTTGTTTTNCANANTNNGT
NAAATANTTTTTCTATNATNNTTNTAAATCTTAAACTTAAATNCTNCCNTGTGTNAACTCCT
NTANNATTGGGNATNNTCNGACCTNTNTATGNNT

SEQ ID NO: 459 GGTACGCGGGGACTGCAAGGCGGCTGCANAGAGAGGTTGTGGCGCTANTTTC
TCTAAGCCATCCANNGCCATCCTCGTGCCTGTCNNNGACACACCGCTCTCGCCGCCGCTTGANTGA
CCAATATNACCTTTCGTGGCACCCTAAAGGGCCACAAACGGTTGGGTAAACCCAAATCNNTANNNCN
CGGATGTTNCGNANATGATCCTTTCCGCNTTTCGANATANAACNTCACANTGNTGGAACNNN
CCAGGGTNGAAACCANCTATGGAATATCCANNNNGTCTTTGCGGGGTNACTCCNACTTGTGNG
AGNNATTNTGGATTATTNCCCTNATATGGCNCANATTTGCCATCTAAGGGATCCTGGNNATGNA
CCNTTGGCCTTTGNGTATTTACNAACTTNGATCCCTCENNAANGGGATTGTGGGGCCATACCT
CATGAATTGCTGAAAGNTGNCNTTTTNNNTNTANANTACNNGNNANAATTGTCTNTCTGGAATCTT
AATATAAAACCATTAAGNTTNGGNGANTACCTGGGNGATGTGAAAANACANTGCTNNGGAANT
ANACCNATNTAAANGNGTTTTT

SEQ ID NO: 460 ACCGCGGGGCTGNCCTCTCTTTTNGACTCAGCCCGCTGCACCCANGTGAAA
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TNGGNGCCATNANTNGGATCGGGGGACCTCCNTNGGGAANNAATCCTCCGNCCTCNGNTCTTT
GCTCCNTNAAAAAATCCNCTACACNTCAGGTCTCAAACCGACAGAGCCCANNAACATTTA
ACACANTTNAAAAATNGGTAAGCAGCCTTTTTTATTTTTTTCAAACCTCCTTCATTATCCNTA
AAACCATTTTCTCTCTTNANTCTNTNCCNNTTNNACTTAANTTTNTCTCTTNTCTTAATTAT
ACATATACCNATATNATTTTCTGTAAGANAAAAAAGAAANANNNNTTTATCCCGTNGG
GCCCCAAAANTTTGCGNCNNTTTGTCNAAAGNNTNGNAAANNNGNAANTCTCCCTNNGGNTNNC
TTAAATAAATGGAAGGGANTGCTCTTNTTATTTATACACNCTATGATTATANGGGGTGNTANTAA
CANTCGGGGAAAAANNNGTTTTGGATTTT

SEQ ID NO: 461 GGNACCCCGAGTCCNTGNCTGGCATACTGAGAACNACCAACACACACCCA
AGCTCGGTCTCCTNTTGGTGATTTCTGGGGAGCANATCTTNATNAAAGGCNNCCGTCCCATGAGAG
GGGGAAAAACATCCCTCTCTTGNAAATNTAAGGAAANTTTTNCNTATNANTCTGTAAAGNAGAA
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NNGTTCTTACCTTGANANTTATATAAANGAAAGTGTTGATATATTNATTGCANNAGNNTTCAANA

AANAAACATCTTATGTTATGTGNANNTNAANTANNCTNANNTGAGGNTTNTTAATNGANNGTTTT
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TNTTGNNAATGTGAGATANTANNGTTTTTTTTTTNGCNTNCTGGNATNTTGGNTATNANTATAAC
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SEQ ID NO: 462 CGAGCGGCCGNCGCCGANGNACTTGAGGCATTACCTCCTCTGAGNCACTGA
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TTNNGCNCNNGGTCNTCTTGGATTNTNTGCTCTTCATCTNCTGNCTATGAATNNTTCTANCTAAAN
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SEQ ID NO: 463 ACTTTTTTTTTTTTTTTTTTTTTTGNACACATTTNAAGGGTTNATTTANANA
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TGGAACCANCTTTNTTACTAATGGCATCTTNACANACTTNGGNAANAAGCACACGGCACTTN
GAANATNAANTTGGAAAAANAANNNTTTNAANAGGCNCACTTNTCTGGGGNTGATNCCCGGTTN
CCACANNTTCTTAGGONNGANACCTNCAATGANCNNCTGATNCGACTTTTNTCTTNGGAGGGGGTG
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ANAAANCCCGGTNAACATTAAANNTTGGTAAAGCCTTGGGGGNGCCCTTAAANGGAGGGGGGCC
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SEQ ID NO: 464 GGACCTCCGNTCANNGCTNNTCATNNCCNCTCNCNCNGCCTGGTGANCA
NGCTGACCNNATCCTCTTNTGNATGGAGGCNCTNTCNGGGANGGGGGAACNNACCATCAANTNA
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CCN

SEQ ID NO: 465 GNGGNGGCCNGGCCGANGNGCACACTTTGGATACACTGGATGCTCATGTCAA
ANGGGGTCAACTCATCTTCACTCTGAGATNCAAAACNTAACNCTTGGCGGCATCAACCAAAAAAAT
CAAACTATCTNTTCCNGAATATTTATAGNCTCCACTNGCTTNNAGGGTTGTTNTGGTTNTTNCNN
NGCTTCTTATCNCCTCNGTTTTGTGNTNTGACTCCACNCTGACATGNAGGCTACTGCTCACTTT
GGTGATGNAAACGACCAACTTGGACANAAAAACCCCGCGNTCTNCCNGGGCNGNCGNTCGAAA
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GCGGGNAGCATAAAATGTCTAAGCCTTGGGNGCCTAATGANTNAAGCTTACTTAGATTGAATNGC
GTAGNNCTCACTGTCGGTTNCCANAGGGGAAACCNCTTGTGCNNGCTGTATTTNCAATCCGGTCA
NCCCGGGG

SEQ ID NO: 466 GGTACCAAANCNANTNACAGGANGGGCGGGACTACCGGAACTACAGGCTGT
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AGCCNCTGCTTTGCTNNTANAGGAANTGGATNCTANNGGCCNTGAANGANNGANNTCCTNTC

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SEQ ID NO: 467 CNGCGGCCNNNCCGNCGGGCTCNCCTNTNCCCAGAAAAGCGGNACTTGCTG
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 CCNNNA

SEQ ID NO: 468 CGCNNNNNCCNNNANGACCTATNCATGCNTATGNNGNATGTNGTTGTGATNN
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 GANCTTGGANGGAAGGATCCACACCCTAAGCANGGAGGNGCTNNGCGANTNNNTNCTANAGAC
 CTGNNNAGNTTGCNNCTNAANAGNNAANNNAATGNTGCCAAGCATCAANTGTNATGGACATGN
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 NCANNACATAATNCTNNGGACGNTGTGGCAANTAGGANTACTGGTGCCTNTAGGCGNATGNTGC
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 TTTAAACCTGGCTGTTTCCCACTGGGTAACTCTGAAGAACAANGCTCNTGGTNGAATAGCTNGGCC
 NAAGTTTAAANGCACTTCTTTATTTGGATGTNTCNGCTTACTATGGTAATACCAACCTTCCATGG
 GGNTTTGGGCTANTTGGAGCGAAATTCCTTGTCTANATNTNGGTAANGGGAATACAGN

SEQ ID NO: 469 TTTTNTTNTNGNTNCTATNTTTTCTNGGGCNGNCACGTGCACTTTATTGAA
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 GTTNCNGCACTTTGCGGTGGNGGCATTAANCCCNNGNCCCCANTAAACNTTCCCAACATNTTNTGT
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 GGGTGNTAACANGGACCAAAATNATGNTNGGNTGACTTCGAAGGTCTNATTTNGGANNNTNNCT
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SEQ ID NO: 470 GGTACNNTNTCANNNNATAAGNGCTGNNGNNNCCNANAATGANGGNGTCA
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 NNGGAGTGATNANCATNANCTGGGACNAACTGAGCATCTCTACTCANANNTAATACCGTGAGANA
 GGCACNTANGCACNAGCTTGTNTACATATGTCCAAGGCTGTAGGANNNTTGAATCTGTTGAATC
 AACGTGAATNTGCTNAATAGTAATGANAGCTTGTGAATATTAGGCNTAAAGGTGNTGGTNAATNT
 NNANNCNCACTGCTCCATNTGAATTACTACTGNGTGTACTTACTGAAGNTGAAATGTNNCNTA
 TGANATATNGTTNNANTGNGCGTTCGANGANGATNNGCTTTGANNNNNATGTACTNNGTGCNAC
 TGAANACNNNNNTCTCACNCTGATNTTNCAAAANNGGACCTGCGGAGGATCACNCTTANACTTT
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 CCATGATANCTATAATGGGTTNCNCTTCTTNNCCGTNNNCNCTCNAAGGCNAATCCATNCTGCG
 GGGCGTTCT

SEQ ID NO: 471 GCGAGGTACCACNATACCAACCAATACAAGTTTGAACCTGGACCTGGGGCTC
 TCCCTGCGCAGCCATCGCGGGCTTCTACCAGAAGCGTTTCCGCGCCCGNCCGACTGAGGCTGGA
 AAGATTNNGGAAGCGCCCTNTACNTGCCGGGCGCGCNGTTCGAATGGTCTNATTNNATTACACTT
 NGCATNCTGTNNNTNNGATNNNANCTTTGNACTNAGTTGTNTGTNATTGANGGTACATNNCTT
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 TATGCTGATTTTNAAGTTNATNTTGTCTATTTTNTTATNAATNTTGTCTAATCTTGTCTGTA

TNTTTTNTTAATTNNINTTCGTTNTAATTTATTTANTTNTATTTTCTACACTTTNTNGTNTNNTATGT
ATCTTANTTTTTNTTGTNTATATATNAAATATNATCTATATTGATTGTTCTATCCNCTTTTTTTING

SEQ ID NO: 472 GTACGCGGGGGTGGGTGGGATTGAGGTGTGCCCTNCNTCATAAAATACAGACT
CANTTTTGCTTGACACTCTGAATCTTNNACCGCATNCTANCCNACGACTNACACAAAGCACGTGN
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CTTNCCTACACTCTGGCCAAAATTTCCATATTANAAACCTTANCCANAAAGGACAAATATGNCTCT
CNGACNCATTCTGNCCNANACCCNCTNCAGANGTTGNNGTGACCAANTAATCTNGACTCANNACA
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SEQ ID NO: 473 TAGGTCCNGCCGACGTACACTCGAAACCAAAATNNCTAAAACTTGGTTNGCNT
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CAGTNTNCTCACACTNNTTCTGGTTTCAAGNCTCAANGCCNGACANNANAAAGGCTTGGAGATT
TTTTNCTTACAGTACAANTCTATCAGCAACINTGAGAGCNTNNTTATGTTNGGTCANGCAACAG
ATCTGTNTCTGCAAGG

SEQ ID NO: 474 GGCGGNGACGACNCGNNCCAACGTGTGCCCTATNAACTCTCCATGGNAATCC
CCNCGCCTACCATGGTGNCCACCNGGTGACGGGGANTAAAGGNTCATTCCCGATANGGAGCCNTA
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NGAGGTAGNTNACNACTGAGTACNTGNNNACNTAANNTNTGGCTTTTGNCTTACNCAAAATG
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SEQ ID NO: 475 CGTGCANTTNANTGCATAAAAAAGGCCTCTCTCCATNANACTCANCACITTTAC
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SEQ ID NO: 476 ACNTCTTTGACATTTTCAAANTGAANAACCTGNCNNNTTTCATTGNAANGG
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SEQ ID NO: 477 CCGNCGGGCCTGCCAGCANCNGGACCCTCANAAGAAANCNCATNACNTCAG
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SEQ ID NO: 478 ACTTTTTTTTTTTTTTTTTTTTTTTTTTCCGNTTTTTTTTTTTTTTTTTTT
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SEQ ID NO: 479 CGCGGCGAGGTACNCGGGGAGTGAAGGGTCTGCTGCTGAAATTTGGGGGC
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SEQ ID NO: 480 ACTCGGGACTGTGCANGAATGATGGAAACCAATCATGGAGAGTTTNNNTG
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TTNGTTACACT

SEQ ID NO: 481 ACGNGGTCGAGGTACACANTGGGGGCTCCTCATACATGGCCTCACATTGAGG
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SEQ ID NO: 482 GTGTGTGTGTGTATGTGTGTGTGTGTGTGTGTGTTTAAGTTTANCCCTTTTGT
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NTTNTTAACTTTGGNCNCTTGAACGTGNTCCATNCCAAACATTTTCAAAATGGGGTTGGGGCNTTA
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SEQ ID NO: 483 ACNTCCNTCTTCCAACCTGCTTGCCAGCAAAGATCATNCTCTGCTGATCAGGGA
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GGGTGATGGTCTTCCNTANGGTTTTACCANAAATCTGCATTTNGGGGGGGCTCCACCTCAANGG
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GNNGCNTTGAAAAATTNCCAGANNTGGNGGGGGAACCTTAAANATTCCTCCAAAAAGCTNGAAAG
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SEQ ID NO: 484 ACTTNNTTTTTTTTTTTTTTTTTTTTNTNAAAGGGTGATAACGCTTTTCANAN
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TTTG

SEQ ID NO: 485 TGCCTAATNACAACATGGATGACTNGCAAAGGANGGGCTCTTTACTTTAAGC
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CGTCTGTGTCCATCNTTGNAAANACTGGCAGCNGTTGNANNTGAANNAGNATGAAGAAAAAGAT
ATGGGAGCTTTTNCCTTTTNTTCTCTGTTAAATCAAACAAAAACAAANGTCAATTGGTN
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SEQ ID NO: 486 ACTTTAAGAAAAAAGCAGGGCCTTGGAAAGTTTGGGTCTTNTTCTCCTCC
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ACTGCCACGGTGGGCGGGCTCCTCTCTANTCTAANGGGACCCACCGTNTANATTCTGNAA
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SEQ ID NO: 487 ACTNATNNTGNTNNCCCAATNGATACTGNTTGNACTAACATCCACTCTNGTAT
GTNGCTGAGATAACTTACTTTGACTGNCATTTGGATATCTCTCANACANACCTTGAACNANATAA
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SEQ ID NO: 488 ACCCATGCTCACACNCACACTTCCAGTTTTATACAGAATTTTTTAANGGA
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NTACNNGTTTACCNCAGCTGAAGGTTCTTTTATTCATTCTNTTTTAAAGTGANCCCATGATTGG
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 NTCNAACTNCATATAGAGAAAAAATCGATNACGAAAAATNCNTGNAATAAGACTNAACTNACTTGGC
 CNTAACAAAGGNCCTTAGTAGATATNTAA

SEQ ID NO: 489 CTCNGNGAGGCCCAACGCTGCTNNTGCTACACTATNGNCAGGATNAATCCG
 GTCCNGTGC GG CANATGGNTANTCTCCTCTGGCCTTGGCNGCCCTCCTTGTTCTGGACANGGGAN
 ATNTCNNGTGGCANNAGGAAAGCTCCNTTTTTCANGANCTGCNCCA

SEQ ID NO: 490 ACACNCGCENNCTGGNNTNANNACGCAAGCTNANNATAGGTCNGGNNAGCG
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SEQ ID NO: 491 ACCACAAGGATGTGAAGCATATGAACTCTGCANGANTCCTGNCCCACTGAG
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SEQ ID NO: 492 GTACANAGTAGCCGTGATGTGGTCATTNGTCTGATGCCAGCCTTGAAGATG
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SEQ ID NO: 494 GGNTCNGGGGAANAGGAGTTGGANTATGGGGGACGCGGNAGGCGGCNTAN
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 GGAAACCANTATAANGGCANAANTGAATACNTGANGACGGCTTAGGGGAANTGNACTTNTCNT
 TTTGACGGANANNCCGCNTCAAGGAAAGGTAAACCTCGCNTTTAAGNCACCTTNAAGAGGCTAN
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SEQ ID NO: 495 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGCTCAGATAAATTATTTATTATTC
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SEQ ID NO: 498 ACGCGGGNNNGTNGNAGCCTGNGGGNCCTANTGNNNNATNGATNGNATNAT
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SEQ ID NO: 499 CATTGANCTCCATAGAGACAGNGCCGGGGCAAGTGAGAGCCGGACGGGCAC
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SEQ ID NO: 500 ACCNNGGNCNNNGCCGACGTGCTAACATGCTTNAACNNATCANTATGGAGNCT
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 ACTACT

SEQ ID NO: 501 CCGGCCGNCNGCTCAGTCTTNNNTATTACANCNNTCATTGANTATAAAAAAN
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SEQ ID NO: 502 AATAAANACCTTATCCGTGGNCNCGGCCGANGNACATGATNCANATTGGTTT
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SEQ ID NO: 503 ACCCGGGGGGCAATCCGTGTCCTTNCGGTGTCTNGGCAACAAANCCGTCCAAA
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SEQ ID NO: 504 ACGCGGGGGGGTCCGGAAGGGGAAAAACAACACTACGGCTGCGGTGTGGTTGGT
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SEQ ID NO: 505 GGTACTATATTGTTTAACTACTGGAACATTGTAGTAAGAATTTATATCAGGAG
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SEQ ID NO: 506 ACTACTAAATTAATAAATTTATTCCACTTTTGAATGACAGCCAAAAATCCAC
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CCC

SEQ ID NO: 507 CGAGGTACTTTTGTATTTTGATATGGACAGTTTATTCATTTGCATACAGTTATT
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SEQ ID NO: 508 ACTGGTTGGGGATGGGAATCGTGCTTTTCTTTAACTTCAGTTTACGAGATGC
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SEQ ID NO: 511 ACATCAGACTAGATACAACATGCNGAATGTTTCTGAACTTATCCGGAATTC
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SEQ ID NO: 515 ACGCGGGGGGCCACGTTTCAGCGGACACGGGAGCAAGATGGCGATTCCGGGC
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SEQ ID NO: 571 ACCTAGCTCTGAAAAACATCTACAGAAGCAAAATGAACTCATCTGCAAAAA
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SEQ ID NO: 573 ACGGTCTCACAGACAACGTTGAGAGAATAGTAGAAAATGAGAAGATTAAATG
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SEQ ID NO: 591 ACAAAGACGCAATTTTCATAGTGCCTAGAAATAGCACAGATCTATTCTACT
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SEQ ID NO: 593 ACOCCTAATTTGCTGGACCTCATGCAGCTTTAGCTAATAAAAGTTTCTTTAAG
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SEQ ID NO: 594 ACATACCCAAAAAGAAATTAAGCAAGGACITGAACAAACATGGTCCCTAGCA
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SEQ ID NO: 606 ACGGAAGGATGCTGCAAGCTGACCCCAATAAAGTTTCTGCAAGGGCGAAGA
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SEQ ID NO: 618 ACTGCGTTTGGGCCTCAAAGGACATCCTTGAAGTCCAGTTTCACATCGTTGT
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[illegible]

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SEQ ID NO: 644 ACTCTAATTTCACTAACTGCCAAAAGGTTTTCCAGAATAATCTCAGTTGCTTC
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GGCAGGGCTGTGCTGATCCCATCTGGCATCGCTGGGAGCTAACATTAAGACATGGCACTTTGGG
TCCGGGTCCAGGTCTGGTTCAGAGCAGCTGCCACCCGTGGCTACTAGAGGATCCTTTTCCGGCT
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CGACTGGAGTGGCCATGTCTCCAGCCACGCCGGCCGACCTCGGCCGCGACCACGCTAAGGGCG

SEQ ID NO: 645 ACCCTAACCTGACAGGAATTAAGTACTGTTTTTTGTGGGGCAGAAAGCAA
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NATGCATGCATTGTGCATTATTTGTAGACAAGCTACTTTTTCTTCTGNCCCTTTAACAAATTTGCA
GCAATTACCTCCCTTTGGGGTCTAGAGTGAAAGCTAATTTGTGGGTAGATGAGATTGCANAAGA
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SEQ ID NO: 646 CTTTTGTTNGCGGCCGAGGTACACAAGTAAATACTACAGAAATTAATTTCTT
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SEQ ID NO: 647 ACCACTCTACCTATACTCCAGGACTTCATCTTTCTTACTGAAAAACCCAAAC
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TGTTAAGTCAACCAGAGGCCAAGTCTTGAATGCTTTCTCTGTTTGGATTATTTCCACGCTGCTGGC
TGCTGCTGGACAGGTCTGTCTGCACATTCTCAAGGNTGAGAAACCCCAACTAGGGNAACCTGC

CCATCAGAAAGGNGAGTTCACTGGGTAATGGGAGCAACTGCTCAATTGTGAAGGTGACATGATGTTA
AAAGGCTTGAAAGGGGCTGCATGGTGGCTAACGCCTGTAAATCCCAGCACTTTGGGATGCTGAGCA
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SEQ ID NO: 648 ACTGGATTCTATAGGTCCACCATTAAGGCTGGTATGGGACACCAATTTATAC
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GCAATTCATTTGCTCCCAACGAACTACCTGTTTGTGTTGTGAGGTAGCATCAAAAGACTATTGATCT
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SEQ ID NO: 649 ACCGGAAGAAGCAGCTGGCAAGCAGCTCCCTGCATGACCAAGGACCCCTTC
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ATGAACATTCCTGGAGGGGATAGAAGCACCCAGCAGCAGTGGGGGCCATGGAGGACAAATCTG
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TGCCATGAACCTCTGGTTGACATGATTTATTTTGGAAAGATGAGAACTATACTGNGGGCAGACA
TTACTGTGACAGCGAGAAACCCCGATGTGCTGGCTGTGACCANCTGATTTTTCANCAATTGAGTA
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SEQ ID NO: 650 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTCGANAACCAAGCCAGTNTTT
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NGGGGCAACANAAGCCATGCTGGAGTCTNTACTTTTGGAAAATGGANAATCAAAAAATTTGCT
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SEQ ID NO: 651 ACTGATATAATCTAACAAATGAAGGTGCACCTTTACTTCTCGGAACATAGAC
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SEQ ID NO: 652 ACTGCCAAGGACAAGTTGATTTCTGGCCAGGCAAGTTAACTCAGTTTTTTAG
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SEQ ID NO: 653 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGCTTCAATCTTTTATTTAAATGCCATG
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SEQ ID NO: 659 ACCTCTATATATAAAATTTGGACGAATAGAAGTAAATATGTTTATTGGTGAAAA
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SEQ ID NO: 660 AGCAAACCTTCTGGATGCCAACATGATTTTCAGTAACCACCCTTTAGAGTAT
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SEQ ID NO: 661 ACTGGATTCTATAGGTCCACCATTAAAGCTGGTATGGGACACCAATTTATAC
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SEQ ID NO: 662 ACTTTTTTTTTTAAAGATTACTAAACATACAGGAAGTGATAAGAAGTATCAT
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SEQ ID NO: 663 ACATTAATATGTTACTTTGGCATTCTCTATTTCTAGGCTTACAGGAATTATTA
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SEQ ID NO: 664 ACAGTCCGGCCCGTGGGGAGGAGGGAGGGAAGGCAGGCACACGAAGACAC
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SEQ ID NO: 665 CGTCAAGTTCTTCTAGCAGGGACCTGTCTCCCTTTACTTCTTACCTCCCACCTT
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SEQ ID NO: 666 ACTTTTTTTTTTTTTTTTTTTTTTTTAAATTAATTAATAAAATTTTAAATGAT
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SEQ ID NO: 667 ACCTGATTTTTTTTTTAAATGGACAGTCTATGCTTTCATGAGGCATGCATATTG
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SEQ ID NO: 668 ACATTGGTTGGGGCCATGGCGGGTTCCACATTCTTATGATTCTAATAGTCAG
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SEQ ID NO: 669 ACAAAGCAGCCTAGGAACCCCTCAAAGACCCCTTCCCTACTTACTTCCACA
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SEQ ID NO: 670 ACCCGCCTGCCATGGACTGGATCTTCCAGTGCATCTCCTACCATGCCCGGAG
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SEQ ID NO: 671 ACGCGGGACAGGAACAAAGCAACCAATTTTAACTTTCTCTTCTCATTCTCT
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SEQ ID NO: 672 ACTTTTTTTTTTTTTTTTTTTTTTNGGNGANATTTTACTAAATAATTGATAT
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SEQ ID NO: 673 ACACCATTACTCTTCTGAAGAGCCTGGTAAACAGCAGATGCTTTATTCAGAA
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SEQ ID NO: 674 ACCTCAACATAACCTGTAAAAGTATTTCTAGATAAACTTTACAAGTGAAGA
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SEQ ID NO: 675 ACCAGGCTGGCGACAGGTGCTACCAGGAGTGGGCTGAGGGGAGAAAACTA
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SEQ ID NO: 676 ACAAATTTAAGACTAGACAATTAACAAAAAACAACAAATTTATAGCCGC
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G

SEQ ID NO: 677 ACGCGGGGGAGGCCGCTNTNTCTCATCGAAGATGGCGGCGCATCTGTGTCTG
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SEQ ID NO: 678 ACTTTNTTTTTTTTTTTTTTTGGCTTTATAAGAGAATTTTTATTGTTAATTATT
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SEQ ID NO: 679 ACCTGGGTGTATCCTGTGTTTGCCAACTCAGCCTCTTGGGTCTAGCAGCTTT
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SEQ ID NO: 680 ACAAGATATTGCGGTTTTGTTTTTATAACCCACTAAGCCAAGATTGTATC
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SEQ ID NO: 681 ACAAATATCATCATTTATTTTTGATTTTTTTACCAGCCCTGAATTTTCAA
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SEQ ID NO: 682 ACACATGCACATCAAAACACTTCAACTGAATATAGATGCCATTACATTATTTA
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SEQ ID NO: 683 ACTTTTTCTTTTTCTTCTTTTTTTTTGGAAATTTATTTCTGAGCCTTTTGT
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SEQ ID NO: 685 ACTTTTGGAGGCCAAGGCAGGTGGATCACTTGAGCTCAGGAGTTTGAGACCA
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SEQ ID NO: 687 ACGCGGGGGGGCGCACCCGCCGATTGTGGCCATGGCGGCCGAGTCTCTAG
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SEQ ID NO: 688 ACGCGGGGGAGACCTGGCTGCTGTGTCCCGGGCTTGCGCTCCGTAGTGGAC
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SEQ ID NO: 689 ACGCGGGGTGAAGATATTATGGCTGCTGCCACGGAGCATAATCGCCCGAGCA
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SEQ ID NO: 690 ACTTTTTTTTTTTTTTTTTTTTTTTTTCAAAAACGCCAGTNTTTATT
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SEQ ID NO: 692 ACCCCACACCTGAAGGTGTCTATGAGTTCACATGGCTCAGGAATGGAGTTT
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SEQ ID NO: 695 ACTAAAGGCTTTTGCATGAATTAAGGAAGGAGAGTCTTGGGGCAGAAOCCAATA
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TGG

SEQ ID NO: 698 ACTAGGGATACAAAGACTTGGTTATTCTTGTGGAGTAATGATTCTCCTCTAT
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SEQ ID NO: 699 GTCGCGGCGAGGTACACAGTCCAGGCTCTCCAAACGGAACCTACAGGCAGC
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SEQ ID NO: 700 ACACCGATTITGGATACTTTCTTTTCAGAGCCGGCCACTGAAACAATGAAGTA
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SEQ ID NO: 701 GTACGCCTGTAATCCAGTGACTTGGGAGGCTGAGGCAGGAGAATCGCTTGA
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SEQ ID NO: 702 ACCTGACAAATTATTGGATTCCAGCAGTGACTCACTTATTCAAGATAACTG
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SEQ ID NO: 703 ACATGACCTTTAGTGAAGATTATTTGTATCAAAATTACCCATATCCAAGTTTC
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SEQ ID NO: 704 ACAGACTGAACAGATTAGGTCTTTGTCTGAAGCTATGTCAGTGGAAAAAATT
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SEQ ID NO: 707 ACTTGCTTACAGGAAGAGTAATTCCTAGCAAAGGTCATTAGCTCCTAAGGC
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SEQ ID NO: 708 ACTTTTTTTTTTTTTTTTTTNGGTATCTATCTAATAAAAGTTTATTGTGTAT
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SEQ ID NO: 709 ACGCGGGAAGCATATGTTACTTACCTTGTATTAAATATTTCTTGAAAAGCAA
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SEQ ID NO: 711 ACATGGCCCTTTAAAAACCGGAGACAACTGGAAATTCATTGGACCTGATCAA
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SEQ ID NO: 712 ACGCGGGGACCTGGGATAACGGCGGCGAGCGGACGGCTGCAATTACGGGGT
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SEQ ID NO: 713 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNAANAACCTTTTTATTCATCATCTA
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SEQ ID NO: 714 ACTTTCATAATTTGCTCCTGCTATCTAAAGGCAGAGCCAGGTATACAGGAT
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SEQ ID NO: 715 ACGCGGGGTGAGAAGGAGAAGGAGCGGCTGGGAGGCGGTTTGGGAGTGGCG
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SEQ ID NO: 716 ACTAAATCTAGTAAAGACATTTTCATACACCAAGGGGAAAAATAGGTAGC
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SEQ ID NO: 717 ACGCGGGGCGAGATCAGGGATCGCGATTGCGAATCCTCCGCTGAGGTGATTT
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- SEQ ID NO: 718 GCTTTTTTTTTTTTTTTTTTTTTTTTACTTTTGGGAGGANATAAACCAGTCTC
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- SEQ ID NO: 719 ACGCGGGATGGGAATGAGGNTCTACCACTCTGGAATAATTCATGCCTGCAGGT
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- SEQ ID NO: 720 ACAAATAAAAGTGATGGTGAGAACCTGGCTCAGGAAATGCAGTAGCAGGGC
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- SEQ ID NO: 721 ACTTTTTTTTTTTTTTTCTTTTGATTTCTCAGGACCTTAGAGGGAAAAACAAAC
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- SEQ ID NO: 722 ACCGGAAGAAGCAGCTGGCAAAGCAGCTCCCTGCACATGACCAGGACCCCTTC
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- SEQ ID NO: 723 ACAGCGTTCACAATGCTGGTATTAATCAGCTACATATTTTGAACATCTACTGT
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- SEQ ID NO: 724 ACGCGGGAGTGCCTGCCGCTCCGCCGACCGAANAGGCTGGACATGACACC
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- SEQ ID NO: 725 ACCTCATCGGTATCCAAGGCCCGACTATGTTCTTGTGCGCTCCGACCGGGTG
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SEQ ID NO: 728 ACCACTGTATTGATTAGCCTGTATGTAGCAGGGCTCCCTTCATTGCATCTGAG
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SEQ ID NO: 729 ACTTCAGGATTAGGAATTTGGGTTTGTATAGATGTATTCTCTGGTGAGGGTG
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SEQ ID NO: 730 ACCTCCTNTTCTTCTATTTTATAGGAANAAGTTATAACAAGTTTTAAATATCT
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SEQ ID NO: 731 ACCTCCTCTTCTTCTATTTTATAGGAAGAAGTTATAACAAGTTTTAAATATCT
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SEQ ID NO: 732 ACTTTTTTTTTTTTTTTTTTTTTTAAATAGTTAATAAAATCAATACAAAT
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SEQ ID NO: 733 ACCAGGCTGGCGACAGGTGCTACCAGGAGTGGGCTGAGGGGAGAAAACTA
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SEQ ID NO: 734 CAGCAGAGATATATGCCTATCGAGAAGAACAGGATTTTGAATTGAGATAGT
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SEQ ID NO: 735 ACATTGAGACAGAGCTAAAGAAGAGGAAAGGGATCGTGAACATGAGGAAC
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SEQ ID NO: 736 ACGCGGGATAGACGGAAATGGAGAGCTGGATTCTCCACTTTTCTGACCATT
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SEQ ID NO: 737 ACATAAACTTCAAAGAGATGCTGTAGAGGATTGGACTGCAGTTTTCTCCTATA
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SEQ ID NO: 738 ACCAAGTGAGTGGGAATACATATTCTAGTTAAAGCATTGTGTCTAGCTACAC
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SEQ ID NO: 739 ACCTTCACTGCTCCAGTGATGANAGCCTCCAGCAACATATAGAAAAGCACA
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SEQ ID NO: 740 ACTTTTTTTTTTTTTTTTTTTTTTAAACANAAAGGTATAAAGTTTATTAACATCT
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SEQ ID NO: 741 GGTACGCGGGTGAAGTATTGCTAATATTACCGNGGTTTATGAACTATGTTCAAG
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SEQ ID NO: 745 GGTACTGCTATAAACTCATTCTGTGTGGTGGCTGTGCTATAGAGTCTGTGT
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SEQ ID NO: 746 ACTTTTTTTTTTTTTTTTTTNGCCTGGAAATGTTTTTAAATANAATGGTCTAG
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SEQ ID NO: 748 CGAGGTACGGGGGTCTTGAGCGCAGAAACACTTACTTTTCCCCCTACCCCTGCT
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SEQ ID NO: 749 ACGCGGGATTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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SEQ ID NO: 750 GGTACGGGGGTCTTGAGCGCAGAAACACTTACTTTTCCCCCTACCCCTGCTCCT
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SEQ ID NO: 751 GGTACGGCGGGAACCTTTGTAAGATGCAAGAGGTTGGATCAAGTTTAAATGAC
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SEQ ID NO: 753 ACGCGGGGGTCTCATTGAATCGCTGCAGCTCTTGGGTTTTTGTGGCTTC
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SEQ ID NO: 755 ACGCGGGGGACGAACACGTGACGCGGTGGGGGGACCACTGCAGACTGAGC
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SEQ ID NO: 756 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTCTTTCAAAGATTTTACTAAATCAT
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SEQ ID NO: 761 GGTACTGGGATTATATAGGCATGAGCCACTGAGCCTGGCCAGAAAGCGTTTT
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SEQ ID NO: 762 ACTTTTTGTTTTATTCTTTCTAGCTTATCCCTGCACAATTATTAGAGTGAA
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SEQ ID NO: 763 GGTACCATAGTCCAGCACTTGGCCAGGGTCTAGACTGCTGGGTAGGTCC
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SEQ ID NO: 764 ACAATAGATGCAACGCCAAAAATGAGATGAAAGAGAATTCAGAATAAAATTC
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SEQ ID NO: 765 ACITTTTTTTTTTTTTTTTTTTTTTTTINACTNGTTTGGTTGGATGCTCTTCCA
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SEQ ID NO: 766 CGAGGTACTGTACCCGGACATACCTATTCTTCAAGTTCTGGTTCTTCAG
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SEQ ID NO: 767 ACTCTATAAATCTAGTGGAACATTTCTGCACAACTAGATTCTGGACACCA
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SEQ ID NO: 768 GGTACGCGGGGATTTGTGGTGAGATTCTCTCCAGGCCACANGACATTTCTCG
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SEQ ID NO: 769 CGAGGTACTTTTAAGAAAAAGTCCAATGTTACAAAAATCAAAATGCTTATATCA
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SEQ ID NO: 772 ACTGTATATCCATATGGCACATTTATGACTTTGTAATATGTAATTCATAATAC
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- SEQ ID NO: 801 ACTTCTTTTTTACAGTTTTTTTTTTTTTACACACATATTATACAACTTTT
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- SEQ ID NO: 805 ACTGGATTCTATAGGTCACCATTAAAAGCTGGTATGGGACCAATTTATAC
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- SEQ ID NO: 806 ACTATTGCTATTAGGGGTTCTGTTTTATAAATATTTCTTATCATACTTTATT
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SEQ ID NO: 808 ACTTTTTTTTTTTTTTTTTTTTTTGGNTTTTTTTTTTTTTTTTTTTTTNA
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SEQ ID NO: 811 ACAGAATGGTATTTGTGTATGTGTGTGGGCTTANAGATTACAAGTAAATATT
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SEQ ID NO: 813 ACAAATATGTATCTGAAACACTTCTATTTGGCAATTTTATAACAAATCAAAT
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SEQ ID NO: 816 ACTGTTGGTTAAATGACAATTTATGTGGATTTTGCATGTAATACACAGTGAGA
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TACT

SEQ ID NO: 817 ACCCAACTTTGCTGGACCTCATGCAGCTTTAGCTAATAAAAGTTTCTTTAAG
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SEQ ID NO: 819 ACATTGGAGAAGCTGTGCAGCAGCATCCTTTCTGTGGTGGGCAGGGCAGGA
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SEQ ID NO: 820 ACTCAGGGGCATCATGTTGCTGCAGAGGCCACACTTCCAGAACTTTTCTCCT
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TTGTNACGAAAA

SEQ ID NO: 821 ACAAATCTTTGGCCTTTCTCTTGACATTTTCGTATGTCAAAAAGCAAAAACC
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SEQ ID NO: 822 ACTTTTTTTTTTTTTTTTTTTTTTCAAAATGAGACTTGGAGTTTAATAAAAA
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SEQ ID NO: 823 ACTATCTCTGCAGCTCAATATAAACAACGATGATTTCTTTGTAGCAGTATG
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SEQ ID NO: 824 ACTTGGGGATATAAA
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SEQ ID NO: 825 ACGGACTTGTGCAAAATGAAGAGAAATTATTCAGCCTGTCTCTAAAAGCGATA
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SEQ ID NO: 826 ACGCGGGGCCCTTACGGCGCCGGAGAGATGGCGGAGTTGGACATCGGGCAG
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SEQ ID NO: 827 ACTCCAGGAAGATGCCATCTTGCACTCAGAAAGATAGTTTAAGGAAGATGGCA
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SEQ ID NO: 828 ACTTTTTTTTTTTTTTTTTTTTTTCTNAGTATTCAACACTTTAATATTTATG
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SEQ ID NO: 830 GGTNCAAGTGATTGTGACAAATGACGTAAAAATGGCATTTCATGATGTCGAA
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SEQ ID NO: 831 GGTACCTTCTTTAGTAGAGACTGGGTTTCACCATGTTGGCCAGGATGGTCTCT
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SEQ ID NO: 834 ACAAGATGGTAGCTTTATATTTTTTTAAATGGCTATACTAAGAGAAAA
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AACCAACTAAAAAAATATTGAAGCACTTTTGAATGGAAGCAAAATGAATAATGCTAGATTTAAA
AACAGNLTGAATCACACTTTGGTCTGTAAACATATTTAGCTTTGCTTTTCAATCAGATGTATACAT
AAACTATTTTCCCGTACC

SEQ ID NO: 835 GGTACTATTTATTTCTCAAGTGTCTCCATGGGGGAAAAATAAAAGTCTAAT
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TCTTACTTTTGGAAATGGAGAAATCAAAATTTTGCTAATCAACAAACAAAAAGGAGGAAACTC
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SEQ ID NO: 836 ACGTGAAGAGCAATTTAGGAGACATAAGACCGTGTGCTGACGAGGCACA
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SEQ ID NO: 837 ACGCGGGGGCTCTCTAAGATGGCTGCGGCTACCGGTGCGGTGGCAGCCTCT
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AGT

SEQ ID NO: 838 ACCAAGCACTGGGTAAGGCACCTTTTGTGGAGCATTAGACAGTAACCCCTCAAG
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SEQ ID NO: 839 ACGCGGGGCTGTGACTTAAATCCATTTTCACTTAGAGAAATAGAAACACAAG
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SEQ ID NO: 840 ACTATTTATTTCTCAAGTCTTCCATGGGGGAAAAAATAAAAGTCTAATATG
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SEQ ID NO: 841 ACTGTACAGAACTTTTACATACATCTCTCAGTCTAGTTGTGAAAGGCCTAAA
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SEQ ID NO: 842 ACTGGGACGATTCCGCGGAGCCGGGCAGAGGTTTTAGGGGAATGATTAACAA
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SEQ ID NO: 843 ACTTTTTTTTTTTTTTTTTTTTTTTTTTANAAAGGATGACTTTTATTTCCATCC
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SEQ ID NO: 844 ACTTTTTTTTTTTTTTTTTTTTANATTGCCTGCTGCTAGGAGGAGGCC
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SEQ ID NO: 845 CGCGTCGAGGTACCCCTGGCAGAGCATTTGCAGATTAAAGAAGCATTTGAGA
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ATCTGNTTAAAC

SEQ ID NO: 846 ACCGCGGGGAGTTGCTCTGCGCGGTGTTCCACGTGCGGCCTGAACCTGAG
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AANATGAATAGCTGCTTGTGCTGNGTCTAAAGATGTGTATGTNGATTCCANAAATCCTGNGTNTTAC
TTG

SEQ ID NO: 847 ACCCTGACCCATGAACACCTGGCCATGACCTTTGACTGCTGTTACTGTCCACC
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SEQ ID NO: 848 TCGCGCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTCTTTATAGG
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GGCCTNTGGCAGTCTAT

SEQ ID NO: 849 CCGCGCGAGGTNCCCTTNNGAATTGAAGTGAANGATCCTGAGCTGGAGG
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SEQ ID NO: 850 ACTGTGAAACCACTTCAAGTTGCTCAGACTCCAGTAATACAACGGTCA
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SEQ ID NO: 851 CCGCGGCGAGGTNCCCTTNGNGAATATGAGGAGTATATTACTAAACTTTTCA
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TCTTCANGATCCAAATGNGGCTGNGTTCNTGGNAAACCAATTCAAGGGTGAATCAAGCGTTTTTG
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SEQ ID NO: 852 CCGCGGCGAGGTNCCCTTNNNGAATTTGAAGTGAANGATCCTGAGCTGGAGG
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SEQ ID NO: 853 ACGCGGGAGGATTTGTTCCACTAAAAATTTATTTTCAAAAAATTTACTTCACAT
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SEQ ID NO: 854 ACTATTTATTTCTCAAGTGCTTCCATGGGGGAAAAATAAAAGTCTAATATG
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SEQ ID NO: 855 ACTACTGTTAATATCTCTAAGAACAAAAACACATTGAACATCCTTCCAGAAAG
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SEQ ID NO: 856 ACCCATCCCACTCTCAAAATCGTTTGGTTTTTTTTATCTTGATTGAGATCCTC
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- SEQ ID NO: 857 ACTGGTGCACTCTCATATCAAGGAAAAGCAAAACACAGAATAATTTAAAT
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- SEQ ID NO: 858 ACTTGAAGGAGAACAGTTTACATCGGGCGTTAGCCACCTTGCAGGAGGAGAC
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- SEQ ID NO: 859 ACCTGCCTTGAATTTAAATGTCTAAGGAAAAATGGGAGATGATTAAGAGTTG
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- SEQ ID NO: 860 ACTCTAAGTCAGGAAAAATTAAGACGACCAATAGTTGCCTGTGAACCTTGGCA
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- SEQ ID NO: 861 ACTTTTTTTTTTTTTTTTTTTTTTTTCCCTTTAAAAAGAAATTTATTAAGCTGTG
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- SEQ ID NO: 862 ACACAAATGCATGAGTATGTTTATACAGTGTAGACTGATGTGAATTTGCATT
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- SEQ ID NO: 863 ACAAAGGCTGCTTAAGGCAGTGCAGCCCTTCTCAAAGTCAGCATGTCAATG
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CCTGGTATAAAAAATACAGCNTACCTACCCNNGGAAAGGAGGAAAAAGGAGANGAAAAAGCTTTT
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SEQ ID NO: 864 ACTTTTTTTTTTTTTTTTTTTTTTTTTTAAAAATAAATCCAAATTTTATTA
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SEQ ID NO: 865 ACCATGAAGAAGAAATAAATGAGGGTAAGGGGCTAGTGTGATAGGGAGAGGG
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SEQ ID NO: 866 ACTTTTTTTTTTTTTTTTTTTTTTTTNAATAAGGNCTCACTCTGTCTCCAGG
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SEQ ID NO: 867 ACATAGGGTCTGTACACCAGTTTATAGGATAAAGAACTGGAAGAATTCCT
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SEQ ID NO: 868 ACCTGTCCCATCTCTAAAAGGATTTGTGGGCAATGCTGGCACTTGGTGGCCAG
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SEQ ID NO: 869 ACCCACTGCTATTGCCTAAGGGTGTAGTCTGAAACTGAAGCCAGTTGCCGA
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SEQ ID NO: 870 ACAGGCTTAAATCTATGTCATTTACACTCACTGAATCATCAACCTNATCACCA
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SEQ ID NO: 871 ACTTACCTTCACTGAAGAGCGTAACATGAATTTCTGCAGTGGTATAAGGAT
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SEQ ID NO: 873 ACGCGGGGGGACAACCTGGCCATCCAGACCCGGGTGGCCAGAAAAGCAT
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SEQ ID NO: 874 ACGCGGGGGGTCTTGGCTTTGACAGCTTCAAAGAATGGACAGTGATAAGTT
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SEQ ID NO: 875 ACTGTCCATATCTTTTGTATTTACTTCAAAGGATTCTGGATCAGCAGTATAAA
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SEQ ID NO: 876 ACGCTGGATAGCCTCCAGGCCAGAAAGAGAGAGTAGCGCGAGCACAGCTAA
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SEQ ID NO: 877 ACGCGGGGAGTGTCTTCTGGGATGGGAACCAAGCCGCTTCCCAAGTCTCTGTGC
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SEQ ID NO: 878 ACAACCAACCACTCCTGTTCCTTCCATTTTTTCTGGCCTAGTGTCACTGCCAGGT
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SEQ ID NO: 879 ACCTTTTGTAGCATAGCCTGGGAAGAGTCACTGAAGGAGATTTAACTGAA
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SEQ ID NO: 880 GGTACTAATCTCTGAATTTGTCTATGCGGAAAAATGGAGACTTGGCTTGTGC
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SEQ ID NO: 881 ACTGAGGAAGACACCACTTCTGACGGTGTCTAAGAAGCCAGGTGGATGTGT
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SEQ ID NO: 882 CCGGGCAGGACTTTTTTTTTTTTTTTTTTTTTTTTNGGNTAAAAGGANAATTG
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SEQ ID NO: 883 ACAGACAAGGTCTATAGAATGTGGTAAAACTTGACTGCAACACAAGGCTTA
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SEQ ID NO: 884 GGTACCTCCAAACAGAGATGGAAGCTACACTGCAGTTCCCAATACTACTTCA
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SEQ ID NO: 885 ACCCTTTTCTTTTCTTTTCTTTTCTTTTAAAGTATTGTTAACAATCCTTTGG
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SEQ ID NO: 886 ACTTTTTTTTTTTTTTTTTTTTTTTTGGGTTATAAAAGCCCTTTTATAAGCC
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SEQ ID NO: 887 ACCAAGGAGCTCTTCTTATTTATTTCCATATGGCCCTCAGCAGCTTTCATCTG
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SEQ ID NO: 888 ACTTATTTTTTTTTTTTTTTTTTTTTTTTNGNNGTTAATTCATTTTAATAGTAT
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SEQ ID NO: 889 ACTTTTTTTTTTTTTTTTTTTTTTTTGGNGACAGTTGATTTTATTTTTTAAGTTA
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SEQ ID NO: 890 GAAGAAGCCAAAAGAAACGAAATAGATGCGGAGCCGCCAGCTAAGCGGCA
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TTC

SEQ ID NO: 891 GGTACCAGCACCAGCCCCTCTGAAAGGAAAAAGTGTAGTCATGACTGTCCAT
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SEQ ID NO: 892 GGTACTACGTACGCAATTTCTCCAAACAGCTGCTCGACAGCATATGGCACCA
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SEQ ID NO: 893 GGTACCGCGGGCATGCGCGTTTCTCTGTCATGGTGTGCGTTTCTGTTCTAGCT
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SEQ ID NO: 903 ACTGCTGACATCCAAACTATGTCCCTTTTAGGGTCTACTCGGAGAAAAATGC
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SEQ ID NO: 912 ACATAGAGAAGAAAAATTTGGTTTTAGCAAATGACAGAGCCTTCAAAAAATATT
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SEQ ID NO: 915 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTATNGAGTATTGTTTTATTAACCAA
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SEQ ID NO: 927 ACCTAGCTTCTGATGTATGCAAAACACTGCAGGAAGAGAGAATGAAAGAAA
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SEQ ID NO: 929 ACTGGTGACCTCTACATATCAAGGAAAAGCAAAACACAGAATAATTTAAT
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SEQ ID NO: 930 ACTCGATGTGAATGAAACCTGAAATAATAAGATAATAAGAAAAGCAATAAT
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SEQ ID NO: 933 ACTTTTTTTTTTTTTTTTTTTTTTTNGAACCCAGTTACAAGAAACAGGCTGA
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SEQ ID NO: 934 ACCGAGCACTTTATTCAGTGCATAGCTTTAAGCCAGTGTGGATTCACTAAGT
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SEQ ID NO: 935 ACCCTGGCATTGCTGACAGGATGCAGAAGGAGATCACAGCCCTGGTCCCCAG
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SEQ ID NO: 937 ACGCGGGGAAATCACTGTTTAGTCTTCTGGAGGCTATGATTTTTGCCTTAC
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 GCCCCTNGCCATNANACCTTNAACAGNAATTTTNCNTNCTNTTAATNCATTTCCAATTCAAGTTT
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SEQ ID NO: 939 CGCGGCGAGGTACAGTGACCTGCAGAACTTAGCCAAGAGTCTGGGTCTCCGG
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SEQ ID NO: 940 ACTGTCTCTCCCCAGAAGGCCTTCAAGGTTAACACACAACANTGCCCTGCC
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SEQ ID NO: 941 ACTCATCACTCTGTCCATACGCGATCACAATATCTCTAGTTCTTCCATCACA
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SEQ ID NO: 942 ACGCGGGGACAGCGCGCGGAAGAAAAACAGCAAGAAAGCGCGGGGGAA
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 TTAATAT

SEQ ID NO: 943 TTAATAAACTTCGAAAGTCACAGACACAGAAATTTAGGAAGCTGAAGGCTGAO
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 ATCCA

SEQ ID NO: 944 ACCTCTCTCTGTTGGAATGGGTTATCCAGTAAAAAGGCGGTGCCCATGCAA
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SEQ ID NO: 947 ACTAAGGGGACAATACACCAAATTTGTTGAGTTTACAATCAAGTCTACTAAG
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SEQ ID NO: 948 ACTTTTTTTTTTTTTTTTTTTTTTGGATATTACACCATAGGTTTATTAA
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GCGT

SEQ ID NO: 950 ACTTCCAGCCAACCTCGTAGCCAGGCGCCAGATAGGCAAACTTTCTTGT
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SEQ ID NO: 951 ACGCGGGGCGCTTACAGTTGCTGAGAGGAGGCGAGAGGCGGGGCGCTAGG
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SEQ ID NO: 953 ACAGTTGAAAGCAGAGTGTAAACAAGGGATATGTCAAGGTAAAGCAGGTAGG
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SEQ ID NO: 954 ACCTAATGAAAAGATCTCCAAGAGGTTTGTCTCATTCTCCTTGGGCTGTAAAA
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SEQ ID NO: 956 TGCTGAAGCTTCACAGGGCGGCCAACTAAGTCTGCTGATTTTGAAGACCA
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SEQ ID NO: 979 GGTACATCTTTGGCTTGTGAAAAACAAACATCTTTCTCTGGGCAATAGTAG
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CTTANCTGGGANGGATGCAAAATTAAGCATGGATTTAGTGAGAANGGANCCTTACCTTTAANTT
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SEQ ID NO: 997 ACTAGTGCTGCAATGCAAGGGTTATGACAAAACCTGTCTGTAATGTAGGA
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SEQ ID NO: 998 GCGTGGNCGCGGCGAGGTAATTNCAAGCAAGCCCTATGATTTGCTACTAT
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SEQ ID NO: 1003 ACTGACACATCCAAGCATGAGTGTGCAGAAATCCCTTGTCTATTCTGTCT
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SEQ ID NO: 1004 ACGCGGGGGTGC CGCGGTGGCGGGACTCTGGGGAATAATGGCTGCGTCTTCGA
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NCCACTTGAATTN

SEQ ID NO: 1005 GGTACACAAGCCATCAATTACCACTCTCTGCTCGCCCTCCATGAAAAATCCAA
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CTATGCAAGANAGCATTTTTNTAAAACTAAGGNCNAAAGNAAANANANGCCTTTGT

SEQ ID NO: 1006 ACGCGGGGGTGC CGCGGTGGCGGGACTCTGGGGAATAATGGCTGCGTCTTCGA
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AGAGCGGCTGCTGTCTGCGCTTGAGGACTTGGAGGTCCCGTCTAGGGAACCTATAGAAATGCTGG
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SEQ ID NO: 1007 ACATCCGGCGAGTAGCTGGCGGTCCCGGGTGTCTGTTAGTGTGCTCTGA
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SEQ ID NO: 1008 GCGTGGGNCGCGGGCCGAGGTACTACTTTCTNACTTTTCTGGTTAGCCAGA
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GNAAGGATGAGGTGANGGATCTCANCCCGGGGNGAACAGTAAAAATTTNTTAGGCCNGC
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CNC

SEQ ID NO: 1014 CGAGGTACTTTGATTCGGTGCTCTGGCCTTTGGAAACCTGCTGTTCCTGACG
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SEQ ID NO: 1015 GGTACAGCAGAGACCTTCCTGCTTTTACTGGGGACTCCAGATTTTCCCCAAA
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CCATCAAA

SEQ ID NO: 1016 ACTTCTGTCTTTGGCACATTTGCCAGCGGATGCAACTTCTATCCTCAGTC
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SEQ ID NO: 1017 GGTACTCAAAGACGAATCATGAAAAAGAAAAAACTTTATTTCAAACAGGT
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SEQ ID NO: 1018 ACTTTTTTTTTTTTTTTTTTTTAAATCAATATTATTTGGGCGCTATTATGTG
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SEQ ID NO: 1019 ACATATATCAATCTCCCTTGCTTGTCTTTAAGAAAGGGCCGTTATAGCATT
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SEQ ID NO: 1020 ACTTANCITGATTTCAAATAAGTAATCTTCCCCCTTTTGTAGGACTTTAAA
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SEQ ID NO: 1021 AAAAAACCCACTTGGGGCTATATGCGATTTCAAGTTGGATAAACGAGTC
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SEQ ID NO: 1022 ACATTCCACAAGCATTGCCTTCTTATTTTACTTCTTTTAGCTGTTAACTTTGT
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SEQ ID NO: 1023 ACTACACCACTTTTCTCACCAACCCCATCTCTATTCTTGAGTTGCAGGATAC
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SEQ ID NO: 1024 ACAAATTTGCCACAGGTGAACACTTAATTTGTGTTCTTAAAAATAATGCT
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SEQ ID NO: 1025 GTACTCTATTCTGATTANGAAAGAGAGGCTAGATACCAAACATCACGAGATC
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SEQ ID NO: 1026 ACGCGGGTTCCTCGGCTGGATTTAAGGTTGCCGTAGCCGCTGGGAATTTA
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SEQ ID NO: 1028 ACAGTCCCTCTCCTATAAGCAAGAAGCTCTCGTGTGCTAGTGTCAAAAGCCA
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SEQ ID NO: 1029 ACAGGAAATGACTTAGCACTTCCCTGTTTTCTATTGCATAATTTTTTTTT
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ACCTTGTG

SEQ ID NO: 1031 ACTGTATAACATCTGTGTTATTATTTAATGTTTCTAAAAATAAAATGTTAGT
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SEQ ID NO: 1032 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGGNGAAAAATACTTATTCATGT
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SEQ ID NO: 1033 ACGCGGGGAGGCTTGAGGGAAGCATGGAGGTCCATGGCAAGCCCCAGGCTA
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SEQ ID NO: 1034 ACTGAAGCAGCATATCAATCCCAATAAGACATTGGACCCTTTTGAACCATG
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SEQ ID NO: 1035 ACTAGGCCTATCAAGAAAAGCTGTGAACAGCAACATCATAGACAAAAAGG
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ANA

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SEQ ID NO: 1038 ACNCGGGGGTAATATGGTNNAAGANAACCCATATAGACAGCTGCCTTGTAAAC
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SEQ ID NO: 1039 ACTTTTAAATTTTTTTTTTTTTTTTTTGGATTTTAGTAGAGACGGAGTTTAC
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SEQ ID NO: 1040 ACAGTAATCCTGTGAGAAAGACAGGACAGAAACCACTGTGCCTATTTACAG
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SEQ ID NO: 1041 ACTACTAGTGGACTCAAGTGATATAAAAAATAAAAAATAAACTTCCAT
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SEQ ID NO: 1042 ACGCGAATTGGAGAAAAAGTTCAAGTGGGAAGCATGTCGTCTTTATCGCTCAG
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GGCCAT

SEQ ID NO: 1043 ACCAGCGGCGCGCCATGGAGTTACTGAAGGTCTCCAAGGACAAACGGGCCCT
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SEQ ID NO: 1044 ACTTCTGTCTTTGGCACATTTGCCAGCGGATGCAACTTCTATCCTCAGTC
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GCAC

SEQ ID NO: 1045 ACAGCTTCTTCGTCTCCATGCTAAGAGATGTAAGGCTTAAGGGTCAAAC
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SEQ ID NO: 1046 ACCAGTAAAACTTAAAGGCACAAATTCCTTGAAGACCTTCTCCCTTTAT
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SEQ ID NO: 1047 ACCCCACAGCTCCACACTGTATCCCCAGCCAAGGGCCATCCCTAGAAAA
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SEQ ID NO: 1048 ACGCGGGGGGCAACGAGGAGGGCTGCGAGGCCATCAGCTTCTCTCTGCTCCCT
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GGGATCTGCGGATATTTCCAGAGGGGAAATCATTCATAGCAGATGTGGAGCCATTTTGTACAG
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TGCTATGACTGTCTGGT

SEQ ID NO: 1049 ACAGATGTGTATGGGAAACCCCAACCCCTATATATTGTAATAGATGGGCTG
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SEQ ID NO: 1050 ACTACTTGATTGTTTATATCCAATTCCTTTCCATCATTTGATTGAATCTTTTGG
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SEQ ID NO: 1051 ACTCTGTTGTAATGGGAAACATTAATATCTGCTTCTTGCACGACAGTAA
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SEQ ID NO: 1052 ACAAAGAATACAAATATGATTGTCAAAAACATATAAAAGACAGCTGCTC
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ATTCCA

SEQ ID NO: 1053 ACTTTTTTTTTTTTTTTTTTNGGGNNCCATNAAAAAGCTTTATTTCCATTGG
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AGNG

SEQ ID NO: 1054 ACTTTTTTTTTTTTTTTTTTTTCTACTTTTCTTTATTGTCTGGCTAAC
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SEQ ID NO: 1055 ACCAGAATACTCTCACATTTTATTCAAGGCACTCTCCAGCAGAAAGTATAAT
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SEQ ID NO: 1056 ACCTCTCATTTTGGCTCTGCCCCCTCTGGAAGATCCTCTCTGTATCCTCATCCTG
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SEQ ID NO: 1057 ACGCGGGGCAACCGTGAGAGCAGAGCGCGGCGGTGGAAGCTGCTAAGTCA
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SEQ ID NO: 1058 ACGCGGGACTCTAAACTGGTGGTTTCTTACTGAAGGTGTTCTCCATTGAAA
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SEQ ID NO: 1059 ACAGAGAAACCAAGGTTGCCCTTTCCACAGCTGGATAGACTTATCCAAAAC
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SEQ ID NO: 1060 ACATACTGCTGAATTTAACTCAAAATATTTCAAGGTAAGTGAAGTGGTGCTA
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SEQ ID NO: 1061 ACATAAGTGCTATCAGAGAAGCCAGCCGATATGGATTGGCCTGCACGACCC
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SEQ ID NO: 1062 ACAGACCAGTGAGTCTGGGGAATTGCGGTCTCCACCAAGATCTGTGGGTGCA
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SEQ ID NO: 1063 ACNCTAAACAGTGGATTGAGTTCACNGNTTATCTTTTNCCTTTTTCANA
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SEQ ID NO: 1071 ACTGCAACTGCCAGAACTGGTATTGTAGCTGCTGCGCCGCTGACTAGCAGCTC
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SEQ ID NO: 1077 ACGCGGATTGTGACAAAGATGGTGATGGAACATAACAACAAAGGAATTGG
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SEQ ID NO: 1078 ACTGTCACTTAACCCCTATTAACATACGGTGTTCAGCCTTCCAGTATCAGCG
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SEQ ID NO: 1079 ACTTTTTTTTTTTTTTTTTTTTTTTTTTAAAAATGTCCAGGCTGCCTTCTGTG
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SEQ ID NO: 1080 ACTGTGAAGTCAAAGGCCAACATTACAGAGCGCACTCTGCCTGAAATACA
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SEQ ID NO: 1081 ACCTTTGTGCATGTTGCCTTCATTCCTGAGCAGGTATCATCCTCAGGGAACCA
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SEQ ID NO: 1082 ACTTTTTTTTTTTTTTTTTTTTTTTTGGTAAGGACCAAGTATTGATTTGACTTT
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SEQ ID NO: 1084 ACTGCTGCCGAAGTTGCCCGAGTCCATGGGGTTCGTGCTTTGGCATCAACA
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SEQ ID NO: 1085 ACAACCTTCAAAACATTCCAGTTTATATAAAAAAGGGGCACACAATCGTGGT
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SEQ ID NO: 1086 CGAGGTACAAATGTTCTGTAAAGTTGTAAACAGAAATGAACCCCACTCTT
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ANNGGAANNANCTGNNNNNTCTTAATTAATNTNATNTNTTNTGTTTGAANGNNTTCTCCANT
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SEQ ID NO: 1087 GGTACTNCANCTANNGGCTCATTGGNATGCTATCNTGAANNACNTGGTNATN
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CTTAGAAAGGAGCAGAGTANCAGATATGTTTACAGATCAAGAAAAGCAACTTATGGAAACAACTA
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SEQ ID NO: 1088 ACTTCTGTGAGATTACGGNCGCTATGACATGGCTCAGTTCGGTTTAAAAA
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SEQ ID NO: 1089 ACTAAAGGAGATAAGTGTAAAGTTTCCCATGACTTGACTCTGGAGAGAAAA
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TGGGATGAGAAAAAGCTCTGAAGAGTATNGAACAANAAGCACNGTGAGGCGGAAAAATAAAAA
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SEQ ID NO: 1090 ACAACCTGTGACTGTGATTGGGTIATTCACAGCGTAATTCAGATTCACTC
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SEQ ID NO: 1091 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCTTAAAAATCCATCTGACTGGG
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C

SEQ ID NO: 1092 ACTTTTTTTTTTTTTTTTTTTTTTTTNGNTNTTTTGGGGCAGTCAAGTTAATACAA
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CAACTNAGGCCNTTCTNACCAAAGGAAGAAAGGNTGGTNTTCCACCCCTNTAGGAAAGGCTG
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ACANAAAAGGTTTTNTNTNAAATGGTGGCNAACGNCANCTTGANCTAAANANCCNAACTTA
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SEQ ID NO: 1093 CATCCTTACAAAGATTCTGCNGTGATTTGTGTGAAGAAGAAACGTTGTCT
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SEQ ID NO: 1094 ACCTGGTNAANCACTGTGGCAACATACCTGTCTCNTTATTAATTATCCATTA
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SEQ ID NO: 1095 GGTACGCGGGGATTCTTCCCCTCTCTACAACCTCTCTCCTCAGCGCTTCTTCT
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CCACCTCCACAAGTACT

SEQ ID NO: 1096 ACTGCCCTTTCACATCAAAGAACTACTGACAACGAAGGCCCGCGCTGCCCTT
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GTCCTGCAGGCTGTAATGCAGTTAATCAGAGTGCCATTTTTTTTTTTGTCAAATGAATTTAATTA
TTGGAATGCACAATTTTTTAATATGCAATAAAAAAGTTTAAAAACTTA

SEQ ID NO: 1097 NGTACCACCATTTGNACCTTAACGAAGAANAANATCTTCAAGTNGACCOCTAN
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TATATGNTCCCTNNCCGGCGCGCGGNTAAGGNCGAATCCCNCTCNCCTTGGCGNCCGGANTTA
GGGGANTCCGAACCTTGGGCCCAANTTGGNGTAATNTGGCTNAANCTGGGTTCCNNGGAAAT
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NTG

SEQ ID NO: 1098 GGTACGCGGGATGGACTCTGCCACTGCCCGGACAAGATCAGAAAGCTGTAT
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NTCCATCAANTAATAGNTTCTNNCCNGGNCNGGNTNGTTTNAANGGATAAATTTANNTCTCC
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SEQ ID NO: 1099 ACTTGTNCCTAGTTTTCAAGGTATGGCTGTTCTATAGATGCANTGATTGTC
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SEQ ID NO: 1100 ACTTTTTTTTTTTTTTTTTTTTTTTTGGCTNNTNTTTTTTTTTTTTTTGA
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TGNAAAACATTAATTTCTTAAAAAANGNTGCCACATGTCCCTNTAANATGCCCAAN
GCTGGTACAAATTTCCACCAANATNGGTCCTAACAGTTNAGGNAAACTAANAATGAANGGNTT
TGCAACCAATC

SEQ ID NO: 1101 GTTCNCGGGGAGAANCCTGGACCGCATNCTAGCCGNCGACTCNCACAAGGCA
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CCANACCTCTTCAGAGGTTGGGTTGACCAACNCATTGGGACTCACACATATGAANAATCTCTAT
ATNNANTTCNAGACANGNAACNAACCTGGATGATTATTCATCATTGNATGANNCTCTANACA
GNTNAANTTTANANAAAGAGNNTGCTGATAAAAAATTAATTCAGANAATTGGCNATNCNT
GNAGGGGCTTCTCAATACCTTGGNTNATGAANACNAATGNNCNAACACCTTNTTCNANGGC
CANNTTNTCCCTGGANTNATNTTGTGGACCTCCNNGNNTGTTANTAGCCCGTTTNNANTTG
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SEQ ID NO: 1102 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCCTTAATGGGGG
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SEQ ID NO: 1103 ACACTGAAACCAAAATTTCTAAACTGTGTTTTCTTAAAAATAGTTGTGTA
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SEQ ID NO: 1104 ACTGTTTATTAACCAACCAGCTTAGAAAAATAATCATGGTAGACACCTTAGT
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ATTTCAATNNTNATANCNANCG

SEQ ID NO: 1105 ACTTTTTTTTTTTTTTTTTTTTTTCTCAGCTAAGCCCATACAGAAGAAC
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CTGCCATCCCANTGTCACTGGGTCTGGTCCCTATTATTCATAACAATTGCAATGCTTGTGTTTCC
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SEQ ID NO: 1106 ACTAAATGGTATCCTTAGATTAATAATTTTGTGCTTGATAACAGCTGNTTTTC
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CATACTGNTAATATTTTATTGAAATTTATTTAGAGCGGAGAACTTAAGCTAAAAGCTGTTATA
CAGAATTGAAAGCCTTCGTATCTGGACCTTCCAACCATTTTTCTTATGGCTGTTNGAAAGTATN
NAAGCTAAATNGNTTAAATACCACTTTCCTTTGTACCTTTGGCCGCGAACACGC

SEQ ID NO: 1107 ACTTCGTGTGCTCCGACCCATGGTGACGATGACACACCCTGGTGGCATGCC
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CTGAACCATGACTTGGAGCGGGCAGAGTAGGCTGTGGCTGTGGACITTCAGCACAACCATCAACAT
TGCTGTTCAAAGAAATACAGTTTACGTCCATTCCAAGTTGTAAATGCTAGTCTTTTTTTTTTTTT
TCCAATAAAAGACCATTAACTNAAAAAATAAATNAAAAAAGTACCTNGGCGTNACCAC
GC

SEQ ID NO: 1108 ACCAGTAAGGCTGGATCTTACAGAGAAAGACTATGAAATACTTTTCAAATCT
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TTCCGTGAAGAAATTTACAATGAATGAAAANGTTTAAAGAAAGTTTAAATNGTCTTACTTTCCA
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SEQ ID NO: 1109 ACGCGGGGATGCCAAGGTATGAAGGATGCAAGAGCGAAGAGGTANTAGA
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GACACATTTGGCCGCTGTGATTGTTGCCTACAAGAAAAATCTGGTANAACAGCACATTCAGGAC
ATTGTGGTCCACTCACGTTCAACAAGGTGCTCATGCTGCAGGANCCCTGCTGGTGGTGGCGCCTT
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SEQ ID NO: 4323 ACTCTCTGCAGATGGTCCAAAATTGTAATGGAGTCTGTATTAGAAGAAAAATA
AGGGTAAAAATCAGGCTGAACCTGCATGTATATGGCTCCACTGTGGCTTGTGACACTTTTAAAAATCAT
CCGTATGTCAGTGTATCTGGATACACGAGGAAAAGGAAAGAGTCTCAGAGTGGAACAAAGAGTG
GGAAGAGGTGATCTGTAATGTNACAAAATTGTGCTATTACTCCAAGGTCCAACCTTTCCAGTGCAAT
ACATGG

SEQ ID NO: 4324 ACCAGGTGGGGAGAAGGTAGCAAATCTCAGTGCCAATTTGAGGGGAAGCC
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CAGTCACCTCTGCCACATGGCAGAAAGCCAGGTGGCAGTGTGGTGGTGGGGAAACAAAACA
CACAGTCTCTGGCAAGCCCCACCGGGAAAGGAGGGCTCA

SEQ ID NO: 4325 ACTATCCCTGTAAGTCCAAAGAGCTCAGGAGCCAGGCTAGTGATCACACCAG
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CTCTGACTTATAAAGCGAGGTGTAATAAATTACAAGTTCATGACTGAAAAAATGCTTTAGGGGG
AAAATCAGTCATATCTTAAACACCAACAAGCAATTTCCCAACCAACGAATGTAGT

SEQ ID NO: 4326 ACAGAGTCTTTTGCTTCTCCACCCCTAGGGGGAAAAACTGCTTTGTGCTTT
GGGAAGTTGTCTCTGAAACCCGGGGACAGAGGACGAGGACAGACTAGGAGGGAGCCGGGAGGA
TGGGCTGCAGCTGTGGAGGAGGGTTTCAGAGGAGAGAGGTCCGAGAGCANAGGCTGAGAAGCC
AGAGGCAGGTGGAGAGAGGGTGGAAAGTGAGCANCGGGCTGGGCTGGAGCCGCACACNCTCTCC
TNCCATGTTAAATAGCACCTTTAGAAAAATTACAAGTCCCCATCCA

SEQ ID NO: 4327 ACATAAGCATAATCAGTTATGGACAGCTTCTTGTATAAATTGCTATTTCAGCAA
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TCTGAAAATATGGGCACATTTTAAAAACATATTAAGACAGTTCTGTAAACATAATAGTCCACAGT
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GGGGANGT

SEQ ID NO: 4328 ACTGGCACAGCTCATCTGGAGCCGAGCCTTAGGCTTCCCTCTAGAAAGGCC
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CTTTAAAGACTTAAAGATTAAATTATCTGAGGCACTGATAATATGTTTGAGGTTAAAAATATAAAT
TAAGACTTTAAAAAGATGAAAAATGGTCCCTTCTTCTAATCANCTNCCTTCCCTGCCTGGTATGA
GTTGGCCCATCATACNCAATTGGTCCTGGANGATGAC

SEQ ID NO: 4329 ACGCGGGGAAAGGAGAGACAATTATGTTCTGAGGTCTCAGCCTTGGATCAG
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AACCTCAGGTCACTCAGCCTACAGTTGGGATGAATTTCAAAACGCCTCGGGGACCTGTTGAATT
TTTTCTGTAGTGCTGATTATTTTCAATAAATCTGGGACAACANATANAAAAAAT

SEQ ID NO: 4330 ACATCTTTAGAAACATCACTTTTAGCTCTGTGATCAGTCTTTGAACAATCATC
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SEQ ID NO: 4331 ACGCGGGGCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGGTGTCGTGAAA
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CTTGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAATTTGA
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SEQ ID NO: 4332 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAACACANTCTTGCTCTGTTG
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ATTATCCTGCCTCAGCCTTCCGAGTAGCTGGGACTACAGGCGCCCGCCACCACGCTGGCTAATTG
TTNGTATTTTNANTAAAAACGGGGTTTACCCGTGTTANCCAGGATGGTCTCAATCTCCTGACCTG
GTGATCTGCCCTCTCGGCCACCCAAAGTGTGGGATTACAGGNGTGAGCCACTGTACTT

SEQ ID NO: 4333 ACGCGGGGGATGAGGTTTTNAAGATTATGCCATTNCANAANCAGACCCNTGC
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SEQ ID NO: 4334 ACTTGGGTCGCTGTCTACTGCTCCTTCATCAGCTTGCCAACTCTCGGAGCTC
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GCAGAAATCCTCAGCCCATGACGCCCATGGTGATATCAGCCTAGAAAGGGTCACATTTTGGACCCT
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SEQ ID NO: 4335 ACTGCTACTTGAATAACTCAGTTAACGCTGTTTTGAAGCTTACATGGACAAAT
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SEQ ID NO: 4336 ACAGAGGGTGCCAGCAGGGTCTTCTACAGTGGCTGTTGAAGAGGCTGAAGG
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SEQ ID NO: 4337 ACTACCAGAGCGAGGAGCAGGCAGAGGAGGAGCTCCTGGACATGGCGGTGC
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SEQ ID NO: 4338 ACTGAACTGGAAGGAAGAGGAAAAAAGAAATATTACGATGCTAAAACTGA
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SEQ ID NO: 4339 ACTTGCAATGATAGGACAACCTCAGTTAGAAAAAGTATAGTGAATGGATGGAATCT
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SEQ ID NO: 4347 ACGCGGGCGCTCCTAATTTCAATATTGTTGCGTTTCAGGGAATAGGGAAGCC
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SEQ ID NO: 4348 ACCAGAAGACCTTAGAAAAAGGAGGAAAGGAGGAGAGGCAGATAATTTGGA
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SEQ ID NO: 4350 ACCAAGTAAAAATGCAGTCATTTTGGATGAAAAATGTATAACATGGTCACAT
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SEQ ID NO: 4357 ACTGAGGATACTTGCAAAGGTCAACTACGGGACACAAAAACGATTGTTA
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SEQ ID NO: 4361 ACTACCAGATAGAAATTCTGAAATTGGAATTGGAGGCCAAAGCCTTAATCT
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SEQ ID NO: 4362 ACGCGGATTGTTGCAAGATGGCCGCGCCAGTGATGGATTCAAGCCTCGTG
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SEQ ID NO: 4363 ACCCTTTATGGCTCTTCCAGGTTACATGAGAACTGGTGATCTCGGTGGGGT
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SEQ ID NO: 4364 ACGCGGGGAAACGACAGGGTAAAGGAGGTCTCACTGAGCACCGTCCCAGCA
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SEQ ID NO: 4365 ACGTCTACTGTAAAACCATCCGAGGCACAAGCAGAGACAGATGTAGACCTT
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SEQ ID NO: 4366 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGCATTTACAAATAGTTTATAAGANAAT
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SEQ ID NO: 4367 ACAGTAGTCTGACGTATTTCCCTTCTGTCCCTAGTAAGCCCAGTTGCTGTA
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SEQ ID NO: 4368 AAAAAAAAAAAAAAAAAAGCCTCAGCATTTTATCATTTCCATGGAAGGAGAAT
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SEQ ID NO: 4371 ACATCTCTGGCACAGATGCTATTGGTCCTTAATGTCCTGTGATTTTAGGAAAT
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ANT

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SEQ ID NO: 4377 ACCACATCCTGCTATGACTCCCGGGCCTGGGTATCCAGGTCCCATTGAGTGG
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SEQ ID NO: 4378 ACACCTTGAGACGCAGGAAGCAGCTGAAAGAGCTATTGAAAAATGAATGG
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SEQ ID NO: 4379 ACAGTTTAAACAACAGCTGAAAGAACTAAAGAAGCAATGTGGTCTTCAAGCT
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SEQ ID NO: 4380 ACTACCAGATAGAAATCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCT
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SEQ ID NO: 4381 ACCATATAATCCAACATCATGGTAAGGCCAGAAATCTTCTAACCTACCAGA
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SEQ ID NO: 4382 ACTGGGAGTCAGAACGCTCTGGGTTCTAGTCTTGACTGCCATTAACCTAGCGAG
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SEQ ID NO: 4383 ACGCGGGGCTGCTCCGCTTGAGGAGAAGCGCCAAGTGCGCATGGGGACGCT
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SEQ ID NO: 4384 ACTAGGTGCTGCAATGCAAAAGGGTTATGACAAAACTGTCTGTAATGTAGGA
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SEQ ID NO: 4385 ACACAAGCTTTGAGGAAGTGCNAAGGACTGACCTCTAGGCCAGAACAAAGAT
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SEQ ID NO: 4389 CGTACCTCTATAATTTGGGTGACCANTATGCACTGAAGATGAGGTTTGTGGAC
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SEQ ID NO: 4401 ACGCGGGGAGGATAGGCCGAAGCTNGACCCGGAGGAGATGAAACGGAAGGT
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CAAGCACAGGGAGATGCGTGGGCTGACATCTGCAGGCCGAAAGACCCGTGGNCTTGGAAAGGGC
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SEQ ID NO: 4411 ACCAATCCTTTTGACGCTATTCCATTAAGATAGAGAAAGAGAATCCTCCCTAA
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CTCAGCNAAATTGGCAGACAAGGAGACATACCTAANTGCTATNCAAAAGTCATCTATTGACAAACC
C

SEQ ID NO: 4412 ACTGTGTGCAGCAGCTCAAGGAATTTGATGGGAAGAGCCTGGTCTCAGTTAC
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CACCTGGAGATCAACCTGACCACCCCATTTGTGGAGACGCTGCGGCAGAAAGGCTGAGGCCGACA
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SEQ ID NO: 4413 ACCGCTCCAGGCCAGCTGTGTCTNNANATCTGAGCCTTGACAGCAGCGGTGCC
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SEQ ID NO: 4414 GGTACTCAACACCAACATCGATGGGCGGCGGAAAAATAGCCTTTGCCATCACT
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SEQ ID NO: 4415 GGTACTCTTGATGAAAGACCGTGAAACCAACAAATCAAGAGGATTGCTTNT
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SEQ ID NO: 4416 GCGTGGTGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTGGAGCAGAA
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 TGNNGACGGCACAGGTTCATNANGGACCGCTCCNTNTCNNTGGGGAACNAATCNGGCCATCCCN
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SEQ ID NO: 4417 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNNAAAAATNAAATTTT
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SEQ ID NO: 4418 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTNGCTTTTTTTTTTTTTTTTTTT
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SEQ ID NO: 4419 GCGTGGNCNCGGCCGACGTNCGCNGGTAAGATAGTTAANCGTGCNTAANN
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 ATNGGAAANTTGGTATAATGAATGAAACATTTTGNATATAAGATTTCATATNNACTTCTTATACNT
 TTGATAAAGNNAGGCTTGGTTGTGGTTAATCTGGNTTATTTTGNCCACNNGTTAANTNTNTCNT
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 AAACNTNTCCTATNGANTTNNCTTCTCNTANAGTTTNTAGNGNNNTNTNNCTNGTTAAAAATGNT
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SEQ ID NO: 4420 ACTTTTTTTTTTTTTTTTTTTTTTTTATTTTTTTTTTTTTTTTTTTTTTTTTT
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 CCCNGGNGNAAANTNGTTTCCCTCACAATTTCCACAANATANCAACCCGNANCTTNAAGGG
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SEQ ID NO: 4421 NCCAGCGGCCGNCNCGNCNGGCNCTTTTTTTTTTTTTTTTTTTGGTTGGNN
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 CTNGTCTTATATNGCTTNCATANANGATGGAACNTGCCCTTCCATTTAGCCTTTTACTNGCTTC
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CCTACCCTTAAAGAAGGNACCTTTCCTTTTAAANAA

SEQ ID NO: 4422 GGTACTNCTNCTNCTNCTTTTNTNTTTTGNNTTTTNNAACTTNNCACTTT
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SEQ ID NO: 4423 ACAGGAGAGAATCAATAAGGAGATAGTTAATTCACCACTACAGCTTTGTGCA
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SEQ ID NO: 4424 ACTTTTTTTTTTTTTTTTTTTTTTTTATTAATTTGGGNCTTACAAATGA
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SEQ ID NO: 4425 ACGCGGGGTATTGAACTGGGGGTGGTCTGGCCTACTGGGCTGACATTAAC
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GGGGGAANANCNTANNCCNTNANANTINTNCNTCTANNAAAANCATTNTCTGCNTNTGCCAAAAA
TTAANCATAA

SEQ ID NO: 4426 ACACAAGCTTTGAGGAAGTGCAAAGGACTGACCTCTAGGCCAGAACAAAGAT
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SEQ ID NO: 4427 ACTTCCAGCCACTAATTGAGATGTAGTTATGAAAGATTAGAATTGCCTTAA
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SEQ ID NO: 4428 ACAAGTCATTTTAGGAATAATAGAAATAGGAATGTGGGAAGGCCAAGTGGT
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SEQ ID NO: 4429 ACTCTGGATGCCAGCACCAAGATCTATGCTGTGCGCGTGGATGCCGNCATG
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SEQ ID NO: 4430 CGTGCCCNACGATTNCNCGCTTTGAAAGTGAAACTATGGNTACCAAAACAN
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SEQ ID NO: 4431 ACTTTTTTTTTTTTTTTTTTTTGTNTNTAACCCTGAANCANTTGATTCCAGT
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SEQ ID NO: 4432 GNCCTGNCGCCCTTTNNNGTCTCNCAACCAANCCCATNGNNGCNCNGTAACTCT
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CACTTTACAGGATGATTAGGTGGACCTGCAATGAANANAATACATTTCAAAGATGGGTTCTGA
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SEQ ID NO: 4433 ACGCGGGGGCGTCTGTCTTGCCTGGTGTGCGGTGGTTAGTTTCTGCGACTTG
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AACC

SEQ ID NO: 4434 ACGCGGGGGCTGCGCGCCGCTAGGTGTCTGGGCGATCTATGGGCAAGAGCA
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SEQ ID NO: 4435 ACGCGGGGCGAGTCAGCGAGCCACGTGCTTGTGTTGACTGGACAACCTTCCT
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SEQ ID NO: 4436 ACCGCCGGGTTGAAAAAGAAACAAAGGAATACTTTGAGAGTTGGGGAGAAA
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SEQ ID NO: 4437 ACTTTTTTTTTTTTTTTTTTTTCAGNGNAAAATAACTTTTATTGAAACCCNACC
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SEQ ID NO: 4438 ACCCTNCAGANNATNGTGTNTTTTACNCCATTTTCTACAACCTCTGGATTGCTT
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SEQ ID NO: 4439 ACANGNGGAACAATCNGGNTTTTTTAATCAAAGAAGGNGGTGTTCAAGTTGCT
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SEQ ID NO: 4440 ACCATAGCCAAATCTGGGACAAGCGAGTGTTTAAACAAAATGACTGAAGCAC
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AAATATTACAGTTCATAAACTTTCCTATTTATGTATGGAGCACAAGACTGAAACTGGTTGAGGGA
CCCATGGAGGAANAANAACNCCCNNGAANAAGANAATTTTGTGATTAACTGCNNTNNNN
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SEQ ID NO: 4441 GGTACTGGATCCAGGTGAGGTGTGGGCTGNGNCCCGAAGGTGCTTGGCTCC
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GGNCATCTGGGGTAACCCCGCGTACCTNCCNCGGCGGNCGNTNAAANGGGCNAATTCACNC
NCTNGNNGGCGGTNANNANNGGNCCNANCTNGNCCNANCTTGGNNNAATNATGGNNTAANN

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SEQ ID NO: 4442 GGTACGCGGGGAGGAGATCGCCATTATCCCCAGCAAAAAGCTCCGCAACAA
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TCAAGCTGCAGGAGGAGAGAGAGAAAGGAGAGACAATTATGTTCTGAGGTCTCAGCCTTGGAT
CAGGAGATTATTGAAGTAGATCCTGACACTAAGGAAATGCTGAAGCTTTGGACTTCGGCAGTCT
GTCCAACCTTCAGGTCACTCAGCCTACAGTTGGGATGAATTTCAAACGCCTCGGGACCTGTTTG
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NNTTTNCCGGTNGGNCNTTCNAAAGGGGGGAATTNNNNCCCTCCCCGGNCCCTTTTAAAGGGG
TTTTTCCCNCTTNGGGGNNNNNTNTAAAAANCCNCTGNCNCAANTTTTGTNNCCNTNN

SEQ ID NO: 4443 ACCTATTAGTAGTCACCGCCTTTTCCCTTCTCTCCAGCCCCCTAACAACTA
ATCTACTTCTGTCTCTACGGATTGTCCTACTCTGGACATTTTATATAAATAGGTTAATACGATGCG
TCCTTTTATACAAAAATGTTTCATAGCAGCATTAATCATAAAAAGCCCCAAAGCGAAACACCTCAAGT
GTCCATCAACCGATGAATGGATAAAACAAAATGTAATATATCCACACAATAGAATCTTATTCGTCA
ATAAAAAAGGAATGAAGTACTTTTTTTTTTTTTTTTGGGATTTTTAGGTAGNGGGGTGTGAGCT
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SEQ ID NO: 4444 GGTACGAUTGNTAGTGATGAGTTTGCTAATACAATGCCNGTCAGGCCACCT
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ACCCTATGAAGCCAATTGATNTCATAGCTCAGACCAATTCCTATGTATCCAAATGGTCTTTTTTCC
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SEQ ID NO: 4445 ACNCGGGTGCAAGAGTCTCGCTCAGCNNNAAATANGNTNGCTTTCTTTAAT
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TGAATGGTTTTGTATTAAATTTGCTTTGAAATAGATTTTATTCTTGTGCACACAGCCAAGATTTCTT
CAATGGGNCGTGAGCTAGTTGAGGGNTAACCTTGTANGTTGCANAGTGCAATNGCTTGNTTGNNTG
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SEQ ID NO: 4446 ACAAATGTTTTTTATTCAAAAATACAAAATAAATTATCTGTAGGCATGGACA
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SEQ ID NO: 4447 ACTTTGGGAGAATCGTGGTGTCTGGATGGCCTGATCAATGTATTAATAATCA
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 TNCANAANAGGNGGGGNGCGGGGCCNNNAANATAGNNGNGNCCCAAGNGGGTCCAAAAAAA
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SEQ ID NO: 4448 ACCTACTGGTAGTTGGGTTCAAGGAAATGGGATTGACTTGGCCTTCAGGCTCC
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 ACCC

SEQ ID NO: 4449 ACGCGGTGCACACTTTGGGAAGCATCACCATGAAGGTGAGGGACAGAGCTC
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SEQ ID NO: 4450 GCGTNGNCCCGCCGTTTNTCTGGCNGAGCTGAGGCTCNAATTCNNNAGG
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 NCCCCATCTGTTNTGCCCTGGNTGCNTCANCCCTACCATCACTGGGCANGNCTANNGGGCCTCGTA
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SEQ ID NO: 4451 ACTTTTTTTTTTTTTTTTTTTTTTTTATTAGGCAAGTGCATGTTCTGTA
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SEQ ID NO: 4452 GGTACAATGCCTATCGCTTCTTAATCCAAACGTTCTGNGGCTCCAGANGGA
 GGAAGAAATAGAATTTCTCTACANTGAAACNCGGNTAGAGAAAGCCCCAACATTNCANACCGG
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 GTNATTCCTCTNTCAATTTANANAAANTTTCCGNNNTTNNAGCCATATANGGNAACNNTCN

GNGNNCGCNATANAAT

SEQ ID NO: 4453 ACNGCGGGGCTCACTGAGCACCGTCCCAGCATCCGGACACCACAGCGGNCCT
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SEQ ID NO: 4454 GCGTGGCCGCGGNCGATGTNCANCACAGGCTACATGTAGGCAAGCTAAAGCT
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CATCCTATAGGGAAATTNCTTTTGAAAAGGCNNATGAANATCTANTTATTTAATTCANAATGNGAC
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SEQ ID NO: 4455 ATNTNCCATGAAATATCCATGAACATACTTATANGTNAAGTATTATTTATTTG
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SEQ ID NO: 4456 ACGCGGGGAGGGCGGTGGCTCAGGCTCCTGGAAAGGACCGTCCACCCCTCC
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SEQ ID NO: 4457 GGTACTTNAATTG
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SEQ ID NO: 4458 GCGNGGGCNGGCCGANGNNCACNGGCTGCTNCCNNGTNTTATNNNNGT
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SEQ ID NO: 4459 GGTACTTTTTTTTTTTTTTTTTTTTTTTTATAGGGCCAGGTTTATCCCTCACAT
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SEQ ID NO: 4460 GGTANTTTNGGGAGCTACAGATAGTAAAGATGATGATGACATTGACCTCTTT
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SEQ ID NO: 4461 NCNAGCGGCCGCNCGNCGGGNACGCGGGGCTCTTCTGCNCTACATNATGG
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SEQ ID NO: 4462 GGTACTTGCATGTAGGACAACCTCAGTTAGAAAAGTATAGTGAATGGATGGAA
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SEQ ID NO: 4463 ACANAGTNTTTTCAACAACCTGAATTTTAAAGTTTCTTCTNCAATGTCTGCCCT
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SEQ ID NO: 4464 ACCACCCTGAGTTCCTGTCCAGGCCTATCAAGCCCTCCCCACCATACTTTGGC
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SEQ ID NO: 4465 GTACGCGGGGGATTTCNATGCGGGGAANANGTGGTTTTGACANAATGCCTC
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SEQ ID NO: 4466 ACNAGAAAAGGGTCCGAGCACAAGCCAAGAAGTTTGGCCCTCATAAGCAG
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SEQ ID NO: 4467 GGTACTTTTTTTTTTTTTTTTTTTTAAATCATCACANGCNCGTGCACTTTATT
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TCTTGTCCNCTAGACTTCACTNGTNTTANGCGAATTGCTTTTGAAAGCCCCATNANANTCNTCCNC
TTATATNTAAANANNNNGNTTGNACAATGGGCTCNNTACNTNANTNGTNTGGTCCCGGNATGGT
NTNTCCTNTGGATNTTTGATCACCTCTCTCAACCNTNNNAAAGAAATGGTNTNTNGGGGNNCCTCC
ANGANAACNCTNATTTTNTNCTGGNNNTNTATTGGCNTTGGGCANGGAAATTN

SEQ ID NO: 4468 ANATTTGGCCCTGGTTGATTCTCTCTGAATAGTTTCCATCCCNATGAAGAG
GACCTCTCAAGTATTAGTGCACACCACTTCCAGAGGAGTTTGAATTANAAGGATTTTGGCATTTG
AGANCTTCTTTCAAGGAACCTGGATTNTNNAAAGGTCACCANGGTATTACAGGGGACAAAANAAGG
TNAGCNCGACGAATACNACNGCAANGCTNGATCTNTATNGGNAAATGGATTGTTGATAATCATC
CTAGGCTNATTCAGTGTGAAANTGANGNAGGGAAATTTGTTGGGTATCACGANANATCCNGAATT
AATACTGGAAGACNCCAGNGTAGCNAAGAGAACCGATTCTACAAGAACATCTGANATAGAGT
CGCTTGTNTAANTGGGANTCCANGGTNTAAAANCAGGGTGNNTNTACAAANCNCGAAAAANNA
NNATATNTTTTNNCNCNNGANANGAATNCANTTNGGNCCTTNCANANGATNTTTTGGGNACCAN
GGNTTGGNCCTTTCCTAAAATCTTGGNGGCCTTNAATATTAAACTTNAAGGGGANTTTNGGNGGTT
TANTNTCTTT

SEQ ID NO: 4469 GGTACCTGCAGGCCTCTACACCTACCTCTCTCTGGGCTTCTATTTCGACCGC
GATGATGTGGCTCTGGAAGGCGTGAGCCACTTCTTCGNGAACTGGCCGAGGAGAGCGCGAGGG
CTACGAGCGTCTCNTGAAGATGCAAAACAGCGTGGCGGGCCGCTCTCTTCCAGGACATCANAG
AANCCAGCTGAAGATGAGTGGGGTAAAACCNAGACGCCATGAAAGCTGCNATGGCCCTGNANA
NAAAGNTGANCCAGNCCCTTTTGGAACTTAATGCCCTGGGNGNNTGTNGCGCNCCTGGCNCNCAAT
NTTGTANANTNTCTGGANNNTTANCTTCTNTATNANGTGGGAANTTGANACTGTATNAGNAN
NATTGTTNGATNANTNTNANCTAANNNTNTATNTGTTGNGGGTGCNCANGTTGCTTTGGCTNGTC
TGAAATNTTCTNTAGATNGGATAANCANTTTCAGCTATGTATTTAAGATTATCTNCNNNAATTCT
NNNGNTGACCNNTGGGATANGGCTNTCTTCTTATTTAAAAATNGGTTATGTATATCNTNTATNTCTT

TNTNTCATGAGGNTTGCTNTTTNAATNNTCANACANCTCNCCTTG

SEQ ID NO: 4470 GTACGAGATGGCACCCCTCCAGAGCCCNCTTCTATGGAGATNAGATGAATCTT
TTNTCNCTGTGCCATAAGATCAANCNGTGTGACTACCCACCACTCCCNNGNGAGCACTACTCCGA
NAAGTNACCANAACNGTCAGCATGTNCAATNTGCCNTGACCCCACCANATAOCTGANATCENNAT
ACGTGCACCAGGTGGCCAAGCAGATNCACATATNGATGTCCAGCACCTGAGCATGNATGCACCNG
TCCTATCAAANNCANGCACCCTTTGCCTTACTTGAGTCGTCTCTNTTCAAGTGGCCACCTGGTA
GCCTANACAGATAANACCCAGGGNTCAGNANGTTCCCCAAANGCTGCNCAACCTTACANCANAT
GCTTNAGGCATANNNACTGANGGAGGGGCGCTGGCCACAATGTGNACTGATGGNTAGATTNCA
AANTTCCTTTNTTTATACTGTGTGNAGCANNTCTAAANTTGGTCAANTAANGCAAGGGGNGGTCA
ACNCAGC

Figure 3.

SEQ ID NO: 4471

MASRSMRLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELEC
QSYGNGAHLASILSLKEASTIAEYISGYQRSQPTWIGLHDPQKRQQWQWIDGAMYLIRS
WSGKSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP

SEQ ID NO: 4473

MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYE
EALYKSKTSNKPLMIHHLDECPSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHL
PDGQYVPRIMFVPSLTVRADITGRYSNRLYAYEPADTALLDNMCKALKLLKTEL

SEQ ID NO: 4475

MRAWIFLLCLAGRALAAPQQEALPDETEVVEETVAEVTEVSVGANPVQVEVGEFDDG
AEETEEVVVAENPCQNHCKHGKVCELDENNTPMCVCQDPTSCPAIGEFKVCSDN
KTFDSSCHFFATKCTLEGTKKGKHLHDYIGPCKYIPPCLDSELTEFPLMRDWLKNVL
VTLYERDEDNNLLTEKQKL RVKKIHENEKRL EAGDHPVELLARDFEKNYNMYIFPVHW
QFGQLDQHPIDGYLSHTELA PLRAPLIPMEHCTTRFFETCDLDNDKYIALDEWAGCFGIK
QKDIDKDLVI

SEQ ID NO: 4477

MEKLVQLKESFGGSSEIVDQLEVEIRNMTLLVEKLETLDKNNVLAIIRREIVALKTKLKE
CEASKDQNTPVVHPPTPGSCGHGGVNVISKPSVVQLNWRGFSYLYGAWGRDYSPQHP
NKGLYWVAPLNTDGRLLLEYILYNTLDDLLYNARELRITYGQGSGTAVYNNNMVYN
MYNTGNIRVNLTTNTIAVTQTLPNAAYNRRFSYANVAWQAY

SEQ ID NO: 4479

MTERRVPFSLLRGPSWDPF RDWYPHSRLFDQAFGLPRLPEEWSQWLGGSSWP GYVRPL
PPAAIESPAVAAPAYSRA LSRQLSSGVSEIRHTADRWVSLDVNHFAPDELTVKTKDG
VEITGKHEERQDEHGYISRCFTRKYTLPPGVDPQTQVSSSLSP EGTLTVEAPMPK LATQSN
EITIPVTFESRAQLGGPEAAKSDETAAK

SEQ ID NO: 4481

MSSTSPNLQKAIDLASKAAQEDKAGNYEALQLYQH AVQYFLHVVKYEAQGD KAKQS
IRAKCTEYLDRAEKLKEYLKNKEKKAQKPVKEGQPSADEKGNDSDGEGESDDPEK RK
LQNQLQGAVIDRPNVKWSDVAGLEGAKEALKEAVILPIKFPHLFTGKRTPWRGILLFGP
PGTGKSYLAKA VATEANNSTFFSISSSDLVSKWLGESEKLVKNLFQLARENKPSIIFIDEID
SLCGSRSENESEAARRIKTEFLVQM QGVGVNDNGILVLGATNIPWVLDSAIRRRFEKRIY
IPLPEPHARAAMFKLHLGTTQNSLTEADFRELGRKTDGYSGADIGIIVRDALMQPVRKV
QSATHFKKVRGPSRADPNHLVDDLLTPCSPGDPGAIEMTWMDVPGDKLLEPVVMSMDM
LRSLSNTKPTVNEHDLLKLLKFTEDFGQEG

SEQ ID NO: 4483

MHKEEHEVAVLGAPPSTILPRSTVINIHSETSVDPDHVVWSLFNTLFLNWCCLGFIAFAYS
VKSRDRKMVG DVTGAQAYASTAKCLNIWALILGILMTIGFILLVFGSVTVYHIMLQIIQ
EKRGY

SEQ ID NO: 4485

MRTIALAAILLVALQAQAESLQERADEATTQKQSGEDNQDLAISFAGNGLSALRTSGSQ
ARATCYCRTGRCATRESLSGVCEISGRLYRLCCR

SEQ ID NO: 4487

MPAPEQASLVEEGQPQTRQEAASTGPGMEPETTATTLASVKEQELQFQRLTRELEVER
QIVASQLERCRLGAESPSIASTSSTEKSFPWRSTDVPNTGVSKPRVSDAVQPNNYLIRTEP
EQGTLYSPEQTSLHESEGLGNSRSSTQMNSYSDSGYQEAGSFHNSQNVSKADNRQQHS
FIGSTNNHVVNRNSRAEGQTLVQPSVANRAMRRVSSVPSRAQSPSYVISTGVSPSRGSLRT
SLGSGFGSPSVTDPRPLNPSAYSSTTLPAARAASPYSQRPASPTAIRRIGSVTSRQTSNPNG
PTPQYQTTARVGSPLTLTDAQTRVASPSQGVGSSSPKRSGMTAVPQHLGPSLQRTVHD
MEQFGQQQYDIYERMVPPRPSLTGLRSSYASQHSQGLQDLRSAVSPDLHITPIYEGRTY
YSPVYRSPNHGTVELQGSQTALYRTGVSGIGNLQRTSSQRSTLTQYRNNYALNTTATYA
EPYRPIQYRVQECNYNRLQHAVPADDGTTSPSIDSIQKDPREFAWRDPPELPEVIHMLEH
QFPSVQANAAAYLQHLGFDNKVKMEVCRLGGIKHLVDLLDHRVLEVQKNACGALRN
LVFGKSTDENKIAMKNVGGIPALLRLLRKSIDAEVRELVTGVLWNLSSCDAVKMTIIRD
ALSTLTNTVIVPHSGWNNSSFDDHKKIKFQTSVLNRNTTGCLRNLTSAGBEEKQMRSC
EGLVDSLLYVIHTCVNTSDYDSKTVENCVCTLRNLSYRLELEVPQARLLGLNELDDLGLG
KESPSKDSEPCWGKKKKKKKRTQEDQWDGVGPIGLSKSPKGVEMLWHPVVKPYL
TLAESSNPATLEGSAGSLQNLASNWKFAAYIRGGPRPKRGLPILVELLRMDNDRVVS
SGATALRNMALDVRNKELIGKYAMRDLVNRLPGNGGPSVLSDETMAAICCALHEVTSK
NMENAKALADSGGIEKLVNITKGRGDRSSLKVVKAAAQVLNTLWQYRDLRSIYKKDG
WNQNHFITPVSTLERDRFKSHPSLSTTNQQMSPHQS SVGSTSSSPALLGIRDPRSEYDRTQP
PMQYYSNQGDATHKGLYPGSSKPSPIYISSYSPAREQNRRLLQHQQLYYSQDDSNRKNF
DAYRLYLQSPHSYEDPYFDDR VHFPASTDYSTQYGLKSTTNYVDFYSTKRPSYRAEQYP
GSPDSWVYDQDAQQRNSFFLTLFRLR

SEQ ID NO: 4489

MSGIALSRLAQERKAWRKDHFPFGFVAVPTKNPDGTMNLMNWECAIPGKKGTPWEGGL
FKLRMLFKDDYPSSPKCKFEPPLFHPNVYPSGTVCLSILEEDKDWRAITIKQILLGIQEL
LNEPNIQDPAQAEAYTIYCQNRVEYEKRVRAQAKKFAPS

SEQ ID NO: 4491

MCDRAVIKNADMSEEMQQDSVECATQALEKYNIEKDIAAHIKKEFDKKYNPTWHCIV
GRNFGSYVTHETKHFIYFYLGQVAILLFKSG

SEQ ID NO: 4493

MENFQKVEKIGEGTYGVVYKARNKLTGEVVALKKIRXDTETEGVPSTAIREISLLKELN
HPNIVKLLDVIHTENKLYLVFEFLHQDLKKFMDASALTGIPLPLIKSYLFQLLQGLAFCHS
HRVLHRDLKPQNLLINTEGAIKLADFLARAFGVVVRTYTHEVVTLWYRAPEILLGCKY
YSTAVDIWSLGCIFAEMVTRRALFPGDSEIDQLFRIFRTLGTPEVVWPGVTSMPDYKPS
FPKWARQDFSKVVPPLDEDGRSLLSQMLHYDPNKRISAKAALAHPPFQDVTKPVPHRLR

Figure 2.

SEQ ID NO: 4472

AAGATATAAAAGCTCCAGAAACGTTGACTGGGACCACTGGAGACACTGAAGAAGGC
AGGGGCCCTTAGAGTCTTGGTTGCCAAACAGATTTGCA'GATCAAGGAGAACCCAGG
AGTTTCAAAGAAGCGCTAGTAAGGTCTCTGAGATCCTT'GCACTAGCTACATCCTCAG
GGTAGGAGGAAGATGGCTTCCAGAAGCATGCGGCTGCTCCTATTGCTGAGCTGCCT
GGCCAAAACAGGAGTCTGGGTGATATCATCATGAGACCCAGCTGTGCTCCTGGAT
GGTTTACCACAAGTCCAATTGCTATGGTTACTTCAGGAAGCTGAGGAAGTGGTCTG
ATGCCGAGCTCGAGTGTCAGTCTTACGGAAACGGAGCCACCTGGCATCTATCCTGA
GTTTAAAGGAAGCCAGCACCATAGCAGAGTACATAAGTGGCTATCAGAGAAGCCAG
CCGATATGGATTGGCTGACGACCCACAGAAGAGGCAGCAGTGGCAGTGGATTGA
TGGGGCCATGTATCTGTACAGATCCTGGTCTGGCAAGTCCATGGGTGGGAACAAGC
ACTGTGCTGAGATGAGCTCCATAAACAACCTTTTAACTTGGAGCAGCAACGAATGCA
ACAAGCGCCAACACTTCTGTGCAAGTACCGACCATAGAGCAAGAATCAAGATTCT
GCTAATCCTGTCACAGCCCCGTCCTCTTCTTTCTGCTAGCCTGGCTAAATCTGCTCA
TTATTCAGAGGGGAAACCTAGCAAACCTAAGAGTGATAAGGGCCCTACTACACTGG
CTTTTTTAGGCTTAGAGACAGAAACTTTAGCATTGGCCAGTAGTGCTTCTAGCTC
TAAATGTTTGCCCCGCCATCCCTTTCCACAGTATCCTTCTTCCCTCCTCCCCTGTCTCT
GGCTGTCTCGAGCAGTCTAGAAGAGTGCATCTCCAGCCTATGAAACAGCTGGGTCTT
TGGCCATAAGAAAGTAAAGATTTGAAGACAGAAGGAAGAAACTCAGGAGTAAGCTTC
TAGACCCCTTCAGCTTCTACACCCTTCTGCCCTCTCTCCATTGCCTGCACCCCAACCC
AGCCACTCAACTCCTGCTTGTTTTTCTTTGGCCATAGGAAGGTTTACCAGTAGAATC
CTTGCTAGGTTGATGTGGGCCATACATTCTTTAATAAACCATTTGTGTACATAAGAA
AAAAAAA

SEQ ID NO: 4474

ACCGCATCTAGCCGCCGACTCACACAAGGCAGGTGGGTGAGGAAATCCAGAGTTG
CCATGGAGAAAAATTCCAGTGTCAAGCATTCTTGCTCCTTGTGGCCCTCTCCTACACTCT
GGCCAGAGATACCACAGTCAAACCTGGAGCCAAAAAGGACACAAAGGACTCTCGA
CCCAAACTGCCCCAGACCCTCTCCAGAGGTGGGGTGACCAACTCATCTGGACTCAG
ACATATGAAGAAGCTCTATATAAATCCAAGACAAGCAACAAACCCCTTGATGATTAT
TCATCACTTGGATGAGTGCCACACAGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAA
TAAAGAAATCCAGAAATTGGCAGAGCAGTTTGTCTCCTCAATCTGGTTTATGAAAC
AACTGACAAACACCTTCTCCTGATGGCCAGTATGTCCCAGGATTATGTTTGTGTA
CCCATCTCTGACAGTTAGAGCCGATATCACTGGAAGATATTCAAATCGTCTCTATGC
TTACGAACCTGCAGATACAGCTCTGTTGCTTGACAACATGAAGAAAGCTCTCAAGTT
GCTGAAGACTGAATTGTAAAGAAAAAAATCTCCAAGCCCTTCTGTCTGTCAGGCCT
TGAGACTTGAAACCAGAAAGAGTGTGAGAAGACTGGCTAGTGTGGAAGCATAGTGA
ACACACTGATTAGGTTATGGTTAATGTTACAACAACATATTTTTAAGAAAAACATG
TTTTAGAAATTTGGTTTCAAGTGTACATGTGTGAAACAATATTGTATACTACCATA
GTGAGCCATGATTTTCTAAAAAAAATAAATGTTTTGGGGGTGTTCTGTTTTCTCC
AACTTGGTCTTTCACAGTGGTTCGTTTACCAAATAGGATTAAACACACACAAAAATGC
TCAAGGAAGGGACAAGACAAAACCAAACTAGTTCAAATGATGAAGACCAAGAC
CAAGTTATCATCTACCACACCACAGGTTCTCACTAGATGACTGTAAGTAGACACGA
GCTTAATCAACAGAAATATCAAGCCATGTGCTTTAGCATAAAAAAAACAAAAA
A

SEQ ID NO: 4476

CGGGAGAGCGCGCTCTGCCTGCCGCTGCCTGCCACTGAGGGTTCCCAGCACCC
ATGAGGGCCTGGATCTTCTTTCTCCTTTGCCTGGCCGGGAGGGCCTTGGCAGCCCT
CAGCAAGAAGCCCTGCCTGATGAGACAGAGGTGGTGGAAAGAACTGTGGCAGAGG
TGACTGAGGTATCTGTGGGAGCTAATCCTGTCCAGGTGGAAGTAGGAGAATTTGAT
GATGGTGCAGAGGAAACCGAAGAGGAGGTGGTGGCGGAAAAATCCCTGCCAGAACC
ACCACTGCAAAACACGGCAAGGTGTGCGAGCTGGATGAGAACAACACCCCATGTGC
GTGTGCCAGGACCCACCAGCTGCCAGCCCCATTGGCGAGTTTGAGAAGGTGTG
CAGCAATGACAACAAGACCTTCGACTCTTCTGCCACTTCTTGGCACAAGTGCAC
CCTGGAGGGCACCAGAAGGGGCCACAAGCTCCACCTGGACTACATCGGGCCTTGCA
AATACATCCCCCTTGCCTGGACTCTGAGCTGACCGAATTCCCCCTGCGCATGCGGG
ACTGGCTCAAGAACGTCCTGGTCACCTGTATGAGAGGGATGAGGACAACAACCTT
CTGACTGAGAAGCAGAAGCTGCGGGTGAAGAAGATCCATGAGAATGAGAAGCGCC
TGGAGGCAGGAGACCACCCCGTGGAGCTGCTGGCCCCGGGACTTCGAGAAGAACTAT
AACATGTACATCTTCCCTGTACACTGGCAGTTCGGCCAGCTGGACCAGCACCCCAT
GACGGGTACCTCTCCACACCGAGCTGGCTCCACTGCGTGCTCCCTCATCCCCATG
GAGCATTGCACCACCCGCTTTTTCGAGACCTGTGACCTGGACAATGACAAGTACATC
GCCCTGGATGAGTGGGCGGCTGCTTCGGCATCAAGCAGAAGGATATCGACAAGGA
TCTTGTGATCTAAATCCACTCCTTCCACAGTACCGGATTCTCTCTTTAACCCCTCCCT
TCGTGTTTTCCCCAATGTTTAAAAATGTTTGGATGGTTTGTGTTCTGCCTGGAGACAA
GGTGCTAACATAGATTTAAGTGAATACATTAACGGTGCTAAAAATGAAAAATTCTAA
CCCAAGACATGACATTCTTAGCTGTAACCTAACTATTAAGGCCTTTTCCACACGCAT
TAATAGTCCCATTCTTCTTGCATTTGTAGCTTTGCCCATGTGCTTATTGGCACATG
GGTGGACACGGATCTGCTGGGCTCTGCCTTAAACACACATTGCAGCTTCAACTTTTC
TCTTTAGTGTCTGTTTGAACCTAATACTTACCGAGTCAGACTTTGTGTTCAATTCAT
TTCAGGGTCTTGGCTGCCTGTGGGCTTCCCCAGGTGGCCTGGAGGTGGGCAAAGGG
AAGTAACAGACACACGATGTTGTCAAGGATGGTTTTGGGACTAGAGGCTCAGTGGT
GGGAGAGATCCCTGCAGAATCCACCAACCAGAACGTTGCTTGCCTGAGGCTGTAAC
TGAGAGAAAGATTCTGGGGCTGTCTTATGAAAATATAGACATTCTCACATAAGCCCA
GTTTCATCACCATTTCCTCCTTTACCTTTCAGTGCAGTTTCTTTTCACATTAGGCTGTTG
GTTCAAACCTTTTGGGAGCACGGACTGTCAGTTCTCTGGGAAGTGGTCAGCGCATCCT
GCAGGGCTTCTCCTCCTCTGTCTTTTGGAGAACCAGGGCTCTTCTCAGGGGCTCAG
GGACTGCCAGGCTGTTTCAGCCAGGAAGGCCAAAAATCAAGAGTGAGATGTAGAAAG
TTGTAATAATAGAAAAAGTGGAGTTGGTGAATCGGTTGTTCTTCTCCTCACATTGGAT
GATTGTCATAAGGTTTTTAGCATGTTCCCTCCTTTTCTTCACCCTCCCTTTGTTCTCT
ATTAATCAAGAGAACTTCAAAGTTAATGGGATGGTTCGGATCTCACAGGCTGAGAA
CTCGTTCACCTCCAAGCATTTTCATGAAAAAGCTGCTTCTTATTAATCATACAACTCT
CACCATGATGTGAAGAGTTTCACAAATCTTTCAAAAATAAAAAGTAATGACTTAGAA
ACTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 4478

CGGCCTCTCATTTCTCCTAGCCCTTCTGTTCTTCTTGGCCAAGCTGCAGGGGATTTG
GGGGATGTGGGACCTCCAATTTCCAGCCCCGGCTTCAGCTCTTCCCAGGTGTTGAC
TCCAGCTCCAGCTTCAGCTCCAGCTCCAGGTCCGGCTCCAGCTCCAGCCGCAGCTTA
GGCAGCGGAGGTTCTGTGTCCAGTTGTTTCCAATTTACCGGCTCCGTGGATGAC
CGTGGGACCTGCCAGTGCTCTGTTTCCCTGCCAGACACCACCTTCCCGTGGACAGA
GTGGAACGCTTGAATTCACAGCTCATGTTCTTCTCAGAAGTTTGAGAAAGAACTT
TCCAAAGTGAGGGAATATGTCCAATTAATTAGTTTGTATGAAAAGAACTGTTAAAC
CTAAGTGTCCGAATTGACATCATGGGAGAAGGATACATTTCTTACACTGAAGTGGAC
TTCGAGCTGATAAGGTAGAAGTGAAGGAGATGGAAAACTGGTCATACAGCTGAAG
GAGAGTTTTGGTGAAGCTCAGAAATTGTTGACCAGCTGGAGGTGGAGATAAGAAA

TATGACTCTCTTGGTAGAGAAGCTTGAGACACTAGACAAAAACAATGTCCTTGCCAT
TCGCCGAGAAATCGTGGCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAG
ATCAAAACACCCCTGTCGTCCACCCTCCTCCCACTCCAGGGAGCTGTGGTCATGGTG
GTGTGGTGAACATCAGCAAACCGTCTGTGGTTCAGCTCAACTGGAGAGGGTTTTCTT
ATCTATATGGTGCTTGGGGTAGGGATTACTCTCCCCAGCATCCAAACAAAGGACTGT
ATTGGGTGGCGCCATTGAATACAGATGGGAGACTGTTGGAGTATTATATACTGTACA
ACACACTGGATGATTGTCTATTGTATATAAATGCTCGAGAGTTGCGGATCACCTATG
GCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACATGTACAAC
ACCGGGAATATTGCCAGAGTTAACCTGACCACCAACACGATTGCTGTGACTCAAAT
CTCCCTAATGCTGCCTATAATAACCGCTTTTCATATGCTAATGTTGCTTGGCAAGCAT
ATTGACTTTGCTGTGGATGAGAATGGATTGTGGGTTATTTATTCAACTGAAGCCAGC
ACTGGTTAACATGGTGATTAGTAACTCAATGACACCACACTTCAGGTGCTAAACAC
TTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACGCCTTCATGGTATGTGGGGT
TCTGTATGCCACCCGTACTATGAACACCAGAACAGAAGAGATTTTTTACTATTATGA
CACAAACACAGGGAAAGAGGGCAAACTAGACATTGTAATGCATAAGATGCAGGAA
AAAGTGCAGAGCATTAACTATAACCCTTTTGACCAGAACTTTATGTCTATAACGAT
GGTTACCTTCTGAATTATGATCTTTCTGTCTTGCAAGCCCCAGTAAGCTGTTTAGG
AGTTAGGGTGAAAGAGAAAATGTTTGTGAAAAAATAGTCTTCTCCACTTACTTAGA
TATCTGCAGATATCTAAGTAAGTGGAAGACTATTTTTCAACAAACATTTCTCTT
TCACCCTAACTCCTAAACAGCTTACTGGGGCTTCTGCAAGACAGAAAGATCATAATT
CAGAAAGGTAACCATCGTTATAGACATAAAGTTTCTGGTCAAAAGGGTTATAGTTAAT
GCTCTGCACTTTTCTGCATCTTATGCATTACAATGTCTAGTTTGCCTCTTTCCCTG
TGTTTGTGTCTATAATAGTAAAAAATCTCTTCTGTTTGGCGTATAGGGATTCTTTGTAC
AGGAAATATTGCCCAATGACTAGTCCTCATCCATGTAGCACCCTAATTCTTCCATG
CCTGGAAGAAACCTGGGGACTTAGTTAGGTAGATTAATATCTGGAGCTCCTCGAGG
GACCAAATCTCCAACCTTTTTTCCCTCACTAGCACCTGGAATGATGCTTTGTATGT
GGCAGATAAGTAAATTTGGCATGCTTATATATTCTACATCTGTAAAGTGCTGAGTTT
TATGGAGAGAGGCCTTTTTATGCATTAAATGTACATGGCAAATAAATCCCAGAAGG
ATCTGTAGATGAGGCACCTGCTTTTTCTTTCTCTCATTGTCCACCTTACTAAAAAGTC
AGTAGAATCTTCTACCTCATAACTTCCTTCCAAAGGCAGCTCAGAAGATTAGAACCA
GACTTACTAACCAATTCCACCCCCACCAACCCCCCTTCTACTGCCTACTTTAAAAA
ATTAATAGTTTTCTATGGAACCTGATCTAAGATTAGAAAAATTAATTTTCTTTAATTC
ATTATGAACTTTTATTTACATGACTCTAAGACTATAAGAAAATCTGATGGCAGTGAC
AAAGTGCTAGCATTATTTATGTTATCTAATAAAGACCTTGGAGCATAATGTCAACTTAT
GAGTGTAATCAGTTGTTGCATGTAATTTTTGCCTTTGTTTAAAGCCTGGAACCTGTAAGA
AAATGAAAATTTAATTTTTTTTTCTAGGACGAGCTATAGAAAAGCTATTGAGAGTAT
CTAGTTAATCAGTGCAGTAGTTGGAACCTTGCTGGTGATGTGATGTGCTTCTGTG
CTTTTGAATGACTTTATCATCTAGTCTTTGTCTATTTTTCTTTGATGTTCAAGTCCTA
GTCTATAGGATTGGCAGTTTAAATGCTTTACTCCCCCTTTTAAAAATAAATGATTAAA
ATGTGCTTCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 4480

CTCAAAACACCGCCTGCTAAAAATACCCGACTGGAGGAGCATAAAAGCGCAGCCGAG
CCCAGCGCCCCGCACTTTTCTGAGCAGACGTCCAGAGCAGAGTCAGCCAGCATGAC
CGAGCGCCCGTCCCCTTCTCGCTCCTGCGGGGCCCCAGCTGGGACCCCTTCCGCGA
CTGGTACCCGCATAGCCGCCTCTTCGACCAGGCCTTCGGGCTGCCCCGGCTGCCGGA
GGAGTGGTGCAGTGGTTAGGCGGCAGCAGCTGGCCAGGCTACGTGCGCCCCCTGC
CCCCCGCCGCCATCGAGAGCCCCGCAGTGGCCGCGCCCGCTACAGCCGCGCGCTC
AGCCGGCAACTCAGCAGCGGGGTCTCGGAGATCCGGCACACTGCGGACCGCTGGCG
CGTGCCCTGGATGTCAACCACTTCGCCCCGACGAGCTGACGGTCAAGACCAAGG
ATGGCGTGGTGGAGATCACC GGCAAGCAGGAGCGGCAGGACGAGCATGGCTA
CATCTCCCGTGCTTCACGCGGAAATACACGCTGCCCGCGGTGTGGACCCACCCA

AGTTTCCTCCTCCCTGTCCCCTGAGGGGCACACTGACCGTGGAGGGCCCCCATGCCCAA
GCTAGCCACGCAGTCCAACGAGATCACCATCCCAGTCACCTTCGAGTCGCGGGCCC
AGCTTGGGGGGCCAGAAGCTGCAAAATCCGATGAGACTGCCGCCAAGTAAAGCCTT
AGCCTGGATGCCCACCCCTGCTGCCGCCACTGGCTGTGCCTCCCCGCCACCTGTGT
GTTCTTTTGATACATTTATCTTCTGTTTTCTCAAATAAAGTTCAAAGCAACCACCTG
TAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 4482

GGGGGAGGGTTCGGAGCTCTGGTGGAGAGAGTGTGTCTAAAACAAGTTCGGGAAGG
GAGGCTGCCCTTCGCGGTCCGAGAACCACCGGCTCCCCAGTTTGAGGGCTGTTACC
CCGTGCGCGCTTCGACGTTGCTGCTGTTGGCTCTCCTCGCCCCCTGTTCCCTTGGGAA
CCGCTGGGAACTCCGCCATGTATCCACTTCGCCCCAACCTCCAGAAAGCGATAGAT
CTGGCTAGCAAAGCAGCGCAAGAAGACAAGGCTGGGAACTACGAAGAAGCCCTTC
AGCTCTATCAGCATGCTGTGCAGTATTTTCTTCATGTGCTTAAATATGAAGCACAAG
GTGATAAAGCCAAGCAAAGTATCAGGGCAAAGTGTACAGAATATCTTGATAGAGCA
GAAAAACTAAAGGAGTACCTGAAAAATAAAGAGAAAAAAGCACAGAAGCCAGTGA
AAGAAGGACAGCCGAGTCCAGCAGATGAGAAGGGGAATGACAGTGATGGGGAAGG
AGAATCTGATGATCCTGAAAAAAGGAACTACAGAATCAACTTCAAGGTGCCATTG
TTATAGACCGACCAAATGTGAAATGGAGTGACGTTGCTGGACTTGAAGGAGCCAAA
GAAGCACTGAAAGAGGCTGTGATACTGCCTATTAATTTCTCTATCTTTTTACAGGC
AAGAGAACACCTTGGAGGGGAATCCTATTATTTGGGCCGCTGGAACAGGAAAAGTC
CTACTTAGCCAAAGCTGTAGCAACAGAAGCCAACAACCTCAACATTTTTTTCAATATC
TTCCTCTGATCTTGTCTTAAGTGGCTAGGTGAAAGTGAAGAACTGGTTAAGAATTT
ATTCCAATTGCCAGAGAGAACAAGCCCTCCATTATCTTCATTGATGAAATTGATTCT
TCTCTGTGTTCAAGAAGTGAAAAATGAAAGTGAAGCCGCACGTAGAAATTAAGACGG
AGTTCCTAGTGCAAATGCAAGGGGTTGGTGTAGACAATGATGGAATTTTGGTCTGG
GAGCTACAAATATACCCTGGGTTCTGGATTCTGCCATTAGGCGAAGATTTGAGAAAC
GAATTTATATTCCCTTGGCGGAACCCCATGCCCCGAGCAGCAATGTTTAAACTGCACC
TAGGGACCACTCAGAACAGTCTCACGGAAGCAGACTTTCGGGAACTTGGGAGGAAA
ACAGATGGTTATTCAGGGGCAGATATAGGTATCATTGTACGTGATGCCCTTATGCAG
CCTGTTAGGAAAGTACAGTCAGTACTCAATTTAAAAAGGTTTCGCGGACCTTCCCGA
GCTGATCCTAACCATCTTGTAGATGATCTGCTAACACCTTGCTCTCCAGGTGACCTT
GGTGCCATTGAAATGACGTGGATGGATGTCCCTGGAGATAAACTTTTGGAGCCAGTT
GTTTCCATGTGCGATATGTTGCGGTCACTATCTAACACAAAACCTACAGTCAATGAA
CATGACTTGTGAAATTAAGAAGTTTACAGAAGATTTTGGTCAAGAAGGCTAAGC
CAAAGACAAGGAAGATGCTTACCATATGTATTCTTTCTTTTCATAGATATTTTTGTCTA
TTTGGATCGCATTAAATTGTTTCCAGTAAACTCTTTTACCACAGGGAAATACACATC
TCACTTCAGAGTTCATTAGGTTTTATATTGTACTTTTCTCCATTACTTATTAATAC
TCCTATTAACAAAAGGTACAAAATAACAGGTTATGAGGAAATGAGCGATATATGAA
CGGCATAAAAAACAGAAATTACCCAGTAAAAAGGATGTCAGAAATTGACATACAAAT
ATTTACAATTTTTATGAATGGTGGTCTTTGCAAAGAGCATTTATATTTCTTTTTTTT
TACTAAAATGATATATGGGTTTATTTTATATTTTCAAAAAAATTGTTAAACATCATTC
TTATCAATGTAAATTTACGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 4484

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SEQ ID NO: 4486

ATATCCACTCCTGCTCTCCCTCCTGCAGGTGACCCCAGCCATGAGGACCATCGCCAT
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SEQ ID NO: 4488

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SEQ ID NO: 4490

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SEQ ID NO: 4492

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SEQ ID NO: 4494

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SEQ ID NO: 1110 GGTACTATTATACTAAAAGCTCCTACTGTGATGTGAAATGCTCATACTTTATA
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TGT

SEQ ID NO: 1111 GGTACTACAAGTTTAGTGGCTTCACGCAGAAAGTTGGCAGGAGCATGGGCTTC
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SEQ ID NO: 1112 CGAGGTACATGCTCTATCTGATGCTCGATGTGTGTTGACATGGCTGGAGAAA
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SEQ ID NO: 1114 NCTTTTAGTAACGACCAATCTAAGGAGCCTTGGAGGCTTGTGAAAAAGAGC
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SEQ ID NO: 1115 ACGCGGGAGAACTGCCGAGAAAGCGAGACCTTAGAAGGCAGCGCTTCCCGC
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[illegible]

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SEQ ID NO: 1131 GGTACTCAAAAATCTCCCTACTCAAAATCAGAAATCTGTTACTAGATGTGT
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SEQ ID NO: 1132 ACGCGGGATTGTNGGAGTCTGTGCACAGATTACAAGGACTTAATCTGGGT
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SEQ ID NO: 1133 ACCTAGCTCAGAACTGAGGGTTTTACTTTTTGGAAGAAGTCAGGAGTGGATG
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SEQ ID NO: 1134 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAGGATTTAA
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SEQ ID NO: 1135 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTCTTNGAANATGGTTATTTTAC
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SEQ ID NO: 1137 ACTTTTTTTTTTTTTTTTTTTTTTTTTTGGTTTTTTTTTTTTTTTTTTNGACT
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SEQ ID NO: 1138 GCGTGGTCGCGCCGAGGTACTAGTCTCTACTTGGGACAAGAAAAAGAATA
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SEQ ID NO: 1139 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAATCAAAAGCAGGGT
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SEQ ID NO: 1140 ACITTTTTTTTTTTTTTTTTTTTGANATGGAGTTTCGCTCTGTTGTCCAGGCT
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SEQ ID NO: 1141 ACCTGAGATCCTGGTGACACAACATAGTGATCTTCATGCGAAGTTTCAGTGAAG
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SEQ ID NO: 1142 GGTACTTTTTTTTTTTTTTTTTTTTTTTTNGAAATTAATACITTTAATTA
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SEQ ID NO: 1143 ACTTTTTTTTTTTTTTTTTTTTTTTTGGTTTTTTTTTTTTTTTTTTTNA
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SEQ ID NO: 1144 GGTACTCAGAACTGTGTAAAGTTAAACCAAAACCATGTTTTAAAGAAAA
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SEQ ID NO: 1145 ACTAAGCGGCCTTGGATACCTGGCCGCGGATGCTGGGCGGCGTCAGGTGAG
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N

SEQ ID NO: 1146 ACITTTTTTTTTTTTTTTTTTTTTTTTNGAGGCTTGNGITTTATTCAAGGCTT
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SEQ ID NO: 1147 ACACTGTTGGTGTTATATGGGGATGGGGTTCCTCGTAATTTTGTTATTATTTA
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SEQ ID NO: 1148 ACCATTGGGCCCTTTGCTTCATGCCAGGAAAACTTGTCCATACTAATGAAG
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SEQ ID NO: 1149 ACAAAAACTGTGACATCAAGAAGGCGAGGAGAAACAAAAGGCATTTCTAT
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SEQ ID NO: 1151 ACTACCACAGCCTTTAGGTGACATTGATTATAACTTGGTCACAAATTCAGTC
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SEQ ID NO: 1152 ACCAGTGAGAAGACAGCTTTGCAGTCACACTGGAGATCAGAGTTCAGGCTG
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SEQ ID NO: 1153 NGTACTCAGCTCTGTTCTCCTACTCAGGCTGGGACACCCCTCAACTATGTCAC
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SEQ ID NO: 1156 TCGAGCGGGCGCGCGGCCAGGTCTGCAAAGACCATCTTCCCTCAGTTAA
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SEQ ID NO: 1157 ACCTAGTGGCTGCTGTCTGTTTGTCTCCATTTTTTTCAGCTTCTTATCCAGTT
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SEQ ID NO: 1158 ACACCTTGAAACCAAAATTTCTAAAACTTGTTTTCTTAAAAAATAGTTGTTGTA
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SEQ ID NO: 1160 ACACGTTCTTGTGTCTGGCTCGGCAACAAACACCACTTCTGGCCAGTCTTC
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SEQ ID NO: 1167 CGAGGTACGCGGAAAGAGGATGGTCAGGAGTATGCTCAGGTAATCAAAAT
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SEQ ID NO: 1187 GGTACACAGCTTAAAGCTATAGGTTGCAGCTTGGCTCTATCTGTCTCAAT
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SEQ ID NO: 1188 GGTACCTTTTGTGTTTTACTTCAGTGAGGAGATTGGAGTCTGAATGGATCTGT
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SEQ ID NO: 1190 AGGTACCACGCTGGTCTAATGCAAAAATGGAGATTGCTACAAAGGACCCCTT
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SEQ ID NO: 1197 GGTACTGATTTCATCGTTGCATTTACAAGTCTACAAAAATGCCAGCACTCC
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SEQ ID NO: 1200 ACTTTTTTTTTTTTTTTTTTTTTTGGCTAAAAATTTTATTTTTTATAATTT
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SEQ ID NO: 1203 ACTGAACACAATATTGTGTTTTTATTTATGCCACGTGAGTGGGGCAAGA
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SEQ ID NO: 1204 GGTACTCACTTTTCCAAATGATCCTAGTAATTGCCTAGAAATATCTTCTCT
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SEQ ID NO: 1205 ACCAAAGGATAGCTGTTCTGTTAAGTAGGGACCTCTCATGCGCTACAGGCTT
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SEQ ID NO: 1206 ACGCTTTTACCCACCCCAAGTCCTGGGAGAAATGCAGGCAACACTGAGA
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SEQ ID NO: 1214 ACATTTTCATAAAATATGAAGGGATAACTACAACTGGAGTAAAAATGACGG
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SEQ ID NO: 1215 GGTACCTTCATGAAAACGGTATTATACACCGTGACTTAAAGCCAGAGAATGT
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AGTGGAAAAATACAACCTTATCTGAACTGTGGGCAGAAAGTCTCAGAGAAAGCTCTGGACCTTGT
CAAGAAAGTTGTTGGTGTAGTGGATCCAAAGGCACCGTTTACGACAGAAAGAGCCTTAAGACACCCG
TGGCTTTCAGGATGAAGACATGAAGAGAAAGTTTCAAGATCTTCTGTCTGAGGAAAAATGAATCC
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SEQ ID NO: 1216 GGACGATCGAAGGGACTATGCTTCATTGAATTTTGTGTTGAAGACAGTAAG
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SEQ ID NO: 1217 ACGCGGGGATGTAATTTTAAATACAATGCAGACGAAGCTAGAAGTCTGAAG
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SEQ ID NO: 1218 ACGCGGGAAACACAATTICAATGCAAGCTCAGTTTCTGGTGTCAAAAACT
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ACATACCTGAAGGATCTTTCTATTAGCATAGACAAAGCGGAACATGAAATCAGCTCTTCTTGGG
AGTCTGGGAGCCATTATTAACATCCTTGATCTGTCTCAACAGTTCCAACCCAAGTAAATTCAGAAA
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SEQ ID NO: 1219 GGTACTGAAGGACAAAACTGGATGGCCTCAAAAGGTTCTTGAACACCACT
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TCGTGATTAGAATTTAACTGATGGTTTTGTATTATAACTTCTAAGACCTGCCAGAAATGCTAGTCTG
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SEQ ID NO: 1220 GGTACATGGTGGTGGTTATAAATATTGGGACTTAAGGCAGCTTGTCTATG
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SEQ ID NO: 1221 ACTTCCTGAGACATGGATCTGGGATTGGTGGTGGTAAACTCAGCAGGTGT
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SEQ ID NO: 1222 AATAAAGAACCTCTATCAGTGAGACTTCTCATTTTATAGCAAAATACATTTTGG
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TCTTAGTAATTTGCGACATTTCTGAAAAGCATGTGAAACGGGTATAAACTTCAACTCTGTGCTTAAT
TCAGAAATTCCTGTTTGTCTCTCAAACTTTTATCTTCTAAAGCATCTTGGCAGAGACTACAAAGG
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ACTCTTGGATTTTNCATCATATCTTCAAGGCATGGNTTCTTTGGCCCAATTTTGGGCCACTNA
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NCCCTGGCTTTTCNC

SEQ ID NO: 1223 ACAAGTTCGGCTTTGAGCTTCTCAGGGGCTCTGGGAACATCCTTCAAAGG
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GTGTCTGTAAAAAAGAAAAAGTTTCTGCAATGTTCATTCCTGATGGGCGGTGTCTGTCTCT
CTCGAATTGACAGAAAAAGGATTTCTGTGAAGGTGATGAGATTTCCATCCATGCTGACTTTGAGAATA
CATGTTCCCGAATTGTGGTCCCAAGCTGCCATTTGGCCCGCCACACTTACCTTGCCAAATGGCC
AGACCAAGGTGCTGACTCANAAGTTGTCACTAGTCAAGGCAATCATATTAATCTCAGGGACATGC
NCATCATGGCGTGGCAAGAACCTTCGGGTTCAAGAAATCAGGCCTTCTATNCTTGGGCTGCAACAT
CCTTCGAGTTGAATATTCCTTACTGATCTATGTTAANCCTTCTGGATCCAAAAAAGNCATCCTTG
CCCTGNCCTGGTAAATTTGGCAGC

SEQ ID NO: 1224 GGTACTATGATCCAAACACCAAAAGCTGTGCAAGATTCTGGTATGGAGGTTG
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SEQ ID NO: 1225 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTATACAANAACCTTATGTTTATTGCAA
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CTGGCAATCCCTGCAATGGCCTGGCGGGACACGTGACTTNTAACACGAGGGTCTTNGTAGTTGGGC
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GCCAACAAATGACACATAATCTACACTGCATATTAGNGGGGCCCAANAATACCACTGGTGANAC
TGTGTAAACATAACAACTNTCACAGGCTCTCCCTAAAAANAGGATTCTGAGGCTGGACGTGGCCCCA
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SEQ ID NO: 1226 ACTCTGGATCCCAAGGTGACTGGTGTGTTAATCGTGTGCATAGAACGAGCCA
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SEQ ID NO: 1227 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGCGGTTCCACACTGCCCTTATT
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SEQ ID NO: 1228 ACTGGGACAGTTGGGTGTGTTATGGATACATAACCTGAGGAGCCGGGGAAG
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SEQ ID NO: 1229 ACAGACAAAGTGGGAGGTTTATTTCTTGGTCTCTCTCTCTGGATAAAGTC
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GATCTGACACTAAGGAAATGCTGAAGCTTTGGACTTCGGCAGTCTGTCCAACCTTCAAGTCACT
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SEQ ID NO: 1230 ACGCGGGCTTCTCCAAGATGGCGGCGATCGGCGGCGTTGAGGCGGGATCCG
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SEQ ID NO: 1231 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGAAANATGGGTTTCACCATN
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SEQ ID NO: 1232 ACCCCTTAACCCCTTCTCCTTACCCCTTAGCAGCAAGTCCCACTTTTCTAGGG
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SEQ ID NO: 1233 ACTACTGTCCAGCCTCCTCAGGAGAACCAACATCCAGTATACTTCAACAG
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SEQ ID NO: 1234 GGNACTTNTNTNTTTTTNTNTTTTTTTTTTATAGGGGTCATCGTCANANCTG
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N

SEQ ID NO: 1235 GGACGTGCGGGACGTCCGCGGTGACACAGAAACATATCCAGGAGTGGG
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SEQ ID NO: 1236 GGACGCGGGGAGTCACTCCAGTCAGGACACAGCATGGACATGAGGGTCC
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CTGCTTCAATTTGCAAACTGGAGTCCATCAAGATTCAAGTCCAGTGGATTGGGACAGAGTTCA
CTCTCACCATCAGTGTCTGAGCCTGAAGATTTGGGAATTACTATTGTCAACAGAGTTACACTT
ATCCTTCCACCTTCCNCCAAAGGACACGGCTGGACCTCAAACGAACTGTGGCTGACCATCTGTCT
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SEQ ID NO: 1237 GGTACCATCCCTCCATATTGCCACCAAGATGCGTGAATACACAGGCTCAT
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CTTGGNGC

SEQ ID NO: 1238 GGTACTTCTGTCTTCCAGTTTTCCTTACCAAAATCGCACTGGGCTCCTGGACTCT
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SEQ ID NO: 1239 ACATGGGTAATCTGTCCCCATGACCCAAACATCTCCCATAGGCTCCACCTCCA
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SEQ ID NO: 1240 TCCTCCCGCCGCCAATATGCCGAAAGGAAAGAAAGGCCAAGGGAAAGAAAGG
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AAAAAGGCTANNAATTTTGGCATTGGACAGGACATCCAGCCCAAAAGAGACCTCACCCGCTTGT
GAAATGGCCCCGCTATATCAGGNTG

SEQ ID NO: 1241 CCGGGCAGGTACATAGGTAAACCAAAGTATATAGCTTATTTGGTGAATCTTCAT
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CGAATCTCTTTGAGTGCCGAGGTGCACGCTTCTTGAAGCCCACTCCATGGATGCGCTTGTGAAT
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SEQ ID NO: 1242 GGTACTCTGGATCCCAAGGTGACTGGTTGTTAATCGTGTGCATAGAACGAG
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SEQ ID NO: 1243 GGTACATGGCAATTAGAAGTTGTATGGCAAAAGAAAACACAGCTGGCGCTG
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CCA

SEQ ID NO: 1244 ACAAGACAAAGGCGAATGAGACTTCTCTTATATCTGAGTAACATTAAGATGG
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SEQ ID NO: 1245 ACTGTCTTCAATCCTATGCGTGCAGGTGTCTACCACAGGCAACAGTTTTCTC
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SEQ ID NO: 1246 AATTCGCCCTTAGCGTGGTTCGGGCCGAGGTACATCATGCCGCTGATGAAGG
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ANAAAACT

SEQ ID NO: 1249 ACAACACTATTTTCATTATCTGGATTGTCCATGCTAGAAATAAATTCATCCTTG
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SEQ ID NO: 1250 ACTNNTNTTTTTTTTTTTTTTTTAAACANCAAGANCGGGAGCAGGATTGGGT
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SEQ ID NO: 1251 ACAACACCATCTGGCTTCTATTTTGAAACTCCACACCAGGTAAATCTTGTT
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SEQ ID NO: 1252 ACATTCTACCGAAGACTTCCCGCCGAAGTCTGCTGCCAGTGAGATAAGTGTGA
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SEQ ID NO: 1253 ACGCGGGGGCAATGCAACAGTCTCATTTTCCATGACGATGGCAACACCGG
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SEQ ID NO: 1254 ACCCAGACACAGAAAGTTTAGGGTAAATAGTAAACTACAAATACCCCTCTTG
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SEQ ID NO: 1256 ACCCACTGGGAGATGATTGAATTATGGGAGCGGGTCTTTCCCATGCTGTCTCT
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SEQ ID NO: 1257 ACCTAGAAGAGAGGCGGGTCAAAGAAAGTAGTGAAGAAGCATTTCTAGTTCAT
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SEQ ID NO: 1258 ACAGTTGGAGGTGTTCTAGGTGGGCGGATTGCTTGAGGTGAGGAGTTCAAG
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SEQ ID NO: 1259 ACAAAGTCCAAATCTTACTTTATGGATGTAATGTCCAGGTTGCTACAAAG
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SEQ ID NO: 1260 ACTTTTTTTTTTCAAACCATGCTATTGAATCAAGAAAAGTAGAAAACTGAA
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SEQ ID NO: 1261 GGTACGCGGGGGGAGTGTGCGAAAGCATGGCGTGGTGGTGGCGCTGA
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CANATCACTATGATTTNCCCCGGTGTTCATTTGGCTGGTATTTCTTTGTTCTCTTTCTAACCTTC
ANTTTTGGAGGACAANAAACCTGGNGAATTTAAATATTTATTTTAACTTTGGGAAACTAATTTT
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SEQ ID NO: 1262 GGTACAGACATTTTCAAAGTTGCCAGTGTTACTTTAATTGGACTGCCTTCGTA
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SEQ ID NO: 1263 ACTGTGTGCAGCAGCTCAAGGAATTTGATGGGAAGAGCCTGGTCTCAGTTAC
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SEQ ID NO: 1265 GGTACGCGGGGAGAAGGGGAAGAATATGGAGGATAGGAGAGGGTGATGATG
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SEQ ID NO: 1266 ACTTTTTTTTTTTTTTTTTTTTTTTTNNCCAAAANATANAATCATANAATTTA
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SEQ ID NO: 1267 GGTACACAAAGAGGGGGTGGGTGTCGGATGCAGAGTGTGTGGCCTGATGCTC
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GAAAACCGTTCTCANCANAAATCACAAAAGTAAGTAAAGAAAGCCTNCCAAAGGCTGGATCATTC
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SEQ ID NO: 1268 GGTACTAGCCGGACTTGGATTTTCTGGAAAGATTTCAAGTTGAGGAACGGGAA
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SEQ ID NO: 1269 GGTACCCCCAGATTACACAGCTTTGAACAAGTGAAACTATGGTTACCAAC
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SEQ ID NO: 1270 GGTACAAGACACTACGGGAACAGTTTGCTCCCTCCAGCCTCAACCACAAT
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SEQ ID NO: 1271 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNCNAAAGGTTTATGAAATA
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CCAT

SEQ ID NO: 1272 GGTACAACTTATAGAAAAGGTAAAGGAAACCCCAACATGCATGCACTGCCTT
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SEQ ID NO: 1273 GGTACTATGATCCAAACACCAAAAGCTGTGCAAGATTCTGGTATGGAGGTG
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SEQ ID NO: 1274 ACACAGGCTGCTACCCAAGTTGTTCTGAATGTTCTGAAACAAGAGTAACAT
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GCA

SEQ ID NO: 1275 ACCCTTGGAGATGGGAAAGGTGAGGGAAATATTTGAAGCAGGGTCAGAAC
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SEQ ID NO: 1276 ACTTTTTTTTTTTTTTTTTTTTTTNGGTANAATATAAAAGAAATGAGAGCA
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CGTACCT

SEQ ID NO: 1277 ACGCGGATTGATAATAGGGTGCAATTGTTGCTTTACTTTATTTACCTTTTGG
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AAA

SEQ ID NO: 1278 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTNTCTCAANANAAATTTAATCT
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TAACAAAC

SEQ ID NO: 1279 GGTACGCATCGAAAGGATTGACGGCGTGAGTTTACTGGTGACAGAGAACCATT
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SEQ ID NO: 1280 ACAATTACCCACCACTGGATTGACTCAGAGAGGACCCCCAGAGGGTGTCTC
CATCTTCCCTATTTATTTTTCAGCCCTTGAGGGCTTCAATTGTAGATCAAAAGCCAAGGCCCAAGGAA
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SEQ ID NO: 1281 ACTTTTTTTTTTTTTTTTTTTTTTGGGCTTATTTCTTTGGAGGGAGGGTCTTGT
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SEQ ID NO: 1282 ACTTTTTTTTTTTTTTTTTTTTTTGGANATGGAGTCTTGTCTGTANC
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CCGNGACCACGC

SEQ ID NO: 1283 GGTACTTTTTTTTTTTTTTTTTTTTTTGGCCACACCTGCCCTTTATTGGTCTC
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SEQ ID NO: 1284 ACGCGGGGAGCGTCTCGAAACCAAGCAAGTGAGCAGATCCTCCGAGGC
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GCTGCTATTTTCTTTGTTGCTACATGTGTGACCTGCACACCAAGATACCAATTCATCAACTGGCCCT
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SEQ ID NO: 1285 ACTGGAATTTTGCATATCTGTAGAGTGTATCTAAATATTCCTGCCTAAAAACA
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SEQ ID NO: 1286 GGTACAGACCAAGTTATTTGTAAAAATGTTCCCAAGTGTGGGTTATCTGAGGT
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SEQ ID NO: 1287 ACCCAATAGCTAAGTTTAAATTTTAAAGAAATCCGAGAATTAGTTTAAAT
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SEQ ID NO: 1288 GGTACTTTTTTTTTTTTTTTTTTTTTTGGGTCCTTCCCAACAGCAGTTGGAA
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SEQ ID NO: 1289 GGTACCATAAGGAGACACAAGAAGAAAGGTGACACTAAGGCTACAGTGAC
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SEQ ID NO: 1290 ACACACCCAGGAAATTTGTCTCCACCCTGAGAGTAACAACCTTATTATCATT
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SEQ ID NO: 1291 ACAGGGGCAAGTCAGTGGAGGGCGAGTGGTTTCGAAAAAAGAAAAA
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CTACAACGAAATATACACAGCTTTTTTCACTCTTAACCTTTTAAAGGATTCACACGCAACTCAA
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ATAGG

SEQ ID NO: 1292 GGTACAAGCTTTTGTCCAAAATGGCACAGTGAGCACAATGAGTTCCTGTGT
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GGGATGCCCCCTGGGAAAGTCTTATATGTGCAACAAAGAGCAAACTGTTTCAAGTGTCTGGAGC
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SEQ ID NO: 1293 ACTTTTTTTTTTTTTTTTTTTTTTTTGGGGGAAAGATATATATATATAT
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CCA

SEQ ID NO: 1294 ACTTTTTTTTTTTTTTTTTTTTTTTTGGGGGAAAGATATATATATATAT
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SEQ ID NO: 1295 GGTACGCGGGGAAGTCGCTTGTGTATGAACGCAGCGGGGACCTGTGAGGGG
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SEQ ID NO: 1296 ACGTCATAGAAATAGCAGCTCCACCTTGTATCAATGGTATCAAAATTTGGTA
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SEQ ID NO: 1297 GGTACTTTTTTTTTTTTTTTTTTTTCCACACCTGCCCTTATTGGTCTCTNT
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SEQ ID NO: 1298 AATTGCGCCTTAGCGGTGGTGGCGGGCCGAGGTACAAAGGCAAAAGGACCA
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SEQ ID NO: 1299 GGTACAATGTGGGCGAGGCACCAAGCTGGGCAAGGAAAGGCTCGGATACC
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TNTT

SEQ ID NO: 1300 ACACTCCAGATATAACTGGGACTTCTGTGTAGATCTGAACGAGTGCAACCA
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SEQ ID NO: 1301 ACGCGGGGCTCTTCCCTGCCGCCGCCGAGCCGCGGAGGCGGAGGCTGTG
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SEQ ID NO: 1302 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTAGGAAATCAATGTTTTCTT
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SEQ ID NO: 1303 GGTACGGGAGTTCTTGTTAAATCCAGAATCAGGATACAATGTCTTTGCTA
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SEQ ID NO: 1304 ACTGGATGGCCCCACAAGATGCTGCCACTTTAATAAGGCTGCAATACACTGT
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SEQ ID NO: 1305 GGTACTTTTTTTTTTTTTTTTTTTTTTTTGGTNTAATGATGTTTTTAATTGACAAT
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SEQ ID NO: 1307 GGTACTTGCCCACTTTTCTCTTGTGGGCTGTCTCTAGAATCCATTATGTTCT
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AAATCC

SEQ ID NO: 1308 ACTAGGAAAAGATACAGTTACCAAGATAATGGCATCCGTCCTTCTCACTG
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SEQ ID NO: 1309 ACTTTTTTTTTTTTTTTTTTTTTTTTNGCTGGGGTATTCATTCTGCATGTATAG
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SEQ ID NO: 1310 GGTACGAAAAACAGAACCAATCTAAAAATGGCTGATGTTACTTTAGGAGCCTG
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SEQ ID NO: 1311 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGAAAGNGTAAATTTATTTAATACCA
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SEQ ID NO: 1312 GGTACTTTTTTTTTTTTTTTTTTTTTTTTNGCATTTANACTCCACAT
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SEQ ID NO: 1313 ACAAAGTAATGACCATAATACCTTGTCTAAATCAGTAGCAGGGCTTCATGGC
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SEQ ID NO: 1314 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTGGNGGTCAGGGTTTATTAAGTANA
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SEQ ID NO: 1315 ACGCGGGATTTCGCCATGGATGAGGATGGGGACGAGAGCATTACAAAAGTGA
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SEQ ID NO: 1316 GGTACTCCAGATTGCTCTAAATGTCTGTCTGTCAGATTACTTTGCTTCTG
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SEQ ID NO: 1317 ACTGCACCAAGCCTGGGCCTTGGCCTTGAGCATTCAAAGCCACGGTCTC
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AGTATCCCTCGTTATTCAGCAGCAGGCTGCTCTGGACGCTCCAGTGTGGCTTGGCTTANCACC
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SEQ ID NO: 1318 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGAGCANATTGGGTAATAAATGT
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SEQ ID NO: 1319 GGTACGCGGGGAGGAGTGAGAGAGCTGCTGGATATGCGGAGGGAGTGGGCG
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SEQ ID NO: 1320 GGTACTGACAAAGTCTGAACTACAATGAGAGGAAACACATTGCCCTACTT
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GATT

SEQ ID NO: 1321 AATTGCGCCTTAGCGNGGTGNGGCGGAGGTACNGCGGGCTCACTCTGCGC
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CTCAA

SEQ ID NO: 1322 ACGCGGGTCTTGTCCAGTGAAACACCTCGGCTGGGAAGTCAGTTCGTCTC
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SEQ ID NO: 1323 ACCAAAAAGAAAAAGAAAAAGGAAAGGTTTCTACTGCTGATTATCTATAACT
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SEQ ID NO: 1324 GGTACACAGTATTTTTATATCTATGTTTCTGTCTCTGGCGCAAGATATTC
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SEQ ID NO: 1325 ACGCGGGGGGCGAGCAGTGGACCTATGAGCAGAGGAAAAATCGTGAAGTTTCA
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SEQ ID NO: 1375 GGTACTTTTTTTTTTTTTTTTTTTTATGATANANACATGGTTTCGCCATGTTG
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SEQ ID NO: 1407 ACTTTTTTTTTTTTTTTTTTTTGGGAGGGGTGAATAATCTTAAATATTACAC
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SEQ ID NO: 1408 ACTTTGAATTTGAGAAGTGGGTGATCCCTCTAGGCTTCTGGAGGTCACATT
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CCT

SEQ ID NO: 1409 ACTTTTAACTAGTAATAGAATTTCTGAAGAATATCCAAATAAACCAACAA
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SEQ ID NO: 1410 ACGCGGGATTGACATGAATGATATCAAAGCATTCTATCAGAAGATGTATGGT
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SEQ ID NO: 1411 ACNCGGGGCGCGTCTTGTTCTTGCTGGTGTGCGGTGGTTAGTTTCTGCGACTT
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SEQ ID NO: 1412 ACTCCTCATAATCCTGATAGGTATCAGAAAACTCAGACGTATTTCCCTATGA
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SEQ ID NO: 1413 ACGCGGGGGGAGTCAGTCCCAACCAGGACACAGCACGGACATGAGGGTCCC
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SEQ ID NO: 1414 ACATTGGTGATCGGAGTATAGTTGGAGCGCTTTGTCATGATTTCCAGGTTGGC
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SEQ ID NO: 1415 ACAACAGTTGATGATGAAGAACACGATGATAAGGAAGAAGAGGAGGAGGAA
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SEQ ID NO: 1416 ACTTGATTTTGAACACAGCACGAAAAACATTTTGGAGCTGGTGGAAATCAGCG
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SEQ ID NO: 1417 ACAGCCAACGGTTTCCCTTGGGGGCTTTGAAATAACACCACCAAGTGGTCTTA
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SEQ ID NO: 1418 ACAGCTTAAACCACAATGGTATAAAATCTTCATTTTGTAAATTAATAATTTCTTG
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SEQ ID NO: 1421 ACAGCAGCAGCAGACACGCATCGCAGAGCTGGAGAAGACGTCAGCTGAACA
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SEQ ID NO: 1425 ACAGAAAAGCCCAGATTAAATACATTAAATATGTCGTTTTAAAAATGATTTT
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SEQ ID NO: 1427 ACCCCTTAACCCCTTCTCCTTACCCTTAGCAGCAAGTCCCACCTTTTCTAGGG
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SEQ ID NO: 1428 ACTTCTACACATCTGCCTAACTTGGAATGAATGTGGGAGAAAAATCGCTGCT
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SEQ ID NO: 1429 ATATCCGCNTNAATTCGCCCTTTNGNGCGGCCNNCCGGGCGNGTNCACCTA
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SEQ ID NO: 1430 ACACAGAGGGCTATAATCAGAGATCGAGCAGCTTTAGAGAAACAAGAAAAA
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SEQ ID NO: 1431 ACCAGGTGGGAGAAAGTGTAGCAAATCTCAGTGCCAATTTGAGGGGAAGCC
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SEQ ID NO: 1433 ACTATCACTTTGCCTTGCTCAGTCTCTCCTTCTCCGGGGCCACAGAAGGAG
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SEQ ID NO: 1434 ACNGCGGGATAATAATTATCTTTGAAGTANAACANTTCTGTTAACTGGAAAA
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SEQ ID NO: 1440 TTATCATCCTAATGTAGACAAGTTGGGAAGAATATGTTTAGATATTTTGAAG
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SEQ ID NO: 1442 ACTGAATTCAGTGCTTAGAACTGAAGTTATTGAGAGGACAGCTTTAAAGAT
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TTTTAATTTTTCTTTACAGTAAATATTCATTCTGATTTATATAAATTAACATTTATGCCTCCCTTT
GTGTTGACACTGTAGCTCATACTGGAAAAGTCGATCAATGTTTGCAGTTTATTGAAAGTAGTTCT
ATATATAACAATGTTATAAGCATTTCTTTAGAAATGGTTGAAAATGCTTCTAAAATGTGATTATCG
ACCATGGTATGCATGATCGTTGTAATTGTTGACATTCCTTTTAGAAGTTGTGAAATGTTACAACCTG
TGCTTATGTAGACACAATCTTCTGTCTCAGTCC

SEQ ID NO: 1443 ACAAAGCAGCAACTGCAATACTCAAGGNTAAAAACATTAGAAAAGCATTGTG
TGACAGGTATATTACAGTATTATCAAAATATTACATTTTCAGACTTACTTAGCAGATAATCATCCA
CCAGAGCTTAAATCTTTAAATTATTTCCATAGNCTTAAAAAATATGTAATGNCAGAAATGCATATAA
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TAACTGTTAATAATCAGCTCAACACCACCATTCTCTAAACTCAATTTAATTCTTATAGGAATAAT
GAACTGTCAAATGCCATGGCATAATTATTTATTTCCAAAGCTATCATCAATGATTAGAAGTAAAAAA
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SEQ ID NO: 1444 ACTTGTGCCTAGTTTTTCAAGGTATTGGCTGTTCTATAGATGCAGTGATTGTC
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CAGGTGATGTAGCACTTCTGTTTTTAATAATTATTGCTTAAAATACCTATTAATAGTTTGGGTCA
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GAGTGAAGCAAGTGGGTGAGTAAACTATTTTGACGTGGGAGCGTTTTCAGATAGGAGTTTAATC
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TGCCACTCGCATNTGGGCAATGTTGACATTTGAG

SEQ ID NO: 1445 ACTTTTTTTTTTTTTTTTTTTTTTTTATCAAAGTTTTAGTGTTAATAATGAAT
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TTATTAGCAACCTTCAACTNTTTTGGCTGGCAGGTATCTTGTTTCACTTTCCAGTTCTTCCACCCC
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CTCCCAATGATCTGGTCANACATGGTCTGAAATTTATCTTGCATCTGCTGCAGGAGTGTCTGCACC
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SEQ ID NO: 1446 ACAATAGCGTCTTCTTCCAGCAGTCAACTCAAGCACAAAAGCCAGACTGACT
CACCTGATGGTAGCAGTGGGCTGGGAATTTTCATCCCCTAAAGAGTTTCAGTGCAGGAGAAAGCTCT
ACTTCTCTCGATGCTAATCACACAGGGGCAGTCGTTGAGCCTTTGAGAACTTCTGTTCCAAGACTC
CCATCAGAGAGTAAGAAGGAAGACTCCTCTGGCGCTACCCAAGTCCCCAAGCAAGTCTCAAAGT
CAGTGATCTCTGACTTTCAATCAGTTTCCAAGCTAAACCAGGGCAAGCCATGCACATGCATAGG
CAAGGAATGCCAGTGTAAAGAGATGGCATGATATGGAAGTGTATTCTTTTCAGGCCTGCAGAGTG
TCCCTCCCTTGGCTCCAGAACGAAGATCCACACTTGAGGACTACTCTCAGTCGCTGCACGCCAGAA
CTCTGTCTGGCTCTCCCCGATCCTGTTCTGAGCAAGCTCGAGTCTTCGTGGATGATGTGACCATTGA
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SEQ ID NO: 1447 ACTTTTTTTTTTTTTTTTTTTTTTTTGAACAGNGGTTTTATTGGTAAANAT
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CGAATAAANAAAAGGAATGGATGGTCCGCGAGTGAAATTTNTTCGGGCATCAACATGCAAAAAGT
TGCNATGCCTGTGTGGCAGCTGCCGCTNTGTTCCCTNTTCATTCACTTCCACAAATGACTTGNG
GACAATTTTTGATATAAAAAATATCTCTGGCTCCTGACATGCCAAACANATCAGCCTTGCTACTGTT
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CCTGGGCAAGCTGACATTAACTTCAATGAAATCGAAGATTCTCAGGTTTAGTCCACTCATGCAACT
TTTCCAAAGTCAACTGTTCTCTCAATCTNTTCAGG

SEQ ID NO: 1448 ACTGATGGGGAAGTGCCGCGCTTCTTGGATGAACTAGATGTGGTTTCAGATG
GACTGAGCTTGGATGCTTCTGAGGCAAGCTGAAGCTTTGGGTTCTGACTGACCCACCTACAGGAC
TGCTGAACAGAGAGCCAGTGTGACTAGGGATCCTGAGTTTCTGGGACAATTCCAGCTTTAATCA
ATACATTTTGTAAATGTGCCATAAAATGAGACTTTTTACGCCTTTATAAGGCCTTAGATGTAAAT
AAACTCACCCCANCAAAAAAAAAAAAAAAAAAAAAAAAAAAGTACCTNGGCCGNAANCACGCTAAG
GGCG

SEQ ID NO: 1449 ACACCTCTTGCAATTCGCTTTATGTGCCCAATGGAAGAGGTGTCCTCTGGAGC
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AGGGTCTATATCTGTCAGATCAACCACAAAGTTTGGGTGAAAGGATGTGTCTTCCCAAATGTCTTT
ACCGAATTCTGTAGTTCTCCCCATCTCCCANANCATTAAAAATGTCTGAAC

SEQ ID NO: 1450 ACCATTTTACGAATTTCTGTCTTCATAATATAAGTGAAAATACTGTCATTTCA
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GTGTCATGTCTTGGGTTTGATGTCGTTGGACAGAAAAGTGATCAATTATTTTAAATGAATTTTCCC
CCTGTTTGGAGCTTAGTCTGNAAATGNGTTGCTGNAACAGAAAAAT

SEQ ID NO: 1451 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGGGGGGANAGTTCTGTANATGTC
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AATTTTAGACCAATATCCTTGATGAACATTGATGCAAAAATCCTCAATAAAATACTGGCAAACCG
AATCCAGCAGCATCAAAAAGCTTATTCACCATGATCAAGTTGGATTTCCTGGGATGCAAG
GCTGGTTCAACATACGCAAAATGAATAAACATAATCCAGCATATAAACAGAACCAAAGACAAAA
CCACATGATTATCTCAATAGATGCAGAAAAGGCCCTTTGACAAAATTCAACAACCTACATGCTACA
AACTCTCAATAAAATTAAGTATTGATGGGATGTATCNCAAAATAATAGGAGCTATCTATGACAAAC
CCACAGCCAGTATCATACTGAATGGGGCAAAAACCTGGAAGCATTNCCTTTG

SEQ ID NO: 1452 ACGCGGGGAGCACCTCCTTGATTCTCAGTTTTGCTGGAGGCCGCAACCAGGC
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AAAAATTCTCCATGTTGACAACCATATTGGTATCTCAATTGCGGGGCTTACTGCTGATGCTAGACT
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TCTCGTCTTGATCTCTAATTGGAAGCAAGACCCAGATACCAACACAACGATATGGCCGGAGACC
ATATGGTGTGGTCTCCTTATTGCTGGTTATGATGATATGGGCCCTCACATTTTCAAACCTGTCCA
TCTGCTAACTATTTGACTGNAANAGCCATGTCCATTGGAACCCCGTT

SEQ ID NO: 1453 ACAAACAAATTATGACCGTTGGAAACATCCCTTCTTCCTTGATGATCGCAGAA
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GTCCTGTCAACAAAACCTGTCTCAACAAGCTGACCGTATACACAACCTTGATAGATGTTACCAAA
GGTCAATTCGAAACTTACCTGCGGGACTGCCCTGACCTTGTATAGGTTGGTGAGCACACGCTCGG
CCTACAGAATGCGGCCCTCTGAGACATGAAGACACCATCTCCATGTGACCGAACACTGCAGCTGTC
TGACCTTCCAAGACTAAGACTCGCGGAGGTTCTCTTTGAGTCAATAGCTTGCTTCGCTCCACCT
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TAGGGGAAGTAAACAAGTCATCTAGAATCACTGAGTTTTGTTTCACTTTGACATTTGGGGATCT
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SEQ ID NO: 1454 ACTCTAGGAACCCAGGGTCACCCAGATGTCCCTTTGATGGCCGTTGTTGAAG
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NAATCTAAACCATGGGCNTANAATTGNAAAACCTGGGCTCATCAAAATCGGGACTATTATNGCTC
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SEQ ID NO: 1455 GGACAAAGATGACTATAACAAGATGCAGCCCTCGGTTTCCATGAACAGCAC
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CTTTCCGAAGAAGATCATGACTTTCAAAGGTTCCACTTGCTGGAAAGTTCAAGTAACTGGAATACT
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TGGNCCCGTTACCGNTANTNGACCCCGCGCTCACTTTTCGTTTTCCCC

SEQ ID NO: 1456 ACACATAAGAAAAGGATTTAGTAACACTTGGGCAAGTAATAAACTGTAGAAC
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SEQ ID NO: 1457 ACATTTGGAGGATCATCTTCCAGGGTCTTTTAAAGACTTTCTGAAAAAGCCTT
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GCCAGCTTTTCCTTACAATCTTATCTGTCAGCCTCAAGTCCAGGAGGAAATCTGTGATAGCTGCTT

CGCTGCTTGCACTCTTAACAACTTAATGATTCTCGAATCGTGGGCAACGGAGGGAGACGGCAAG
TGCTGAGTTTTCCGGAGGCAGCCATGATACGGGCAAGGCACCATCCACCCCTACCTACCCAGG
CCCCGCGTACAAAAGGAATGTTCTTTATAAATCACAGAAGAAAATGACAATATCTGNTGGATA
TTTGATATAATTTAATGGTGTTATAAAACCTTTAAGANGATTTCATGGG

SEQ ID NO: 1458 ACAAGCCTCACCAAGGGCAACCCAGAAAAGTGAATGAGTTTGTCTCTCCA
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ATGACACCAGCAGCACCAAGAGCTGTTCAAGGATAATTATAAATTAATTGCCTGTTAATAAAGCA
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CCAACAGGAAGCCTTCATCTAAATAGGAATCTGCCAAACTTCCTCCTAGCTTCTTGATAATATGAA
TTGCCTCCAGTTGCCAGAGCCITTCAGTCTGAGAACTG

SEQ ID NO: 1459 ACAAGATGCTGTGTAAGTGTTTAATACAGCAAATAGTAACTCTCCAAATCCT
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ATAACTTGTGTGATTTCAAATTAAGCTTGCATTATGTGTTAATTTTCTTGCATCTAAAAAAGCATAG
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CCTAAATGAAAGTGTGTAATTAAGAAGCTGGCGATCTTTTGATATGCTGNTTCACAGGACCTG
CCACTGGAGGGCAGCTGCTTGTGCATTACTTGGTTCCNGCA

SEQ ID NO: 1460 ACACTTGAAACCAAAATTTCTAAAACCTGTTTTTCTTAAAAAATAGTTGTTGTA
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SEQ ID NO: 1461 GGTACTTNTTTTTTTTTTTTTTTTTTTTTTTTNCCAAATTTGTTTTATTTAT
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GCTGTGGNGGTTTGAAGTTTGGACAGGTCTCCTCAGGGAGCGGGGTTNTCCTCGGCTNTGG
NNCTGCATNTTNTCCTGCTGGCNACCCTGCTGAAACTGATGTTTCNGCTGCTGTTGNTTACTANNA
TTCCTCATGNATGNGTGGGATTTAACTATATCTGGGGCTCATTTTCATNNACTCTGTCCATCAACAA
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SEQ ID NO: 1462 ACGCGGGGGGGCGCAGAGGCCTGCGGGAAGCCAAGATGGCGCATAGGGGTT
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TGGCAAACGCCCTCTCCGCCGTCATGGCCCGGCATCGGAATGTTTCGAGGCTATAACTACGATGAA
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GCTGCTCAGTTTATTTATTCACGGCGTGACAAACCTTCCGTTGAGCCTGTGGAAGAATATGATTAT
GAAGATCTGAAAGAATCTTCCAATTCGTTTCAAACCATCAGCTCAGTGGATTGATCAAGCTCGT
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SEQ ID NO: 1463 ACTGGGATGGCCCTGAGGATCACAGTAATTTCTTGTAGTCATGAAAATCACCC
GCCAATCCAATTTCTGCTTCAGGAATAGGTCTAAGACCTTGCCTTTGGAGCATATCCATTATTGAC
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ACCTCCAAAGACAACCTGCGGAACCTCAATTTCTTATGCTGTTTGGCATTCAAAAAATAAATGTTTT
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TCATCAAGAGGTGGGTAAAACTTTCAATTTGTGGAGGCTGCTTCTTGGACTCAACTGCTTTTCAGG
AATTCAGTAAAAATTTCTGGCTTTACAATTTGGACGTCCACAAATGAGTGCACATATTGTTTAATG
GTAACCTTCACTGATACCATGACAAGGGNGAGTGCATTCTTCTG

SEQ ID NO: 1464 ACAACAATTTCAAAGGCATATATATGGGTAATTAGTGTTCACATATACCAA
ACCAGGAACTAAACAAATCTCAAGGATGAGAAACATGAAGAAAACCTTCACTAAAGCGTATCAT
AATTAAATTGTCCAAAACCATGTATAAGAGAGAAAATCTAAAAGCAGCCAGAGACAAAAAACAT
ATTATTTACAGAGAACAAAATAAGAGTGTCTGCAGATTTCTCACCAGAAAATAATGCAAGTGAAAA
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ACACACACACACACATGAACCTATAATCCTATACCCNAAAAAAAAAAAAAAAAAAAAAAAAAATTGG
TNCCTCGCCGCGACACGCTAAGGGCG

SEQ ID NO: 1465 ACTGGCTGGCCACCAAAGCACACGGAGATTCTGTCAGGCGCTGAGACACCAC
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CTAGTAATGTCAAGTTGGATGATGAGAAGACTGGAACCTAAGAAGTTAGCAAGACGTGTCNATT
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SEQ ID NO: 1466 ACGCGGGGTTCCGGGGCAGGGCCGTGCTGATTGAGAATGTGGCTTCGCTCTG
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GATGACCCATTTTCCCTCATGACCGATCCCAAGCTCATCTTTGGAGCCCTGTGCGCCGCTCANAT
GTGGCCTGGAACTTTTGAGAAGTTCTCATAGGCCGCGAGGGAGAGCCCTTTCGACGCTACAGCCG
CACCTTTCCAACCATTAACATTGAGCCTGACATTAAGCGCCCTCTTAAAGTTGCATATANATGT
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SEQ ID NO: 1467 ACAGTAACACAACATCAAAAGCAACACAGCTGTATACAGAAACGTAGGTCAT
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TATATGGACTACATGGAGATCATATCCTGTAGTGTAGTGAAAGCTAAGTCTCAAGAGCCATATGT
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ATTGTCCAATTTATACAACCTGTGGGAGACTTATTCAAGGTTTTTGAAAGTCCAGTGATGCN

SEQ ID NO: 1468 ACATTTATATTCAGTGATAATACAAGCTTCTGTGGTGTGTGGACCAGACACAG
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SEQ ID NO: 1469 ACGCGGGGACTTAACGGTGGTGGCTGGTTCTGCGCCGGATCCGGGAGAGGGG
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CAAGAGACTCTTCATTTATATTGGGATTCTGAATATCAGTCTACATCAGCATCAGCATCTGCGTCA
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SEQ ID NO: 1470 ACTTCTGTTTCTCAGTTTATCTGGATGTTATCAGATCACAGACCATGGTCTCA
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CAGGCTTTCTTTTCATGCACTTTACTCATAGCACATTTCTGTGTTAACCATCCCTTTTTGAGCGTGA
CTTGTGTTTGGCCCCATTTCTTACAACCTTCAGAAATCTTAATTTACCAGTGAATTTGAATGTTGTTT
TCTTGCAAATTTACTTTTGGTTTAGAAAGGATTANGTCTTTTCAAANGGTGAGAACAGTCTTA

CATTTTTCTTTTAAATGAAATGCTTTAAAGAAATGGTGGTA

SEQ ID NO: 1471 ACGCGGGGGTTACCGCGATTCTGAGAGGTGGGCTTTTAGTCCCTCCAGACCTC
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ATTCTTGGGACCTAGAGAAGAAGTAACGAGTGAGCCACGCTGTAAAAAATTGAAGTCAACCACAG
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CAAGTNAAGCATTTATAGGACCCATTTACAAACCC

SEQ ID NO: 1472 ACGCGGGGGGAGAAGAAACGGCGGAGACCTGAGACCCGGAGGCTGAGGCTGT
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CAAAATGTTTGCAGTTTCAGGCGCCCTTAGTTGAAAGGCTGTAATTAACAAGTCCGCTGTTTGCC
AGCCAGGCGCCGTTGCAGGCGCTTTCTGTGGATTGTCATTTATTTCTCACAGCAACCCTAGGAGGC
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GCTCCTGTCCCACTCCACAACCTANTTTGTTGACAATTTAACAGTGGGTTTCTGGAAACAGTGCT
GCCTCCTTGATGGTCTAACTAACTACCAGAGTTATTCTTAACANCA

SEQ ID NO: 1473 ACGAAAAGCGGCAGAACTAGCTCTGAAAACCTCTGAGCAAGGTCTGTGTGAAA
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GCTGCNATGGATANGTGCTCGGCTTATTGNANCCAATATTTTCNNTGATGGNAACTTNAANTGTG
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SEQ ID NO: 1474 ACACTGTTGGTGTATATAGGGGATGGGGTTCTCGGTAATTTTGTATTATTATA
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AATCTTCTGTGGGGGTGGGAGGGACAAAAGATTACAAACCAAACTCAGGAGATGGTAACACTG
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SEQ ID NO: 1475 ACNGATACCGGAAAGGCTGGATACCTNNGTTATTAGAGGATTTTGGAGATGG
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SEQ ID NO: 1476 ACGCGGGGGCTAAAGTGTTGTCAATTTTGTTTAACTTTTCAAACAACCAACTT
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SEQ ID NO: 1477 ACATGTTTGAAGAAGTGCCGATTGTAATTAATAAATTCACATCTGATCAATGTC
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CAGCGTCGCCAGCAGGAGAATATGCTGCGCCAGAGCCCGAGAAGAACCCCGCTCCCTGAGGAG
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SEQ ID NO: 1478 ACATTGTTTGTTCATAGGAGTTCATGGAATTTGAAATCAGAAGAAAAATC
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SEQ ID NO: 1479 ACTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAGGGANACAAC
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SEQ ID NO: 1480 AACTCATTAAATAATTAATAGGCGCTTGACCCACAGGCTGTCAAAATTCG
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SEQ ID NO: 1481 ACGTGCCGCGGAAATGCTCCGCTAGCAATCGCATCATCGGTGCCAAGGACCA
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SEQ ID NO: 1482 ACATGTTTGAAGAAGTGCCGATTGTAATTAATAAATTCACATCTGATCAATGTC
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GT

SEQ ID NO: 1483 ACAGCCAACGGTTTCCCTTGCGGGCTTTGAAATAACACCACAGTGGTCTTA
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SEQ ID NO: 1484 ACTTTCTTATTCAACTGTGAATCTGCTCGAGAAAAGACAGAAGGTTACAGAAA
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TGAGGGGGGACCCTGCACCGCATTAGAGCTCGAAATAAAGGCGATAGCTGACTTCATTGGGGCA
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SEQ ID NO: 1485 ACTACACGCGCTGGGCNACGACTTCCACACGAACAAGCGCGTGTGCNAGGA
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SEQ ID NO: 1486 ACTTTTTTTTTTTTTTTTTTTTTTTTCCACANAAATCTAANCNCACTTGTCTT
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SEQ ID NO: 1488 ACAGTTACTCCCGGACCGGCGCGTGAAAGTCTGTATATCATCGTTGAACTA
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SEQ ID NO: 1489 ACCTAGAAGCCGTGACCCAGGGCCATGGCGCTTACCTGATGAGTCAGGATGC
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SEQ ID NO: 1490 ACTCTGGTTCNATANACTTTTTTTTATTTTANGGTTGANGCNGACCCATNATAN
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SEQ ID NO: 1491 ACCAGAGACTCTCCTATCTCACGGTTGAGGCAGACCCAGGATAGAATAGAGA
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SEQ ID NO: 1492 ACCTGCATCAGCATTAGTGATCAACCTGTTAATCCAAGGNCCTTAGAAAAAC
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SEQ ID NO: 1493 ACAAGAATCGACCTCACTGTTACATGGAACTCTGACCAGGNCCTCTCTGC
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SEQ ID NO: 1494 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGGCGNGNTCAATCATATGAACTAGAT
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SEQ ID NO: 1495 ATGCTGATTCTGAAGAGATCAACAGACAAGTTACATATTTTATAACAGGAGG
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SEQ ID NO: 1496 ACGAAGAAAGCATTTCCTCAAGCAATGAGTCTCTTAATGAAAAAATAAAAGA
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SEQ ID NO: 1497 ACAACCAGGGCGAGAAGAAGAACGCCCTGGCCCAATATCAGGAGATGGAGA
AGAAAGTCAGCCTACTCAAGGACAATAGCTCTCTGGAATTTGACTCTGAGATGGTGGAGATGGCT
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SEQ ID NO: 1498 ACTTTTTTTTTTTTTTTTTTTTTTTTGGCCCTTANAAAAAGNAGATCTTTTACA
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AAAACGATATGAATNACNNAANTCTATNTTGCNNGGANCACATTTACTNNGGTTTCTCCTCTA

SEQ ID NO: 1499 ACTGGAGATGTATTTGATAACCAAGGTTTATAGGTAAATTTCCACCAGTATTAG
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SEQ ID NO: 1500 ACAAATCCAGTGTGCAGACCACAACCTCAAAACAAAAAGATCTATTTCTA
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SEQ ID NO: 1501 ACCTCAAAGTGACGGGGAGAATGGAACCAAGTTGGAAAACACTGCAGGATA
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SEQ ID NO: 1502 ACAGGAAAACGCTGCCGCGGTCCACAGTGTGATTCTGGATGACCACATTAG
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SEQ ID NO: 1503 ACGCGGTGATCCATGGGATTTCAATTAATGACCATGTGAAGATGTTTGAGT
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TATTGTTAACTCACTCATATTGAGATCATTTTTAGAGATACCAGGTTTATGTATCANGCACTAGAT
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AATTTGTTACTAAGGCAATCACGCACAGGTGACCGTATGTCTTATCTGATTTGTTTTAACTCCTTGGT
GCCAAACTCAGAAATGGGAATTTCACTGNCANNAATGANCATNCCCTGNNAAGAAAAAGNTA

SEQ ID NO: 1504 ACTCCCAATGGTGGATTTATTACTATTAAAGAAACCAGGGAAAAATATTAAT
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AATAAATGTTTGTAANNAGTGAATAAAAAATCCCTTTGCATTCTTCTGGACCTTNAATGGGAAG
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SEQ ID NO: 1505 ACAGTGGGCATGCAGCGCCTCGGGACGACACCCAGCGTTTATGGGGGTGCTG
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CTACCTANAAAAAGGTGCGGACCCCTGGAGCAGTCCAACCTNCAAACTTGAAGTGCAAAATNAAGCAGT
GGGACTTTNATTTTTTTTTTTTTTTTNTTTGT

SEQ ID NO: 1513 ACAGTTTTTATACTGAAGCTAGTATTGAGCTGCACTTGAATTCACATTCTTAG
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TCTTCTTTGAGCCTGTTGGCCTGCCAGGCCCTTCTTCTGCTTCACTTTGCCCCCTGGCAGCATAT
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TGGCTGACTGCTNANACCACAATTTACCCCAATNTNTTTCNNAATCNCCAAAGGANAGGGCCNG
 GNNGTNNAACTTTTGTCTTGGGCGATGTNCANANCNAANNAGGAATAAGNCAGAATGGNGGCC
 TTTTAGGACATNNGGGG

SEQ ID NO: 1514 ACAATGCCTGCATCCTGGAGTATAAACAGAGTGGCGAGAGCATTGACATCAT
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 CTAGATCNCGATAATAAANAACTCNAGGCCTTCANCATCCGNCCTGGAGGAGCTGCATGTCATTAG
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SEQ ID NO: 1515 ACAGACAAAGTGGGAGGTTTTATTCTTGGTCTCTTCCTCCTTGGATAAAGAC
 TTGATGATCTCCTCCTTCTTGGCCTGGAGGCGCTCTTACGGCGCTTGGCTGCTTCTTGGTCTTAG
 ACCTGCGGGCCTCANCCTGGTCAGCCAGGANCCTTTCGGGGCCTTGTCTGCCTTCAGCTTGTGGA
 TGTGTTCCATGANAATCCGCTTGTTTTGAACACATTCCCTTCACCTACAGGNACTGTAT

SEQ ID NO: 1516 ACGCGGGGGTTCCTTCAGTCCGCTGGTCCCGAGCACGAGCTGTGAGGGGATT
 CACTTGTGTGCGGAACCTCCTCGGAACCATGGCGTCCCTTTCCCTTGCACCTGTAAACATCTTTAAGG
 CAGGAGCTGATGAAGAGAGAGCAGAGACAGCTCGTCTGACTTCTTTATTGGTGCCATCGCCATTG
 GAGACTTGGTAAAGAGCACCTTGGGACCCAAAGGCATGGACAAAATCTTCTAAGCAGTGGACGA
 GATGCCCTCTCTTATGGTAACCAATGATGGTGCCACTATTNTAAAAAACATTGGTGTTGACAATCCA
 GCAGCTAAAGTTTTAGTTGATATTGTCAAGGGTCAAAGATGATGAAATTGGTGATNGCACCTACC
 TTTGTAANNNGTTNNANGCATAATNNTAANGGNNAGCANAATNTTNTTTGATAAAAGATTNTC
 CCAGACCATNTTANCGNGTGGAGNGAAGCCNAANGTTGNAAGAGAGGCTTTGTTGATTNTNAG
 TTGNTCATGGTTNNGATNAGGTNAATTCGTCNNGATTTAATGATATTGGTGONCA

SEQ ID NO: 1517 ACTTCAAGTTAAAGTGAATAACCACTTAAAAAATGTCCATGATGGAATATTC
 CCCTATCTCTAGAATTTTAAGTGCTTTGTAATGGGAACCTGCCTCTTTCCTGTTGTTGTTAATGAAAA
 TGTCAGAAACCAGTTATGTGAATGATCTCTCTGAATCCTAAGGGCTGGTCTCTGCTGAAGGTTGTA
 AGTGGTCGCTTACTTTGAGTGATCCTCCAACTTCATTTGATGCTAAATAGGAGATACCAGGTTGAA
 AGACCTTCTCCAAATGAGATCTAAGCCTTTCCATAAGGAATGTAGCTGGTTTCTCATTCCTGAAA
 GAAACAGTTAACTTTCAGAAAGATGGGCTTGTCTTCTTGCCAATGAGGTCTGAGGGTCC
 TCTGNTGGANTAAAAGGAGGGTTNAACTGTTGNTTGCNNGAATAAGGCNTTANTATGTTACCTCA
 GTGGCATTTATGAAAAGAGGGGACCAGAAGCCAAAGACTTAGTATATTTTTTCTTGTCCCTTC
 CNCCATANCCNCCNTNAGTCTTTGTTTTTTGTTTTNCAAAAACATT

SEQ ID NO: 1518 ACGCGGGGGCTGTGGTCTGAGCTAGAGGGTGAAGCTGGCGGAGCAGGAGGA
 TGGGCGAGCAGTCTGAATGCCAGAATGGATAACCGTTTGTACAGCATTTGTAATGCTTGTGTG
 CTTANCCCTCATTTCCACCATCTACATGGCANCCTCCATTGGCACAGACTTCTGGIATGAATATCGA
 AGTCCAGTTCAAGAAAATTCCAGTGATTTGAATAANAGCATCTGGGATGAATTCATTAGTGATGA
 GGCATATGAAAAGACTTATAATGATTCACTTTTTCNATACA

SEQ ID NO: 1519 ACATGCTCCATCTTCCAGGAGGACCACTCTCTGTGGCACCCCTGGACTACCTGC
 CCCCTGAAATGATTGAAGGTCGATGCATGATGAGAAGGTGGATCTCTGGAGCCTTGGAGTTCTTT
 GCTATGAATTTTTAGTTGGGAAGCCTCCTTTGAGGCAACACATAACCAAGAGACCTACAAAAGA
 ATATCACGGGTGAATTACATTCCCTGACTTTGTAAACAGAGGGAGCCAGGGACCTCATTTCAAGA
 CTGTTGAANCATAATCCCAGCCAGAGGCCAATGCTCAGAGAANTACCTNGGCCGCGACCAAGCTA
 AAGGCG

SEQ ID NO: 1520 ACGCGGGGATTATTGTAAATATTTGATCTTGAATCACTTGACAGTGTTTGT
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 TGTTATGGTGAAGTCTTTAGTCTTTTCATGTATTTTCTCATGATTTTTTCTCTTATGTAGTTTGA
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 TATTACCTTTGGNATNAAATCTTCATGGAGTGTCACTCAAATGNATACTTTGGGTNGGGTACTT
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SEQ ID NO: 1521 ACACAGGACCAATGCTGCCCATCCACATGGAATTTACAAACATTCTACAGCG
 CAAAAGGCTCCAGACTTTGATGTCACTGGATGATTCTGTGGAGAGGCTGTATAACATGCTCGTGG
 AGACGGGGGAGCTGGAGAATACTTACATCATTTACACCGCCGACCATGGTTACCATATTGGGCAG
 TTTGGACTGGTCAAGGGGAAATCCATGCCATATGACTTTGATATTCGTGTGCCTTTTTTATTCTGTG

GTCCAAGTGTAGAACCAGGATCAATAGTCCACAGATCGTTCTCAACATTGACTTGGCCCCACG
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TCCTAGTNGNAAGAGACAAATTTTACNTAAGANGGAAGAATCCAGCANGAATATCCAACAGTCA
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SEQ ID NO: 1522 ACTTTTCTTTCCTTAGACTTTGGCTTACTGGAAGATTTAATTAAGGTAGA
GGAGAAGTAAATTTGCTGTAATAATTTGCTGTAAATAAAACAAAGAGTTTATTTTATTAGATAAA
GAATGTGAAGTAAGCATGAAGAGACAGGCTTTGGGAGAAATACCAGAAAGGGATTTTCAAAGA
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CCCCACTTGTGTTGGGCTCCGAACTCTTACCAACATCAATTTTATTCTTGGGATAGAAAAATA
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GGCTCATTTTCATTGAAAACACTGACTATGATAGACAGCTCCTGATTGGCAAAAGTTCGATGG
TATATTCAGAATTAATTTTGCCTGCNCCCTAAACACTGACACATTTAACTTAAANGGTTTCCATG
GAGAANAGTGGTAAAAGCTGTATTAGCCAAAATTGGCATCC

SEQ ID NO: 1523 GCCCTTNNCNGNGGCCGNNCNGNCGGGNCGCGGGGAGGGGCANGTGTNGCC
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GACTTCGGAGCACGCTCTTTGATTACATCGGCAGCCACCCGTGGGAACTGTTACAACAGCTGCA
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NCGACCA

SEQ ID NO: 1524 ACTTTTTTTTTTTTTTTTTTTTTTTTGGCTTTGAAATTTANAAACAAATTTTA
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TCCTTCAACAATTTGAGCAAGATAGAATGCCTAANAACAACATAGATGGACTTGCANAGGATGG
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ACATTAAAGTTGAACCTTTGGCACTAGGAATCAGGGCGTTTTGTCNCATAGCATTAACGCATATTA
AAAAATTGTGTATGTGTCAAAGGGATNGGAACCACCATTCAAGCAATGTTGTCAACTNNGGC
AANAAAATGTTCTACTGGNATGGTTCTTNTTTGGGCTAATTACCTGNATACNCTGGGGGNCAACTT
TTGAAAATNAANAAAAGGAGCCTACNCTTCTTTTATTTTNTTTTAAA

SEQ ID NO: 1525 ACCTACATCAGATCTAACCTTGATCCCAGCAATGTGGATTCCCTCTTCTACGC
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TCTGGCAGCTGTCAAGTGGAGTCTATCTGTTACCCAGATCTACCATGCAGTTGCAGCTCTAAGTGG
CTTTGGCCTTCCCTTGGCATCCCAAGAAGCACTCAGTCCCTTACTGCTCGTCTCAGCAAGGAGGA
GACTGTGCTGGCAACAGTCCAGGCTCTGCAGACAGCATCCCACTGTCCCAGCAGGCTGACCTGA
GGAGCATCGTGGAGGAGATTGAGGACCTTGTGCTCGCCTGGATGAACTCGGGGGCGTGATCTC
CAGTTTGAAGAAGGACTGGAAACAACAGCGTTATTTGTGGCTGCCACCTACAAGCTCATGGATCA
TGTGGGGACTGAGCCATCCATTAAGGAGGATCAGGTCATCCANCTGATGAACGCCGATCTTCAGCA
AGAAGAACTTTGAGTCCNTTCCGAACCTTTANCGTGGCCTCTGCAACTG

SEQ ID NO: 1526 ACGAAAAACCTGAAATCACATGCCTATGTAAGGAAAGTGCTATTCACCAGT
AAACCCAAAAAAGCAAATGGATAATGCTGGCCATTTTGCTTCTGACATTTCTTGGGAATCTG
CAAGAACCTCCCTTTCCCTTCCCCCAATAAGACCATTAAAGTGTGTGTTAAACAACCTACAGAATA
CTAAATAAAAAAGTTTGGCCAAAACCAACCATGAAGCTGCAAAGGTGCTTGTCTTACTGTTTCAA
TTTTGCAACTCTGTAGTGTCTCACTTTTAAAGGAACAGCTTGATTGCAAAGGAGAAAAATAGATAA
GCAATGAAGTTATCTCAACTTCTTAAAGGCTTATGACTTCTAAAAAGTGAATCTATCAGCATTC
ACATCAGATTTAAAGCATCAAATGCCTGTGAAACAGCAAAGATGGTAAGCAAAGCAAAGTGT
TTCCGTCTAAAGTCAAAATTGAACACTTACCTTCTCATAGTACC

SEQ ID NO: 1527 ACAGACTTGTTTTGAGTGTGAGTGGCAGGGACAAAATAAGGGAATGTTAT
TTTTAAGAAAAATTCATTTTCATTTGTCTCCTTCTTCTGTGAAAGTCTCATACTGAGAAATT
TGTATATTTTATATTAATCACTTACTATTGATTTTGTGTTGATTTCAAAGGTGGATTCCACAG
ATAAAATCTTGGCTATTGCCCCAAAACATAGTAAAGGGTCACGTGTGACTTTTATAATAGGAAGA
AAATTTGCCTTTGTGAGTGCACATGTCCACATTTATCCCTCCTTCCCTCAAACCTAGAGAGG
GGCATTAAAGAATTGTTGATGTATATGCAATGTCTGTTAAGCATGCACTATGTATTTATCCTCATT

TATTGGGTCTGGGACTGAAGTTTTANCCAGCATGGACCTAACCTACTTTTTGGGATAAAAATTCTC
TGTTTTGTTACAGGCAAATCTGGTATGGCGTGAATGCCATGGGTCATTCTGAATATATTTTTTCT
GGAATTTTATCATTACCCCGANGGTTGCAATACCGTGCCTT

SEQ ID NO: 1528 ACACTTTGAGACGCAGGAAGCAGCTGAAAGAGCTATTGAAAAATGAATGG
AATGCTCCTAAATGATCGCAAAGTATTTGTTGGACGATTTAAGTCTCGTAAAGAACGAGAAGCTG
AACTTGGAGCTAGGGCAAAGAATTCACCAATGTTTACATCAAGAATTTGGAGAAGACATGGAT
GATGAGCGCCTTAAGGATCTCTTTGGCAAGTTTGGGCCTGCCTTAAGTGTGAAAGTAATGACTGAT
GAAAGTGGAAAATCCAAAGGATTGGATTGTAAAGCTTTGAAAGGCATGAAGATGCACAGAAAAGC
TGTGGATGAGATGAACGGAAAGGAGCTCAATGGAAAACAAAATTTATGTTGGTTCGAGCTCANAAAA
AGGTGGAACGGCAGACGGAACTTAAGCGCAAATTTGAACAGATGAAACAAGATAGGATCACCAG
ATACCAGGGTGTTAATCTTTATGTGAAAAATCTTGATGATGGTATTGATGATGAACGTCINCGGAA
AAGAGTTTTNTCCNTTGGTACC

SEQ ID NO: 1529 ACGCGGGGAGTCAGCCTGGCTCCTGTTGAATAGTCTACCCCCCTTGCACTCTA
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AACAAAGGTGAACGCCCAGCTGCAGCCATGAAGATCTGTAGCCTCACCTGCTCTCTTCTCTCTAC
TGGCTGCTCAGGTGCTCCTGGTGGAGGGGAAAAAAGTGAAGAATGGACTTTCACAGCAAAGT
GGTCTCAGAACAAAAAGGACACTCTGGGCAACACCCAGATTAAAGCAGAAAAGCAGGCCCGGGAAC
AAAGGCAAGTTTGTACCAAAGACCAAGCCAAGTGCAGATGGGCTGCTACTGAGCAGGAGGAGG
GCATCTCTCTCAAGGTTGAGTGCCTCAATTGGACCATGAATTTCTGTGTCTTTGCTGGCAATCC
AACCTCATGCCTAAAGCTCAAGGATGAAAAGAGTCTATTGGAAACAAGTTGCCCCGAATCTGCGC
TCACAGAAAAGACATTTTGTAGATTTTCCAAGACAGCTTGTGAAAACCA

SEQ ID NO: 1530 ACGCGGGACAGAGAGCATCTCCGTGGCCAAAATCAGTGTCTATGGGACACTC
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AAGTCTGCCCTCATCTGAGAATACTGTCTTTCCATATGGCTAAGTGTGGCCCCACCACCTCTCT
GCCCTCCCGGGACATTGATTGGTCTGTCTTGGGCAGGTCTAGTGAGCTGTANAATTGAATCAATG
TGAATCAGGGAACTGGGGAAGGCTGACCTCCTCTTTGGTGTGCGGTAAGATAACCGACAGGGC
TGGTGAAGAAGTCCAGATGGCAGGATATTTGGTTTCAGAGTAAGGACTAGGTGCACCACCATGAT
TGACTATCGATCAAAATGGTTGGAACCTAAAAATTTTAAATGAAAGGA

SEQ ID NO: 1531 ACAGAGTATGTAGTGGGCATCTGTTGAATGAATGCTTTTCCAGTAGCAGTGT
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TGAGTGAGACCCAGGTGTTCTTCTCCACCCTAGTGGTCCCCTGGGCAGGTCTTTTTTTTTTTGTA
ACACTCACCATTCTGTTCTGTAGTCAATCATGATTGACTTGTCTGTGAACTTGCAGGAACTGTTTC
ATAGTTTCATTAGCACAGAGTAAACATGTTTGCATGCAAGGTTATTTTGCATCTGCATTTAAGTG
ATAATGTTGAATCAATGAAAAGTTTGTATTAAGCAGTAGTTGTAGATATGCTAAGTTTTCAAATT
ACTAATATCAAGTGGAGATGTTTTACTTTTAAAGGGTATTGCNTTTGNGATAGCATAAATAGTGGTT
TTCCTTTTTGTNATGTAAATTAATTTGCTNGCAACTTTTGTATTCCCTTAGACTNGGGGAAGCTT
ATTGCCTTACAAGTNCCTTCCCGGGCGGGCNGTTCAAAAGGGC

SEQ ID NO: 1532 ACTTGATTTTTACAGATGGATTATCTGGGGTAATTTTCTTCAAAGGGAGTTT
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TTATAGCTCAGTGTGCCCTTGAATCCATACAGTTTCTTAAAAAGACAATAAAATCTTATTAATAAAG
TTAATGTAACCTCTAAGTTCTAGAAAAATGCTGATTCTGTCTGCCCCATTCAATTGGGGGCTACTAAT
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TTGATGACAATTACTTTATGGGTGTGATGCACCGATGGTAGCCAAGGAATNTGTTGGGGAAGNTC
GGAAAGAAACCTTTCTTTCTTTTATTTCAGTTAAAGTAAACCTTTATCCTGGATGTTTGAATNAA
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SEQ ID NO: 1533 ACATTTCTTTCGTGTTCAAACCACGGAGTTCACAACACAGCAGCACACACAG
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GCTGGGCTAGAACCCTGGGGTAGAGCTGTGGATTCAATTTCTCAGACAGAAGATCTTGAACCTTTC
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ATCCACTACCAACAACCTTCTTGACAAGGTCCAGAGCTTTCTCTGAGACTTCTGCCAGACTTCAGG
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AGGTGGATACCCACTAAGGCAGATAAAAAAGAATAAATCCTAAACTCCAGCAGTCCACAGCAGCG
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GGGTCTCATGAGAGAAGTCTCTCCAAAAATCTTGGAGTGNCCCCAAATC

SEQ ID NO: 1534 ACTTCTATTTATCTTTGATTTCAGTCTTGGCAATTGTTAAAAAAAATCTA
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TCTTTTGTTAACATATTTGTTATGCCTTATTCTAAAATTGAGCCTCAAAGTGAATGCCTTTGAAGA
CAGATGCTTCTATAGAGGTTCTTTGACCTAAATAGTTTCAGCATTTGTATTTTATTCTGGTATTTAA
TCAGATTCTAATCATAGCCCCGTAAGAAGGAATGTTACTTTAATATTGGACTTTGCTCATGTGCTC
GTGTCCGCATTTTTTTTTTTCTTAAAAATCATAGCCATATGGTAAATTTCTATTTTGTATGGTCTC
TTTTATTGATGGGCATGCAGGTGGGTGTTACTTGGAAATGGCCAATTTTATTTAAATATTTCTGG
AAGAAAAAAN

SEQ ID NO: 1535 ACGCGGGGCTTTCTAACTCCGCTGCCGCCATGGCTCCTGTGAAAAAGCTTGT
GGTGAAGGGGGGCAAAAAAAGAAGCAAGTTCTGAAGTTCACTCTTGATTGCACCCACCCTGTAG
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CATCCGAGGTGCCTTTCTCCAAAAGGTATTTGAAATATCTACCAAAAAATATTTGAAGAAGAATA
ATCTACGTGACTGGTTGCGCGTAGTTGCTAACAGCAAGAGAGTTACGAATTACCGTTNCTTCAAGA
TTAACCAGGACGAAGAANAGGAGGAAGACGAGATTAAATTTCAATTTATCTGGAAAAATTTTGT
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SEQ ID NO: 1536 ACAGATGTCTGCGTGTTCAGCCCCAAGAAGATCTAGAGACCATGCAAGCAT
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GACTGGTGTCTTCTGGCTAATGGAACACTTAATGCATCCATTCTTAATAGCCTTTATAATGAAAA
TTTGGTTAAAGAAGGAGTTTCAGCAGCTTTTGTGTGAAGCTCTTAAATCATGGATAAATGAAAA
AGGTATCAATGCAGTAGCTGCAAGTCTTCGGAAAAGTCAGCATGGATAACAGACTGATGGAACCTC
TTCCTGCCAATAAGCAAAGTGTGAACACTTCACAAAATATTTACTGAGGCAGGCTTGAAAGAG
CTTTCAGAATATGTTTCGGAATCAGCAACCATCGGAGCTCGTAAGGAGCTCCAGAAAGACTTCAAG
AACAAATGTCCCGNGGGNGATCCATTTANGGTATTAATTTTATATGTCAGG

SEQ ID NO: 1537 ACGGGGGCTTTTTCTCTCTTCAGCGTGGGGCGCCCACAATTTGCGCGCTCTC
TTTCTGCTGCTCCCCAGCTCTCGGATACAGCCGACACCATGGGTTTCGGAGACCTGAAAAAGCCCTG
CCGGCCTCCAGGTGCTCAACGATTACCTGGCGGACAAGAGCTACATCGAGGGGTATGTGCCATCA
CAAGCAGATGTGGCAGTATTTGAAGCCGTGTCAGCCCCACGCGCTGCCGACTTGTGTCTATGCCCTA
CGTTGGTATAATCACATCAAGTCTTACGAAAAGGAAAAGGCCAGCCTGCCAGGAGTGAAGAAAGC
TTTGGGCAAAATATGGTCTGCGGATGTGGAAGACACTACAGGAAGTGGAGCTACAGATAGTAAAG
ATGATGATGACATTGACCTCTTGGATCTGATGATGAGGAGGAAAGTGAAGAAGCAAAGAGCTAA
GGGAAGAACGTCTTTGCACAATATGAATCAAAGAAAGCCAAAAAACCTGCCCTTGTGCCAAGTC
TTTCATCTTACTAGATGTGAAACCTTGGGATGATGAGACAGATTGCGGA

SEQ ID NO: 1538 ACGCGGGTGAGGGGATTGATTTGACGCACAATCCTGAGTTACACCACCTGTGA
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TACGATGTTGACTTCACCCACCCCTCCGGCGAATCAACATGGTAGAAGAGCTTGAGAAAGCCCT
GGGGATGAAGCTGCCAGAAACGAACCTCTTTGAAACTGAAGAACTCGCAAAATCTTGATGATA
TCTGTGTGGCAAAAAGCTGTTGAATGCCCTCCACCTCGGACCACAGCCAGGCTCCTTGACAAGCTT
GTTGGGGAAGTTCTTGAAGTNACTNGCATTAACTCTACATTCTGTGATCCCCCAGATATTGA
NCCCTTTGGCTTAATGGNCCCGCTCTAAANAGGGGTCTGACTTGGNCGCTTGANCTGTTTGTNA
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SEQ ID NO: 1539 ACAAACACTGAACGCCCTGATACACCTACAAACACGCCAAATGCACCTGGAA
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GAGATCCATTAGTGTGTTGCAACTGTAGGAAGCAACAGAGTTACCTTGTATGAATGTCATTACAAG
GAGAAATCCGGTTGTTGCAATCTTACGTGGATGCTGATGCTGATGAAAACCTTTACACTTGTGCAT
GGACCTATGATAGCAATACGAGCCATCCTCTGCTGGCTGTAGCTGGATCTAGAGGCATAATTAGG
ATAATAAATCCTATAACAATGCAGTGTATAAGCACTATGTTGGCCATGGAAATGCTATCAATGA
GCTGAAATTCATCCAAGAGATCCAATCTTCTTGTGTCAGTAAAGTAAAGATCATGCTTTACGATT
ATGGAATATCCAGACNGACACTCTGGTGGCAATATTTGGAGGCGTANAAAG

SEQ ID NO: 1540 ACATATTTTAAAAATAGAATAAAATGTGTTAAACATAAAAATTTTAAAAAGTAGTAG
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TATATAAATGACATTTCAAGGACTTTAAGTATGAAGATAATGGGAATTTTATTGTTTTTGTCTTTTAA
AATGAGAGCATTTTTATTGATAATTTTTTTTAAATTTTTTAACTAATTCATATTTTAAAG
TAATCAGTTTTTCAAATCTTGATTTTTGATATCATTATCTAAGGAGNTATCCTNAAAGGCACAAA
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SEQ ID NO: 1541 ACTTTNTTTTTTTTTTTTTTTTTTTTTTANANATGAGGTCTCGCTATGTTGCC
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CAGGACATTATNTTAAAGGTATTATCCAGGAAACAGATAAGGTCATTCAAAAACACACGGCTT
TTTTCTTTAGCTCAGTGTTAACAATGAAAGTAGATTCCACTATTGAAGCACAAGTTGCAAATTGG
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AAAGAAAACACTGNGGACATTTGGGGNCATGAACTTTTAAGTGGCAACAGCCCAAACAGGGCAA
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SEQ ID NO: 1542 ACTTTTTTTTTTTTTTTTTTTTTTTTCTTCNATTCTTCTCAAAGGCATTTGA
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GNGNGGGCTTTNTACATGTAACCTGCCAGGCTGAAGGCTTACACCCTCNTGTTCTACAACACAGAT
CACTAATGATGATAACATGAGTTAAATGGGATTTCTTGCCCTTCTGTGTGGCTTTTGGCTTCTAGGT
TCTATGACCAAACATTTGACATATTTGAAGTCTGTATGCAGNCATTGTGTGATAAATCTACTTTAC
AGCTTTGCTTCTACCTGCAGCTTACATGATAACCATGCTGGGAAGTGCTACATATGCTTCATACAA
TNTGTTGCCCATCTGATAATAAAAAATACAAAGGNGCTCTTTAANCTAAACCATAAACCTTATTAG
AAAATTCTAGTTAAGTGGNTTGTTTTTCCNCATCNNTGTAAATCCCTT

SEQ ID NO: 1543 ACTATTTTGCAGGGTTTGCACAGGCCCGTAAGTGTCTACTACTTTGATATAA
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CTTTTACAAGCGCAAGGTGCAAAAATATATACAATAGTCTCATTGATGACTGTAAAGTGAATTAAC
ATTTGGTGATTATGCCTAGCTTTTGACTAAATATAAAGATCATAGCTCCCCCTCACTTCTGTCTTAAC
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GCCTCTGTGAGTTCATCTGATGATTGAGCAGTAGCATTTGCCTTTTGGGTTTTTGGTTGTATTAT
AGAAGAGATGACTTCTGCTGATTTTGCTTTANAATGGTTACCTTAGAAGAATTTGGGTGGCTCATG
TCGAATTTCACTTNTGCAATAACTTTTCTCATAGCTTTATAAANATGGGTTCAAGNGGTAT
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SEQ ID NO: 1544 ACACACCTAGTTCATAATCCTCATAATTTATCAACAAACACAAAAAAGTGTCT
TACTTGAGAGTGAGTGTGTGTGTGCGTGTGCACGTGCACACATGTGCACGTTTGTATGTATGGA
AATAAACTTATAAATGGGGACGTATTGGAGAAAGGAAATACATAGACCTTCAAACTTGGAGCAAATA
GCAGTGATGTTTTAGGAACTGAAATGTACACTTAAAGTCTTCAGCCAGCTACTTCCCTATTTTGT
TGGGGAGAAGAGGGCCTGATTAGAACTGTTCTGGTTGTGTTTGGCGGGAGGGGAATAATTTTGT
CAGTCCTTCTTAGTGACCAAACCTTTAATTTTAAAGAATAATATATTGACTTACTGAACTGAAGCATT
CTGAGTTGAAAGGAGCTCCAGAGGAGTGGAGTTCTGTGTTGCTCACATGTTAAAACTTGCTCACC
TTCAGAGCAGAGGGAATCCTATCTTCANATATCCGNCCATTTTCATCTCTTAATTGGTAGTCAAAA
GTATTGACTTGAGAAGTGTGCTCTGGTATTCTGGGGTCTGAAGCT

SEQ ID NO: 1545 ACATCACTGTGTCCCTAAAATAACCCACCCAGTGAAAACTCCAGCCAGT
GAACTGGAGGGTGTCTTTTGGCCACGGTAAACTGAGGGATTATGATGAAGCTGAAGTTCAAGGA
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CCAAAGTTGCCCTCAATGATCTTCAGCCGTCTTCTGCCACAGGCTGATGGAATTCAGAATTTCCGA
CAGGCTGTTCTTGGATCTCCGATAAGCCCGGAAATGGAGTTCAAGACACTGAACATCAGCAATTTGA
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TCCATGGTCTTGGCTGGTTCTGATGGCTTTAATTCTGTCTCTGGATGTGATGGGTATAAGGGATG
CGATTAACCTCTGTCTTGGGGTGACTTGTGCCAATCACATTCAAGCAATGGTGGGTTTCCATAAG
CATGGACAGGGACCACTTTCACCTACATAAGCCAGGGTTCACATA

SEQ ID NO: 1546 ACACTGAGCCCAAAAAGGCCCGTAGCCAACACTATGACTTGGTTTTAAATGG
CAATGAAATAGGAGGTGGTTCAATTCGAATTCACAATGCAGAGCTGCAGCGTTATATCCTGGCAA

CCTTACTAAAGGAGGATGTGAAAATGCTCTCCCATCTGCTCCAGGCTTTAGATTATGGGGCACCCC
CTCATGGAGGAATTGCCTTAGGGTTAGACAGACTGATATGCCTTGCTCACTGGATCTCCAAGCATCA
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TCCCTCCTGAGGAAGTGAAGCCCTATCATATCCAAGTCTCCAAGCCAACAGACTCCAAAAGCAGAN
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SEQ ID NO: 1547 ACAGTTTGCTGCAAATGATAATTTAATTTGGATAATGCTTTAAATCATTGATT
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GAACTCTTCTCAAAAACAGAAGAAAGTCATGACCATTGTTGGGAAAGTGTTTTACATTTCCAATG
AAATCTATTCCATTGATCTGTTTGGATGATTGCTTCAACCTATTTGGCTCTAGCCCATAAATTGTA
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GAAAGGTGGTTTTTCATTCACTCTAATAATTGNGCAGGGATAAGC

SEQ ID NO: 1548 ACAAAATACAACATAAAAAGCAAGGAACAATTAATGCCATGCAAGATTTTAA
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TGCTGGTATAATGGTATAAATCAGATCTTCAAATCTATGGGAACGAGTCATCTTCTGTCTCTAT
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SEQ ID NO: 1549 GGACAAAGTTGTATGACAGGGGCATATTCTTTGCTTCCAAGATTTGGGTTGGGG
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SEQ ID NO: 1550 ACCAATAAATGATGTGTTAGCTGAAGATAAGATTTTGGAAGGAACAGAAACA
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GACCAAGGTGGCAGCTACGCAAAGCCTCTTGGGAAGAACGGGACCGAATGATACAAGTTTATTT
CCAAAAAGAGGTGCGTAAAAATTTTGACACCAATAATTTTCAAGGAAGAAAATCTTAGGACTATGT
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CGTTCAACAAGATACTTTGGTGGAATGGTGTGGTATTTTGGAATAATAAAAAANNATGATGGNT
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SEQ ID NO: 1551 ACCTTCGCAGTGATAGGAGATGGAGAGACTGTGGAGTTTGATGTTGTTGAAGG
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CAAAATTACAGAATAGTGAGAGTGGGGAAAAGAACGAGGGATCGGAGAGTGCTCCCGAAGGCC
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GGGCCGTTCGACCAAGTATTCCAAACCTCTGTGTCAGGGAGAAGTGATGGAGGGTGTGACAACC
AGGGTGCANGAGAACAANGTAGACCAAGTGAGGCAGAATATGTATCGGGGATATAAACCACGATT
CCGCGAGGGGCCCTCCTCGCCAAAGACAGCCTANAGAAGGACGGCAATTAAGAAAAGATAAAGAAA
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SEQ ID NO: 1552 ACTCAAAGACGAATCATGAAAAAGAAAAAACTTTATTTCAAACAGGTTTCAG
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ACTCAAAAAACAAAACAAAATAAAACAAAACAAAAAACAGAACTGCATGATGTATAATTTTGACA
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SEQ ID NO: 1553 ACTTTTTTTTTTTTTTTTTTTTTTTAGTAGTCTATACATTTATTGAGTAAAAA
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CCTTTAATTGTAAGCGGGCATCGCACAGCTGGTGTGAGTCAATTAACCAAGGCAGGGAGGGGA
CTCAATGTTTTACAAGCAGAGGGAAAACCAAAGTAGGCAGAGAACTTTCAAGAGAGGAGAGGGC
CAGAACACTGAGAGAAAAAGCTGCAGCANAGGCCCTGCTGGANAACAGTGGTCCGATCTGCTGGC
TCACTTGGGGAACACAGTGACCACTTCATAACCCCTCANGTGGTGTGACTCGCTCCCGGCATGCTT
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SEQ ID NO: 1554 ACACCTGAAGGCGAGGTTAATTAATCCTGTTGTGGAGTTTGAGGGCCGGA
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SEQ ID NO: 1555 ACGCGGGGGCGTCTTGTCTTGCCTGGTGTGCGTGGTTAGTTTCTGCGACTTG
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CAAAGCCACAGCTGTTATGCCAGATGGTCAGTTTAAAGATATCAGCCTGTCTGACTACAAAGGAA
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AGTGATAGGGCAGAGAATTTAAGAAACTCAACTGCCAAGTGATTGGTGCTTNTGTGGATTCTCA
CTTCTGTCATCTGGCATGGGTCAATACACCTAANNAACAAGGAGGACTGNGACCCATGAACATT
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NGCATTTCTGTTACAGGTGCCTTTTTATCATTTGATNATAAGGNNATTCTTTCGGCNGATNACTTTNAAT
GAACTNCCTNTTGGCCNGTCTNTNGGATGATACT

SEQ ID NO: 1556 ACTTTTTAAAAGTAAAAATCAGATGATTCTTTTGGGGAGGAGGATGTGCG
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ATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGAGCCGTATCAATGATGCTTTC
CGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATACAGCCAACACTTGGACCTCCTAACAGCC
CCCTGTTTCCATATGGCTGATTGTTTTGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCTC
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ATGCCTCCATCGATATTAGCAAAGGAGAAAAATAATCCAGGATTCCAAAAACTGATGATGTTCAA
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SEQ ID NO: 1557 ACTTTGGCCTCTCTGGGATAGAAGTTATTCAGCAGGCACACAACAGAGGCAG
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TCAGGCTCCAGTCTGCTGATGGTGAGAGTGAAGTCTGTCCAGACCCACTGCCACTGAACCTGTCT
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GCANCTCTTTCCCGCTACCT

SEQ ID NO: 1558 ACGCGGGAGTTGATGATTTCTTTTAAAGAAATTAGTTTATTTAAAGCAAGA
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CCNAGTTGATTTAATATAATTTATTGGCATTTTTTCNGAANAGGNTTAAGTCNNATTAAINGATT
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SEQ ID NO: 1559 ACGCGGGATCACCTACCACTGCAAGAACAGCATTGCATACATGGATGAGGAG
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GACAAATCATTGAATACAAAACAAATAAGCCATCACGCCTGCCCTTCCTTGATATTGCACCTTTGGA
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SEQ ID NO: 1560 ACCCACCACCTTCTTCTCTACATATCCCTTCCAGATGGNCATCCAGACTCAG
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SEQ ID NO: 1561 ACTTTTTTTTTTTTTTTTTTTTTTTTTTGGGGTCCAAAAATGGNGATTATTTATGGC
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GTTGGGACANAAGCTGGCCAGCGAGCCCCTGGGGGCTGAAGGCAGCTGCTATNAGCAGCAGCC
ACAGAAGTGCTGCGGAGACCTTCATGTTGGAGGCTGAAGGTGTGAGCTTTGGCGTGAGANGTGGT
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SEQ ID NO: 1562 ACACAGATTGGCTTCATATCAATTAAGAATGAGATACTTGACTGGATTTTTG
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AGCAGTAGAAAGAGAACATAAGGGAATAGAGGTTAATTTTACCCANAAGCAGGGATAGAGAAAA
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SEQ ID NO: 1563 ACAAGCCTCACCAAGGGCAACCCAGAAAAGTGAATGAGTTGTCTTCTCCA
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ACCAGTATTTGCAATAAGAATTTAGCATTTTCAATTCGTTTTGGTTGATTTACTCCAATTTTTTAT
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SEQ ID NO: 1564 ACCTATTATATAGAGGGATAGCTGAATAAAGTCTGTCTCAAAACCAGTGTTA
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SEQ ID NO: 1565 ACTGCAGAGGTATGTGCAGAAACACCCACCCATTTAAGCTTTCAATAAATAC
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 CCAAGCTCTTTAGACTTCAGCACTTCTCGCTCTTCAAGCCTCAGCACCTTTTTTGCAGCAATAATGG
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 AACTCTATTTATTCCCACATCAATGACTGCTGCTCCTTCTTGATCATATCTGGCTGTGATCAAGAT
 TTGGGAATACCTGCAGCAGATATTTACAATATCTGCAAGAATTGTATGTTTCTTCCAAGTCTCTTT
 GGGAGATATCGATGAGATATTGTAACAAGTGGGATTACCNCT

SEQ ID NO: 1566 ACTCGTCAATGGGCTCGGTTCATATATACCACCTCGAAGCCCCGTTTCCGCACT
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 ATCAACTCATCACAGCTGTCCATGATGAACACACGNGGACATANAGTTTGATGTTGGTCTTTTTCT
 TTCTTGGTCTCAAAAAGGGCAAAGGGNANCCGACCAAGGAATAAA

SEQ ID NO: 1567 ACAATGACCAAGATGCGACCAGGATCAGAGGTTCCCTGGGGGAAGACCCACCC
 TACGAAGTTGGAAATGAGACCATCAGATGTGATAAGAACTCTTCTAGATGTCAACATAACCAACC
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 TTTAATTTTCAAAGAGGCTCTGTATAGCAGTTTTTGTCTATTTTAACATTGTAGTCATTTGTACCT

SEQ ID NO: 1568 ACCGGATTCTCTCTTTAACCCCTCCCCTTCGTGTTTCCCCCAATGTTTAAATGT
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 TCAAGGATGGTTTTTGGGGACTANGANGGCTCANNTGGGTGGGAGAAANATCCCTGCANAAACCC
 ACCAACCNAGAACCGTNGGTTNCCT

SEQ ID NO: 1569 ACAATCATATTCTCAGGTTTCATGACAGAACTAAAACTCTAGGAACTCAT
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 CCCATCAGGTTTCATGCCTACTGAAGTCACAGAAATCCACATTTTGAATGGTTTGGACTTGAACCT
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SEQ ID NO: 1570 ACCGTTGTGTGTTTTCTGCAATGTGGAGTTGACTTAGCTTGGCATTTTAGATTT
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SEQ ID NO: 1571 ACCTACATCAGATCTAACCTTGATCCCAGCAATGTGGATTCCCTCTTCTACGC
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SEQ ID NO: 1572 ACACCTTTTGTTACAGTTACATATATGAATAGTTAGCAGAGGAGAACTCCTCC
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SEQ ID NO: 1573 CGCCCTTAGCGTGGTGGGCGGAGGTAAGTGGCAACAGCTGATGCGTAAAA
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SEQ ID NO: 1574 ACCCAGTAAAAACCAGAATGACCCATTGCCAGGACGCATCAAAGTTGACTTT
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CTNCTCAAAGAAAATCATGCTTTTAGGATTAAAAAACTTTCCCAAGGGGNCNCGGTTTCTTCTC
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CACTAGCCCCAAATNAAGGGCCAAANAGAANGGGAGGCTGGGGGATNGGC

SEQ ID NO: 1575 ACTTTATTTTTTTTTTTTTTTTTTTTTTGGCAGTTTTTACATTTATTTAAACAGAA
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CTTCCGGAAGCCNCTGGGCANCATGTGCTTTGTTTTTTTGTGCTCCATAACCAATGTTGGGCATC
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SEQ ID NO: 1576 ACATTCATAGGGTTTTTCTTAGAGTGGGTCTTTTCATGTATACGAACATACT
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TTGAATGGGAAATAAAAGTTTTTCCACATTCCTTACAAGCATAGGGTTTCTCTCCAGTGTGATCCCT
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SEQ ID NO: 1577 ACATAAAGTAAGTGTATATGTGCACAAGCATATTGCATTTTTTTTTTTTTTAA
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NCNTTTTNCCTATNTNNGGCCAN

SEQ ID NO: 1578 ACTTGATTGGTCATTTGAAAACACTGCAACAGTGAACCTTTGCATCTCAAGAA
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AAATATGACTTTCCTTTTTGGTAATATTTTTGTGATCTTTGATGGTTCTTAACCTANGAAGTGTAAT
GTATGCATTATATAANTGTTTTGTATTTTGAATCTTGGANAACCTAANTTTATTATATTTTCAANAAT
AGCCTTTGTTTTTAAAAAAGGCCNTTGGCATAACCTTTTTGNNATANTGNAAAAATTGACCTA
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SEQ ID NO: 1585 ACAAGACCAGCAAAGCCAGCTTCTCGGCTGTGAGCTCTGAGAACCTGGGGA
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TTATAATCTTCGACAGAGGTACATCCAGCTTATGCTTTGTTTTGGTTTGGGTGGTTCAAATGGAC
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TAAAGCTCAAAGTCAACGTCTNTCCGCTNCATATCTGCTACAGTNAGGACGGGNATTNACAGCAA
TTCTCAACCATCTTGTCGGTGNCAACTGTTGACCAACTTTGGAA

SEQ ID NO: 1586 ACCACCAAGAATCTTCAAATAAGCCAGCTGTCAACCAAGTCACTGCAG
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CCACCATAAGCCCAAGGCGACTGCCAAAGCAGCTCTATCTCTGCCTGCCAAGCAGGCTCCTCAG
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CACTGACTGCCCAGAATGGAAGCACTTANAACAGTGAGGGGGAGGAAGAAAAAA

SEQ ID NO: 1587 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAANAAGGTCCAAATCAATAGGTCT
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SEQ ID NO: 1588 ACTTTTTTTTTTTTTTTTTTTTTTTTAAAAATCTGAGGAATAAATGCAAGTTTTTAA
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SEQ ID NO: 1589 ACAGTTTCCCAGCCACAGTCATTGCTTCATTCTTGTCTGATCAGATGGTAG
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SEQ ID NO: 1590 ACTACGACATTTCTGCCAAAAGTAACTACAACCTTTGAAAAGCCCTTCTCTGG
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TGCTCTCCCGGATGAGGATGATGACCTGTGAGAATGAAGCTGGAGCCAGCGTCAGAAGTCTAGT
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CAGTTTAAAAATAAATTCATTGTTTGGACCTGCATATTTAGCTGTTTTGGAACGCAATTGATTNCT
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GTTACTGGNCATTTCCCATTTCTTTTTCGTTTAGA

SEQ ID NO: 1591 ACAGTTCACTCTGCAAAAAATACTCCTTCTCAGCATTACATTCCATTTCAGCA
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CAAGAGATGAGTCTAGGGGCCGTTCTCGTTTTATCCTGATGGTGGAGATCAGGAACTGCAAAG
ACTGGGAAGTTCTTAAAAAGGTTACAGATGAAGAGTCTAGAGTATTCCTGCTTGATAGGGGTAA
TACCAGGGATAAAGAGGCTTCAAAAAGAGAAAGGATCAGAGAAAGGGAGGGCAGAGGGAGAATG
GGAAGATCAGGAAGCTTTAGATTACTTCAGTGATAAAGAGTCTGGAAAAACAAAAAGTTTAATGA
TTCANAAGGGGATGACACCAGAGGAGACAGANGATTATAGACAGTTTCAGGAAGTCAGTCCTCGC
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SEQ ID NO: 1592 ACGCTTGATCAGATTTCTGATGCAGATAATATCCCAGGACTTTTGTTCTCAA
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CTACAAGCAGAAAAATGTTTTAGAGAGCTCTTGAGAAAGATACCGAAGTTGCAGAATATCATT
CCAACCTGGATTAACTACTGGTTCATGGGTGAAGAGACAAGAAAAGATNAAACAAAGGCTCTTA
CCCACCTTCTGAAGGCTGCAAGACTGGATACATATATGGGCAAAGTTTTCTGCTATTTAGGTCATT
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TGGGAAATGGNNTTNAGCTTTCCTTAACAACANTTACTCNAAAAAGGC

SEQ ID NO: 1593 ACGCGGGGTCCTGCTTTTGGTTCTTACAGTAGTCGGCGTAGGCCCTTAGGTGGG
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AANNGAAAAATAGGCCAAAACNTGGAANAANACTGNAACAACCNACAAAA

SEQ ID NO: 1594 ACCATCTGTGGTGGCTCTCTGCAAGTTTTAAACTGCCTCTGCTGAGCTCTCA
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CACAAAGTCTCAGACTAGAAATAATTACCCAGTAGATCATGGCATCCAAGACAGAGTCTCAGA
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SEQ ID NO: 1595 ACTTGCCCCTTCCCCAGAAAAGCGGGACTTGCTGCTAAGGGTGAAGGACCAA
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SEQ ID NO: 1596 ACGCGGGGAAACCGGACCCGCAACCACCATGAACAGCAAAGGTCAATATCC
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SEQ ID NO: 1597 TGTACATGTTGTGGGTGCCGCTCCGGGAGTCATAGCGCAGCCAGATCCCGAA.
GTTCTTACCCGCGAGGGGGGACTTCTCAAACACCTGCCACAGTAGACAATCTCCCCTGAAGACTT
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CAAAATTGAAGCTCTACAAAACCATGAAAATGAGTCTTGTGTATAANGCTTCGTTAAGCTTAATTG
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SEQ ID NO: 1598 ACACCTGGCTTGAGGCTGTCTCTCTCATCGGTATCATCGTAGCCAATGTG
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TAAACTGGAACCTGACTCAGAAACCGGATGACAGTGGCCACATGTGGTTTGACAATCAAATCC
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SEQ ID NO: 1599 ACAAGCCTTTAAAGAAGCAAGACAAAATGTTGCTGAAGTTGAGTCATCAAAG
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CGTGAAGCAACTGTCTCAGTGAGCAAAAAGTCAAAGAAACCAAAATATTGGCGAAGAAACCAA
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CAGTGATGGCGGANAAGAAATTTGTGAAGAGGAGAAGGAATATTTTGATGATAGCACAGANA
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SEQ ID NO: 1600 ACTTTTTTTTTTTTTTTTTTTTTTTTGGGCAGAGGCNCAATCATTTTANATTAA
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ANANAACGGTCTCTCCACCAATTTCACTGGTCTGTCTCATCANCTTTGGGCTGANCTGGGGTG
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GCTGTGCCAGTCATAGTAGAAAGGACTGTTTTATCTTNTAGGNCATTGGCCGTCCANGACAGGAA
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SEQ ID NO: 1601 ACAATTTAAAAATAAGTCTATGTTTTCACATTGATTTTAAAAAATATAGCATG
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SEQ ID NO: 1602 ACAGATGGGGTCTTGCTATGTTGCCCAAGCTGGTCTTAAACTCCTGGCCTCAA
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SEQ ID NO: 1603 ACAAACCTTGCTCAGAAGCTGTATCAGCATGAAATCAACTTATTCAAAAG
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SEQ ID NO: 1604 ACTTTNTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAAATATTTATTTTCTTAACGAC
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SEQ ID NO: 1605 ACTGAGCAGGATTACCATGGCAACAACACATCATCAGTAGGGTAAAACTAAC
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SEQ ID NO: 1606 ACGCGGGGCTTTTTTCGAGGTAGGAGTCGACTCCTGTGAGGTATGGTGCTGG
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SEQ ID NO: 1607 ACGCGGGGACGGTTCGTTTTTCTTTAGTCAGGAAGGACGTTGGTGTGAGGT
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SEQ ID NO: 1608 ACGCGGGGCTCTTCTGCTCTCCATCATGGCGCAGGATCAAGGTGAAAAGGA
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SEQ ID NO: 1609 ACTTTTTTTTTTTTTTTTTTTTTTCCACACCTGCCCTTTATTGGTCTCTTCTAGCAA
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SEQ ID NO: 1610 ACAACAGTGAAGTGAACAAAAGGTAATGAATTAACAGGAGGACTAGAGG
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CTCTCTGAAGACAAAGAAGTATTGTGAGCTGAAGTGAAGTCTCTTATGAGGAAAACAATAAACT

CAGTTCAGAAAAAACAGTTGAGTAGGGATTTGGAGGTTTTTTGTCTCAAAAAGAAGATGTTA
TCCTTAAAGAACATATTACTCAATTAGAAAAGAACTTCAGTTAATGGTTGAAGAGCAAGATAAT
TTAAATAAACTGCTTGAAAATGAGCAAGTTTCAGAAGTTATTTGTTAAAACTCAGTTGTATGGTTTT
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SEQ ID NO: 1611 ACCTGGTAGAAATTGTGTCTTGGAAATGACCCTTTCGAGTTATTGACATGGCTC
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SEQ ID NO: 1612 ACAGAGGGGTCTGTTTCTAAGTCTGGAACCTCAACACGAGGCTGGGATGCTT
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CAACAGANAACCTGGAAGCAGCAGAATCTTGGAGGAGCAGGAAGAGAGCCCAGAGGGAGTGTG
TGCTGAGTGACGGTTAACATATGAAACAGAATTTCAATGGAGATTCTTTGTTACAAGGAGAAATTCG
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SEQ ID NO: 1613 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGGGAANACTGCTTTATTGGNGGC
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AACAGTTTTTGTCTCTCCGGAACTTATTTTTAAATGCCTGCGGGAAGCAGTGCTTATCGTNTCTG
CCAATNTGACGAAAACCANCAAAATTC

SEQ ID NO: 1614 ACATAGGTAACCAAAAGTATATAGCTTATTTGGTGAATCTTCATCCTCATTACT
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NTTGTGTGAGCCTGGTGTCAATGCGCACATCTGGGANNTCCANTCCNTCANGGGCAAAATTTCCGA
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SEQ ID NO: 1615 ACAGGATAATATACTCAGATATTTTAAATAAACTACTTAATAATAAGAAA
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SEQ ID NO: 1616 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGNANATTAAGGCTTGTTTTATT
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SEQ ID NO: 1617 ACCTCGGGGACCTGCTGGAGACCTGCCATTTCCAGGCCTTCTGGCAAGCCCT
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GTCGGACAGCCAGCTAAAGGTGTGGATGAGCAAATACGGCTGGAGTGCCGACGAGTCGGGGCAG
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SEQ ID NO: 1618 ACCAGCTGGCACAGGAGCAGGGGGCATGGCACCTCTGTTGTTTATGCCATA
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AATCCTTCTCTGCTGTCGCCGCATCATTTCTTCTGCTGCCGCCGCATCTCTTCTCACGGCGCCTGC
GCTCTTCTCTGCTGCTGAGCTCCAGTTGCTTTCTGTTTTCGACCTCTGGTTGTGTCAGCTCTTCCATC
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TCTCCATCTCAATGAGTGCCTTCAGCGCATGGCATATTATACTCAAGGAG

SEQ ID NO: 1619 ACTTTTATTCTTTTTTTTTTTTTTTTTTTTGTAGACAGAGTCTGTCTCTGTTGCCTG
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TTTTAGTANAGACGGGGGTTTACCGTGTAGCCAGNATGGTCTCGATCTCTGACTTCGNGATC
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SEQ ID NO: 1620 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTNGTTTTTTTTTTTTTNATATT
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GGCAGNAAAAGCAGCCTGAATACNCAACTACNCCAANAGGGCAGCAGCTCTCTGACATCCATG
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SEQ ID NO: 1621 ACACACTTTATTTACTTCGTTTTGGTTAAGTTGGCTTCTGTTTCTAGTTGAGGA
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SEQ ID NO: 1622 ACTTCTCCGTTGACAAAGAAATTCTAGGTGAAATTAAGAGTCATGATCTGAA
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SEQ ID NO: 1623 ACTTAAATATATATTTATTTCATTTCTACATATATAGAACTTGTAGGTAAAGTA
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SEQ ID NO: 1624 ACTGTTAAAATGTGGATGGCACCCCTCCCAAGGATTGAAAAACACACAGCTGGA
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SEQ ID NO: 1625 ACCATTATTTGTCTGCCGCTTTTAAAAAATACCCATTGGCTATGCCACTTGA
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SEQ ID NO: 1626 ACCTACAGACACTTTTACAGAGTTAATACTAAAATTACAAATTGATGACACTT
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TTTAAAAAGCTCAGAATAATCTTCTCACCGGGCGCAGTGGCTCACGCCTGTAATCCAGCACTTCG
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SEQ ID NO: 1630 ACTCCATCCCACAAAAGAATTCTTGTTCTGGTCTTTTCCAGCCAGGTAAATAAGG
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SEQ ID NO: 1632 TACGCGGGGACGTTGCCAGCCGAGGTTTGGACATACCTCATGTAGATGTGGT
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SEQ ID NO: 1634 ACATGGAGAGGAGTATGGTGAGCTATTTCTTTTAAAGGATGAGACCTTCAT
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SEQ ID NO: 1635 ACAGAAGTTTTCATCTATGAACATGGCCTCATCATCACCTGCAGCCTTGGCCT
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SEQ ID NO: 1637 ACCCACCAAATCCATGGAGAGAAAATTTCTGGTGAAGCAATTGATCTGATAAA
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SEQ ID NO: 1638 ACATGACCTAATTTTTACATCATAGTAAACAGGCCCTATGGAGAGAGGACA
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SEQ ID NO: 1639 ACGCGGGAATGAAGGACTTGGCAGATGAACTTGCTCTTGTTGATGTCATCGA
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SEQ ID NO: 1640 CGCGGGGACCGAGGCCCATGCGAAGCTTCCACTATGGCTTCCAGCACTGTCCGGTGAGCGCTGCTGGCTCGGCTAATGAACTCCCGAAATACCGGACAACGTGGGAGATTGGCTTCGGGGCGTCTACCGCTTTGCCACTGATAGGAATGACTTCCGGAGGAAC TTGATACTAAATTTGGGACTCTTTGCTGCGGGAAGTTTGGCTGGCCAGGAACCTTGAGTGACATTGACCTCATGGNACCTCAGCCAGGGGTGTAGCCAAATANTTTCTAATGCCACTGTCNCTTTATCATCTGATTGCAGACANATGGAATNCTGTGCTGAACCCGATCTTCAANAACANCTACATCTGTGACCANCACANGATGTNCCCTGTGG

CNNCTGAATTTGTNTATNTGGCACTTTTCTCCCTCCAGNTAGTA

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SEQ ID NO: 1643 ACTGTAGGAGAGAATTAATAAAAAATAAAGCTGTAGATAATTAAGCTA
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AN

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SEQ ID NO: 1653 ACATTTTGTACAGACAGAAAGGCTGATTTTGGAAAGAAAGAAACAATNGGA
TGTATAGGGGCTTTCTATCAGCAGACTAGTATGTTTAAAAATAGTCTCATCAAGGGTTCTGAATAA
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GCGC

SEQ ID NO: 1654 ACAGCAGTTGCTCAAGAACAAAGTTATTCTCCTTTTCATCTCGAATACTCAGA
ATATGTGATTTTGGATTGAGTTTCTGGCATTATAGTATGAACCTTCATCCTGTGTTGTTGCCATATGCC
TATCTTTGTTATTATGAAATTTGTAGCAACAGTTCTGAAATGGTATCCACGGAGTATTTAGAACAG
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SEQ ID NO: 1655 ACCAGTGTGGAGAAATGGGCTGGTTAACTGTGTGGGGCCAGACAGTCATTTG
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CTCATTTTCCCTATTGTTGAAACATTAGTGAGAGGGACCCATGCATGTTATTTAAATTTAAGTTC
AAAACACTTAAATAATTCTGTATTAGAAACTTGACTCTATCATAAGTCTCTTCTTTTGAAGCAT

ACTGGGCTGGTTAAATGCTCCAATTCATTGTTATTAACATTTAGGAAGCAGAAACTATTCCAGCTA
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SEQ ID NO: 1656 ACATAGACAAGTTTCTTGTAAAGACAGAAAAACAGAGAAATCCACAGTAACTCT
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CTAAGTTCGGGTCTGCTTTAGTGCATTTCATTGAAATAATCTCATTCTCTATAATTTTCTTTTAA
CTTATCCACGGNTGGTCACTGATTGGCATAGACTNTAATGTCAAGAATTGTAAACTCATATGGT
CCAAAATCTTAAANTAAACAGGCCAA

SEQ ID NO: 1657 ACCAGTAGTTTTTATCGGTAATAAGAAAAAGGATGGCTTAATAGTGCCAATA
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CCAGCGAGAGCCATCCAGTCTGATGAGATCTGGACAAGCCCCATTATATCAGGAGCTGGATC
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CACTTGTGGACCTCCCTCTAATAAAATGGCACTTGAGGGTTAACCTGCCTATTGATCCCAGGGTN
CACGTTTNTCTTTTCCACGGTGACCTAGGGGATGGTAATATTANTCTAGTGGTTACAGGACCGCAC
ACAGANGGGTGCTTCCCCTNTNANANAAACGGGCTTTGTNTTTTAGANCCAATANNTGGCANG
NCATTTTACAACCTGCTNGAAAATTTTTT

SEQ ID NO: 1658 ACAAAAAAATCATTTCAAATAACTCAGGAGGATGATAATGGCTGGACTTTT
GTAATTACCTCAAAGACTGTGGGAGAGCCAACTCAACTCACTGTATAGTCTGTGCATATGGTGGC
TTGTAGCATGTAGGTTTTTTCCAAAAGAAGGAAATATAAAATGTTTAGATTAAGAACCATAAAACT
ACAGGGTGCTTATAAAAGGTGGCTTACTCCTTATTGTTATTATACTATCCAATTTTAAATGCAGT
TAAAAAATAACACTGAGTCTTGTATTACAAGGCAGCAAATGTTTCTCCTCATTTTGAAAGACT
GACTGCAATGCTTTCCTGAACATTTAGAAAAGAGGCAGTAAGAGTCCCTCGGCCGCGACCCGCTAA

SEQ ID NO: 1659 ACTGGGATAAATGAAGAAGAAGGCATAAGGACAATAAACATGGAACCTCCAC
TGCAAAATGGATTTTATGCAGCTGAGGAAAGTTGGGCTTATTAGTATTTGCTCCAGCGAACCTCCA
AGTTTTCTCCATTGCGGACAACGTAACCTACCAGCTCCTTGGCTCAGTGGTTCGGCTCCACTCAGAA
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AGGAAGACAGAACCATTANACAGTGACATTGGTGAAATATGTTTCATTGATTCTCACAGAGTAA
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SEQ ID NO: 1660 ACAACTTATAGAAAAGGTAAAGGAAACCCCAACATGCATGCACTGCCTTGGT
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SEQ ID NO: 1661 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATNGGAAAAANACTGCTTTATT
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AACNATGGNGGCTCTATACAGNGGGCTTAACNTCCCCNCCCTTAAANANNANGGGAATTNCAT
NAATCCTCCNGGAACANTTTTGNTTTTCCGGANCTTTTTTTTAAATGCC

SEQ ID NO: 1662 AACTCTCCATCTTAAATGAGCAGCGCATTCGGGGCATTATGCGATGTCACT
ATCATTGTGGAAGATACCAAATTTAAAGCCCATAGCAATGTTCTGGCAGCTTCAAGCCTGTATTTT
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NNNGTNTCTGACTCENNAGCTGCAGNAAAAAGCTGGAATATCGTTCNTGAANGANTCTNCTGGATC
GCTACTTNTCATATTTCCCGNTCCCTNTGTNTCTGGNTTACTGAAAAGGNANTGTTAAAGAANA
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TCGTAACAGAA

SEQ ID NO: 1663 ACATCTTGCCCTAGATGTGCGATGACTGCAAGTAATAATACAGTTTATAATGAA
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CAGTGATGCGATGTTCTAGAACTCTTAAANGCCATTGGCAGACCTTGNCGGACCCCTAGGCAATT
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ATTCCNNANNCAGNGACTTANTGAAGCTGGGGCATAGGG

SEQ ID NO: 1664 ACACGGCCCCCTTCACTTCCCTTTTCAGCCACAGTCTGTAGTTTTCCATCCGAAT
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TTACACTGNTGGACAAAANCTGGGTGCTANCTTGGCCTTAAAGGTTGTGCGCCCCACTCGTGT
GGACTTCAATGCGGTGGAGAGGACCCGAACATNGGACCTTCTGGTACANATCTTCTTGAAGTAT
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SEQ ID NO: 1665 ACTACAGCAGTCAAAGAGATCTCCACTAGAGATCAGAAAGAAGCACCACTAT
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CCCCAGATGTATTCTCCCTTATCATGGAATAAAGAGAGGNGCAAAATTTCTTCTAACTCCTTCT
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SEQ ID NO: 1666 ACAACTTATAGAAAAGGTAAAGGAAACCCCAACATGCATGCACTGCCTTGGT
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SEQ ID NO: 1667 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCAGCNAAAGTTTCATTTATTTGNGC
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CCCCNTGNTTCTGATGAACCAACATAATTCCTAAAATTACACCTAANCAAGTCTGTNTTGCACA
TTGGGGTTGCCTTAAAAACATTTAAATCTATTGGGCAAGGCGGTGGAACGAGGTTGGGATGGC
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TGGGANNATNTNTCTGAACATTTTGGCCNCCTTATTGAAAAAGTTTCTGNACTGGGGGGGCCNAA
GNTAAACTGGGACTNAAAAATTAGGGGANAAANNNGNCCTTNTTNTGNTNAGGGCINNATACTAACNA
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TAAATTTT

SEQ ID NO: 1668 ACAGAGCACATAGACCAAGGATGGCCAGTAGTAAGGCATGCTGTGCTCTCC
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GCCTCTCAGCACGCATGGGGTGTCTGCGGAGGGAAGTCCCTTGGCTTTCTCTGCAAGGCTTCTT
GGCTGTTATGGACCCGCATGGAGTTTAATTATGCTTAGCATATATTTTTGGCATACTAGGATTTCTT

CCCCTAGGATTTGCCAAAAGAGGGGANGGATCAAANTTTGGCATGCTGGGGGAACAACTCNCCCC
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SEQ ID NO: 1669 ACGCGGGGGTCTCTGGTTTCTGGCCCTTGTCTGCAGAGATGGCTCCCAATGC
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 GAGTCAGGTGATGANGCAAAGAAGCCCTCCTTCAGGTGCGAAGNCCAGCTNATGGCACAAGTGA
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 GAAAATGGGAAATATGCAAATACGNTTAAAGGCNATTACTTTCTGATTINTGATGGAAGGTGAC
 ACCTGGGATGGNGTGGANGGTNAAACTTTTNTAATTTTTAA

SEQ ID NO: 1670 ACCCTTGCCAAGTTGTCTACAAATGCTTTGTGCGATTTTCTACTGAGTTAGAC
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 GAGACTTTGACTTGCAACAGGNTTGAAGCATCAACTTANGTG

SEQ ID NO: 1671 ACCAAGAACCGCTTTATCCAGATTAATATAAGTGAAAGCCTTTAAATGCAGG
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SEQ ID NO: 1672 ACCCCCAAATAGAAAAGAGTGACTGGATGTTGGAACCTTAAAAATGATAC
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SEQ ID NO: 1673 CCAGTTCTTTTACAATACAATATTTTGGTATTTAAATGACCTCTAAATGGTTA
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SEQ ID NO: 1674 ACGCGGGGCAACTGATATATCTTTAGGGTGAGTTACTGAGGCTGTTTCACTG
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SEQ ID NO: 1675 ACAAATACGAAACAGGATTATCTGATAGTAGGCCTCTGTGGATGGCATCAAT
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SEQ ID NO: 1676 ACACAATTATGAAACTATGCCAGTAGCGACCTGCATGTTTGTCTCATCTCTTT
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TGGTT

SEQ ID NO: 1677 ACACAAGGAAAGAGCCAGAACCAAGCTCAAGATACCTATTCAAAGATCCCT
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AAACAAGTTCCAGGCCACTCAGCAGTGGTAGGAAAGGGAGGGAGGGCATGGAGGAGGATGGGGC
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TCTGCCAAATTGANCTGGGGCCTCCCTTCGCCTCNACT

SEQ ID NO: 1678 ACGCGGGGGGATTGTCTGAATTAATGACTATTGAATTTAAACTAATTATGA
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CTCAGTAACCATGACCTGCTCCTCCATTTCATTATTCTCAACATTAAATAGTTTTATCTTGTGTG
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SEQ ID NO: 1679 ACTAAACCCAGTAAAAATTGTTGAAAATGTTAAAGGTCAGCATGTTCTAATT
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SEQ ID NO: 1680 ACGGTATATATATTTTAAATATTCTCACACACATGCAATCCATAAAGCAAT
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SEQ ID NO: 1681 ACTAAAAAAGATTTTGAGGATTTATACACTCCTGTGAATGGATCTATAGTGAT
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 GNNACCAATCCTTTTNNANTNGGCCAANAATCATGGGGCCTGACTNAAATCGGGG

SEQ ID NO: 1682 ACGCGGGGATTAAATGTCCCAAGCAAGGATAGGGAAGGGGAATGGTTGAGT
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 GAGCTCTGTN

SEQ ID NO: 1684 ACCGCCAGCTCTCTGCTCTCCACAGGGCTCCCCGCCCCACCCGGCCTGATAAA
 GCGCGCCGACTGGGCTACAAGGCCAAGCAAGGTTACGTTATATATAGGATTCGTGTTCCCGCTGG
 TGGCCGAAAACGCCAGTTCCTAAGGGTGCAACTTACGGCAAGCCTGTCCATCATGGTGTAAACC
 AGNTAAAGTTTGCTCGAAGCCTTCANGTCCGTTGCAAAAGGAGCAAGCTGNACGCCACTGTGGGGC
 TCTGAGAGTCTGAANTTTTANTTGGGTTGGTGAAGATTTCCACATACAAATTTTTTGGAGTTTNC
 TATTTGATCCATTCAATATGTCTTTAGAAANAAATCCTGTACCCAGTGANNACCAAACNNTTN
 ACAAGCTAAAGGGANATNNGGNTNCATTTGCAAGGCTAAANATCTTAGTCTTNAANGGCNANANT
 NTNANACCTNTTGGNGNTNTAGNGGGACNTAGTAAATGGNATACTTTCCAA

SEQ ID NO: 1685 GCGGTGCGGGCCGAGGTAAGTGTGAGCCCTCGGCCAAACGGCCAGACGCGGAC
 GTCGACCAGCAGGGACTGGTAAGAAGTTTGATAGCTGTAGGACTGGGTGTTGCAGCTCTTGCAATT
 GCAGGTGCTACGCATTTCCGAATCTGGAACCTCTAGAACAAGTTATCACAGAACTGCAAAAGAA
 GATTTCAACTCCTAGCTTTTCATCTACTATAAAGGAGGATTTGAACAGAAAATGAGTAGGCGAG
 AAGCTGGTCTTATTTAGGTGTAAGCCCATCTGCTGGCAAGGCTAAGATTAGAACAGCTNATANG
 AGAGTCATGATTTTGATCACCCNATAAAGGTGGATTCTCTTACNGTACACCAAAATAAATGAAGC
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SEQ ID NO: 1686 ACTGTCGGTTTCAGAAATGCCTTGCAAGTGGGGATGTCTCATAATGCCATCAGG
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SEQ ID NO: 1687 ACCGCGGGTCCGTCAGCTGGTGTCAATTGACTAACACATCCACAAAGCACA
 CCATTAATCCACTATGATCAAGTTGGGGGAATCTGGTGAAGGGTTCTGAATATCTCCCTCTTCAT
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 AACTTNANGGGGCNCTTATNTNTCAATTTAGGAACCTTTATTTGGNGCATTTACGCACTGGAATGCA
 AATCCCTTTGCTGTGTAAGTGAAAAATATAGACTGTATCTGTGGCCCTATGAAATCTGCCTTTTA
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 TTTCTNCTGTCAATTAGCTTAATCTGAGACATNTGAGGAAAAATNTATTTTTNAAAATNAAAAT
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AAAAAAGTGGTTTTNAAGGNAATTTTTCCAAGNAGGTTTT

SEQ ID NO: 1688 ACTACCAGATAGAAAATTCTGAAATTGGAAAATTGGAGGCCAAAGCCTTAATCT
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TGTGTCCCCGCTCAGTCTTGAGCGAGCCCATTTGNGGATGTGTCTATGCGCTCATGAGCGTCTGTG
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GAAATCCTTTCNGGCA

SEQ ID NO: 1689 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGCCAATCCGTTTTTTAAITCTTAAATTC
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SEQ ID NO: 1690 ACGCGGAAGATGAATGCCAGAGGACTTGGATCTGAGCTAAAGGACAGTATTC
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GTTTTGAGGGTAATGATGAACTATTGGAATTTAGGATTTTCTTATNTNCAATCCCAACCGNAATC
ATGGGAGANCNCGCTTGTGTTGGGAATATAACTTGGTTACTGTATAGTGGCTGTGATGGAACCGAG
GCTGATCTGTTATAGCATCTTGTNCTC

SEQ ID NO: 1691 ACTGGGATTACAGGCATGAGTCAATATGCCCGGCCCGCAGTCTATCTTCTAA
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SEQ ID NO: 1692 ACAAAGAAAGTTTTAAGTCAAGGCCTCACCAATTCCTACAGTATTAGTATTGT
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GAAAATAGTTTATGTTTACTCATTATCACATGCTAGAAGAAAATTTTGCATGAGAAAACACTGAAG
AGGTAATTTTTAATCCAGATTTTTCACAACTCATGGTGCAAAATGGGCCCGAGCTTCTCTATTAT
AACTGCTCTTAATTGCTGTGCTGTGAAATGTTGAAGTACTCAN

SEQ ID NO: 1693 ACATTACACTAAATTATTAGCATTGTGTTTAGCATTAACCTAATTTTTTCTGCTC
TCCATGCAGACTGTTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGGAAAGTTTTTTCTCCT
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ACCTAAGATTTCTGTCTTGGGGTTTTTGGTGCATGCAGTTGATTCTTCTTATTTTCTTACCAATTG
TGAATGTTGGTGTGAAACAAATTAATGAAGCTTTTGAATCATCCCTATTCTGTGTTTATCTAGTCA
CATAAATGGATTAATTACTAATTTAGTTGANACCTTCTAATTGGTTTTTACTGAAACATTGAGGG
AACACAAATTTATGGGCTTCTGATGATGATTTTAGGCATCATGCCTATAGTTGCATCCCTNCG
AATGTAAGTACACTGTCCAAAGGTTTGTCTTCTNCACTGG

SEQ ID NO: 1694 ACAGTGGCATGATCTCGGCTCACTACAACCTCTGCCTCCCGGGTTTCGAGGGA
TTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTATAGGCTCCTGCCACCATGCCAGCTAATGTTT
TTTGTATTTTAAATAGAGACAGGTTTCGCCATGTTGGCCAGGCTGGTCTTGAACCTCTTGACCTTAG

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SEQ ID NO: 1695 ACTCCAACCTCAAGTTTACAAGTTACACCTTTGCCACAGCCTTGGCTAAATCTT
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SEQ ID NO: 1696 ACCGTCTAAAGGGGCACAAGGATGCCATCACACAAGCATTGTTTCTACGAGA
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SEQ ID NO: 1697 ACAAAGGACGGAGCACCATCAACCCGTCCAAGGCCAGCACAAACCCAGATC
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SEQ ID NO: 1698 ACAAAGAAGCAGAAGTGTAATTTTCTTTTCCAGTATGACGAAAAATTGGA
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SEQ ID NO: 1699 ACGCGGATCCACGGGTGCAACGGCACCCCTGGTGGCAGAGAAGCATGTCTCT
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SEQ ID NO: 1700 ACATGAAGTATATGCTGTGGATGTTCTCGTCAGCTCAGGAGAGGGCAAGGCC
AAGGATGCAGGACAGAGAACCCTATTTACAAACGAGACCCCTCTAAACAGTATGGACTGAAAAT
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AGCATTTGAAGATGAGAAGAAGGCTCGGATGGGTGGTGGAGTGCGCCAAACATGAACTGCTGC
AACCATTAAATGTTCTCTATGAGAAGGAGGGTGAATTTGTTGCCAGTTTAAATTTACAGTTCTGC
TCATGCCCAATGGCCCCATGCGGATAACCAAGTGGTCCCTTCGAGCCTGACCTCAACAGCTGAGA
TGGAGGTCCAGGATGCAGAGCTAAAGGCCCTCCTCCAGAGTCTGCANGCGAAAAACCCAGAAAA
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SEQ ID NO: 1701 ACTTTTTTTTTTTTTTTTTTTTTTGGCTTTTTTTTTTTTTTTTTTTTTTCCAGCC
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AACCAAAGAAAAATGACCGCATNTATTCTAAAGCTACTGGGGNGGTTTCTCATGCTTNANAGT
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SEQ ID NO: 1702 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTGGTTTANANTTATTTTTATTGACAAGG
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SEQ ID NO: 1703 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTGAATCTGAAGTCTTGTGTTTTACTAATG
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CCTTATCATCAATGATAAAAAAGGCCCTGAACGAGATGCCTTCATCAGCCTTAAAGACCCATAAT
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SEQ ID NO: 1704 ACTGGGAGATACAGCCATCCACCTTCAGATGTGTCTACGTGCGCTCTGCCATT
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TTAATTTCCAGGAAAAATAAAAAAGAGTATGAGTCTTCTGTAATTCATTGAGCAGTTAGCTCATTT
GAGATAAAGCANATGCCAACACTACTCTGATATCCCCATCATACTGGTAAAGCG

SEQ ID NO: 1705 ACTTTTATCAAAATCCATCATAAAAGGGAAAGAAGACTACAAAGTTTTGCCT
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SEQ ID NO: 1706 ACGCGGGCCAGTTGCCAGAGTGGAATACTCGCTTGATAATGCACCTTTTATTG
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ATCACTGAGGTGAGGAGTTTGAGACCAGCCTGACCAACATGGTGAAACCCCTCTCTACTAGAAA
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SEQ ID NO: 1707 ACAAATTTGATTGTTAGGAAACCAATGTTCTGAACATTATTTTATTAGAA
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GACAAAGGTCCATATCTCAATGGAGTCCAATAAATCTACAACATGGGACGGTGGAGTGATTGAT
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SEQ ID NO: 1708 ACAAATATTTAAGAGTGTGATTGGGAGTAAGGGAATGTCAACTGCCAATAA
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ACAACTCATACTGCAGCTAAGCATCTACCCCGAGGGACAAGGCAAGCACACACTAGGGCAGCTGG
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SEQ ID NO: 1709 ACAAATGTTTTTTTATTCAAAAATACAAAATAAATTATCTGTAGGCATGGACA
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AACCTTTGTGGGTCAATGATTCTTTTCCCCATATTACAAAATCTCCAGCCTAGCATCATAACCAA
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SEQ ID NO: 1710 ACACGGGGGGAAAGACAATCATTGAATACAAAACAAATAAGCCATCACGCC
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CCAGTCTGTTTCAAATAAAATGAAGTCAATCTAAATTAAGAAAGAAAGAAATTTGAAAAAATTT
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AAATGTCAACCTTTGTAAAGAAAAACCAAAATAAAAAATTTGAAAAATAAAAAACCTAAACATTTGTAA
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SEQ ID NO: 1711 ACTTTTTTTTTTTTTTTTTTTTTTGGCTTTTTTTTTTTTTTTTTTTTTTTTT
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AGAAACCCCAACTAACCGCTGTTTGAATGNTTNTGACCCACTCCTNTAATTTNCCATATCTGNT
CATCATCCCANGGNTTACATTTANTAANATGGAAGACTTGGAAACAAGGGCAGGTTTTTGGNTTTC
TTTGATTATATTGNGCAAAAAGTTTTCCCTTACCTTTTTGTTTTACTTTCTCCCATNATNAAACCA
AAGAGGCAANGCA

SEQ ID NO: 1712 ACCAGCGAAGCACCTCAGCCCCCTCGGAAGAAAAGGGCCCGGGCAGACCCC
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GCACTCAGCTGCTCTACNNTTTGAGAGGCCCCAGTATGCTNAATCCTCTTGCTCACCTGATGCTC
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SEQ ID NO: 1713 ACGCGGGGGCTCACTCTGCGCTTACCATGGCTTTCATTGCCAAGTCCTTCTA
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GAATGACAAGCTCCCCTACCCTTATGATGACCCATTTCCCTCATGACCGATCCCAACTCATNATTT
GGACCCTGGCCCGTCANATGTGCCTGAACCTTGAGAAGTCCTATAGGGCCGAGGGAA

SEQ ID NO: 1714 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTATGGAATGATTAAAGATGTCTTTAT
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GGAAACAAAGCAATCATTTGTGACAAGCCTAAAAAGCTTGACATATTTAACATACTTAGGAAC
TTTTGTGCGGTGGGAATTTCTCTAATTGTATCATGTGGCCTTTTGAAGTAACAAACAGAAGGCCAG
CTGTTGAAGTTTGCTGTGAACATCACATTTCCCCTAANAACCAAGNGGATTGCTCGAG

SEQ ID NO: 1715 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTCGGGANCCAAGGAAGTTTATTT
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GTCTAGGGCNTTNGCAGGANAACACTGGTGTCCAAAGGGAANCACCATGATTCTGGAGTGGCTCAT
GCATGGCTGGAGTTANNAAACTGGAAGTCCCCCAGTCTTATTANTCA

SEQ ID NO: 1716 ACTCTGGTAAGCTTGTTGTGTCCAAAGTGAAGCTCCCTCAGATGAGGCGTGT
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TCTTCATTCCCTGAAAAGCCCCATTTCAATTCTGAGCTCTTCAGCGGATTGGTGCCAGTCTCTAT
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SEQ ID NO: 1717 ACAGCCAACGGTTTCCCTTGGGGGCTTTGAAATAACACCACAGTGGTCTTA
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TGCAGAGTCAGAAGATGAAGAGGAGGAGGATGTGAACTCTTAAGTATATCTGGAAAGCGGTCTG
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GATGATGATGAAGAGGATGATGATGAAGATGATGATGATGATTTTGATGATGAGGAAGCTGA
AGAAAAAGCGCCAGTGAAGAAATCTATACGAGATACTCCAGCCAAAAATGCACAAAAGTCAAAT
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SEQ ID NO: 1718 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGATGCTTTTCATTATCACANAACAC
ACCACCTGTAATGNGTGCAAAAAGGAAATGAGGGGTGGAAGGANAGGAAGTCTAATTGGGAAAG
GCTGGATGGTCACTTCATTTCTTCTCTTCTTCTTATCCTTTTCATTTCATGGCCAGNATCATCATGAG
TTTTCTGAANACAGTAATGAAATCTAANAANAGATCAATGCAGNGCCAGATATAATCTTGATCTC
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CCACATACAGGTTTGCCTGGAAAAACCAATGGATCCAAAGAAAACATTCCCCANGGAAGACAAA
AGCACAAGCTCAGGGCTGCATCAAGATCCTCCAAAAGAGGTAGCTCGGCCCTGCATANAGTGCC
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SEQ ID NO: 1719 ACGTGAACCACAAAGTGATACCAGGCATATGACATGGATCCCCCTGGGGAA
CCAGGCTGATCTCTTCCAGAGGGCACTATCCGACCAGTGCATGATGATATCCTCATCGCTCAGCT
GCGGCCCTGNCCAGAAATTGACCTGCTCATGCACTGTGTCAAGGGCATTGGCAAAGATCATGCCA
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AGGGGAGGCAGCTGAGGAGTTGAGCAGGGTGCTTCTCACCTGGTGTATTGAGGTGCAGGAAGTC
CAAGGTAAAAAGGTGCCAGAGTTGCCAACCCCGGCTGGATACCTTCAGCAGAGAAAATCTCCGG
AATGAGAACTAAAGAAAGTTGTGAGGCTTGCCGGNTCGAGATCATTATATCTTCTGTNAGTAAC
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SEQ ID NO: 1720 ACGCGGGGGGAGGGGGAAAAACGAAAATAAACGAAGCTTGCAGCACACTCT
GCGTTCACTACTAGGTACCTTGCTCTCCGACCTGCTTGCTCATAGCTCTGTGTATCAGCTATGATA
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GCATAATTACTGACACCAGTTGTCTGAAGGAGCCACAGAAAGCAAGACTCAATGGGGACTGCAG
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ACCCTTCAATGCCCCTTAAAAATCCACCCGACTCCTTGGGGAAGATGGATTGTGGCTCCTG
CGTTCTCTAGCACCTGCTCTTAACCTTTCTGTGAAACCTGTTCTCCTCAGTG

SEQ ID NO: 1721 ACCTTTGTCAACATCCTAACACATTATCGGGAGCAGTGTCTCCATAATGTAT
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TACAAAATTTGAAATTTAGCTTGGGTTTTGTACCTTTATGGTTTCTCCAGGTCTCTACTTAATGA
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CTATAAACTTAGTGCGGCAAGTTTAATCCAGATTGCCTTTGCTTAAAGCAG

SEQ ID NO: 1722 ACGCGGGGAGGTTCTGGGAAGATGGCGAAGGTCTCAGAGCTTTACGATGTCA
CTTGGGAAGAAATGAGAGATAAAATGAGAAAATGGAGAGAAGAAAACCAAGAAATAGTGAGCA
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TCAAGAGCTGAGAANACAGTTCCTTGGCANTCACAGAGTCANGCNATTAACAGGCATGANATTTG
AAGCCATGNAAAGATATGATGATGCTATACAGCTATATGATANGATTTTACAAGAAGATCCACTA
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CTNTCA

SEQ ID NO: 1723 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGGNTCAAGTTTAATACAACTAC
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SEQ ID NO: 1724 ACAATACTTGGCCGAAATCTGTCAGGTCAGCCCACTTTCCTTGTCTGTCAA
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ATGTATGGTTATTCAACATCATTTTACTTTGGATATATGGCGGATTACACACCTTGGGATATGGTG
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SEQ ID NO: 1725 ACACATGATGAAATGAAGCAGAAGCTGGGAGTCGGCCTTTCCTCTAGTAACC
ACCACATGGCTCAGCATCTGTGCCAAACATAGGCGCTCCTAGTCTGGTCAGTGCCAAGAGGCTAC
CAGAACATGGGGCAGGTGGCTGGTGTGGTGTCCCAGCCTAAGAGCCACCTGCTGCAGTTACCAT
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TCATTATAAGCTATGAGTTGAAATGTTCTGTCAAATGTGTCTCACATCTACACGTGGNTTGGAGGC
TTTTATGGGGCCCTGTCCAGGTAGAAAANAAATGGTATGTAGAGCTTAGATGTCCCTATTGTGACA
GACCTGGTGTGTNGTATAAT

SEQ ID NO: 1727 ACACTTGAAACCAAATTTCTAAAACCTTGTTTTCTTAAAAAATAGTTGTGTGA
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CAACTGCTCTGCCATTTCTGGATTTCTTATTTACAAAACACTTCTTTAAAGCTTGCTGNGTGGCNC
TCTCCAANGATGAAAATCATCAAGGTTGTTGTTGCTTGG

SEQ ID NO: 1728 ACCTATTTTTTAATTGAGACAGGCCACTTTATTAATAAGGTCCAAATGTAAC
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SEQ ID NO: 1729 ACTGGATGGCCCCACAAGATGCTGCCACTTTAATAAGGCTGCAATACACTGT
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CTCCTTCAAACACACATAACAGGCTTTAATAATTNGAGCTAAATCAACATGAAGTCACCTTNCAG
TCTTTTCTGAAATCTCAGTCCGTTAGATTCAAANNANNACGAACTANCAANCTGNCTTTTATT
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SEQ ID NO: 1731 ACATCATAATCGGCGACACAGGTGTTGGTAAATCATGCTTATTGCTACAGTTT
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SEQ ID NO: 1732 ACTATAATGCCAACAGGGCATTTCAGAAGATGGACACAAAGAAGAAGGAGG
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CCTATTNCCAAACAGGCAGAAATCTTTCTATATTAAATTCACACTACTAAAAATTTTTTCACGGC
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SEQ ID NO: 1733 ACATCCCAAGAGATGTAGATGAAACAGGTATTACTGTAGCCAGTCTTGAAAG
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SEQ ID NO: 1734 ACGCGGGGAGTTTTCAACTGACCTCTGGACGCAGAACTTCAGCCATGAAGGT
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GTGGGACTGATGGAATACTTATCCCAATGAATGCGTGTTATGTTTTGANAATCNGAAACGCCAG
ACTTTTCTCATTNAAAAATTTGGCCTNGCTGNGAACCAAAGTTTGAAATTCATCTAGGTAACC
GNNAGGCANAACTGNCTTATTGTGAATAAATAG

SEQ ID NO: 1735 ACCTCAAATCTGCTCTGGAGTCGATTATGCCACCTGTGTGTCAGGATGCACCT
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CTCTGCANAGGGATACCTTCCAATAGTAAATTATCTGGTTCCTCACTGAAACAAGTTATTTTGCTT
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CANCAGTGAANGATTCTACACAGGGAATCTGCAGTTTGTGCAGAAATGNTTTNNCTCACGTTGCTNA
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SEQ ID NO: 1736 ACGCGGGAACCCAAAACCTATAAGAACTAATAATAATCCACCACCTTTTGCT
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CCTTCTGATATCCNCGTTNAAGNGTAGACNTGCNNGNACCTGCTTGNCTTTCCTTAGNCAGNCCA
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SEQ ID NO: 1737 ACAGTTGATCCCACTTTGGAATAAATGCCAGAAGGTAATAAGCATTATCAG
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SEQ ID NO: 1738 ACGCGGGGCTCTCGAGTCACTCCGGCGCAGNGTTGGGACTGTCTGGGTATCG
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GCCTTGACAAGATNCGCNTTGACAGCCTGACAAACCTTCGAAAGTTGACAGTGGGNTAAGAGCTG
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SEQ ID NO: 1739 ACCTACAGACACTTTTACAGAGTTAATACTAAAAATTACAAATTGATGACACTT
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SEQ ID NO: 1740 TCCCCACCACTGTGATCTATGAGGATAACCAAAGACCTCTGGGGTCCCTG
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SEQ ID NO: 1741 ACTTGTCATCAAAGACCCAGGCAGTCTCTGGAATAGGCTTTCCAGCTGCTCA
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SEQ ID NO: 1742 ACGCGGGGGCCATATTATCAGCGGTTATTTCGGTGAGCGGTGGTGGTTATTCT
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SEQ ID NO: 1743 ACGTAACTGGAAGCAAGGACGGCTGCATCAAATTATGGGATGGTGTTCAAA
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GACTCGAGGACAGCCGAGCGGAGAACCTGCTGCGTTGGGGCACAACAATATTGTACCTCGGCCG
GACCACGCTAAGGCG

SEQ ID NO: 1744 ACTGTATCCAGCACCACAGAAACCTCAGTGTTTTCCTCTGCTGGTTTGGGGC
ACAAGGAAGCCTTAGGGTATGGGNAAGGNTGTTATTANCTAGAGGTTACTCCATNAGGTTTGG
GNTTG

SEQ ID NO: 1745 ACTGAACTTGTGTTGACCATAGCCTTCTTGTCTTTCATCACTTTATCTCCATG
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SEQ ID NO: 1746 ACAAACCTAGGAACACAGAAAAGGACCAGAGAGGATGTTACACTGTAAAGT
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SEQ ID NO: 1748 ACAGTGATTGGCTATAGACTCTCGCCCCCTTCAGGGCAGACTGTCTCAGTTC
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AAGA

SEQ ID NO: 1753 ACTACACGCACCTGGGCAACGACTTCCACACGAACAAGCGCGTGTGCGAGGA
GATCGCCATTATCCCCAGCAAAAAGCTCCGCAACAAGATAGCAGGTTATGTCACGCATCTGATGA
AGCGAATTNNGAGAGGCCCNCTAAGAGGTATCTTTATCAAGCTGCATGAGGANGATAGAGAATG
GTGAGACAATTA

SEQ ID NO: 1754 ACAAAGATGACTATAAACAAGATGCAGCCCTCGGTTTCCATGAACAGCACAC
TATTACAGTAAACCAAGTTTATATTCCACCATCAAGTGTGGCTCTCCCATGACTTCGCTTTGTGATG
GATCATTAAAGATATCCTCAAATCCAATAGTCTCATCATTACCCCTCANAACATCCAGTGAAAGAT
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TAGCGGAGCAATAGACCCTGAATGNTTCTCAGNGTGGNAAAATTNATTTAATNTTGGTGAGCTGG
AAATTTTTTTCNGANNATCAAGGGGATGACTAGACAAATGTTCAATTGTTTCNCACANNAAAAACCT
TNCANANANATCATGACTTTCNAAAGGCCACTTGTNGAANGTANAGNACTGNATCTNCCTTACTN
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CCCCCGTGTCTGCGGCGGCGGTC

SEQ ID NO: 1755 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTATAAGTATATAAAAACATTTATT
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CTNTGGGTTTCANGCGATTCTCTGCCTCANCCCCCTTGNNTAACTGGGATACAGGCNCAACCAATACN
CCCCGGCTTATTTTTTATTTTATAGTANANAGGGGGTCTCCATGTNGGGAGGNTGGNCTCGAACTC
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CCCTGCCAGGGGAAGNACANACTTNAGGTTTGGCTGGANCCATCNTTNAAGGAGTGTTTTGGG
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SEQ ID NO: 1756 ACAAATATCCCCACTTCCCTTGAGAAAGAGTATATCTAAAATACACTTTGAT
GAACACAGAATATTAACACATTATATGCTATAGAAGTGAACACAAATACATTTTCCAAATTTT
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GNTCTTGATGTCTCTCTCCAGCTGAGTAAATGGATTACTGCACTTANACCTGGTGAATCAAGAAG
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AAGAATCAGTTCTTCTTCCCAACATCTGAAATCCTTTTTTTGTAGTATTAATACTCTGTCTCCCC
NCNAGAGAGGCAACTCATTANTCCTGATAANATCCCTNAGGTGNTNTNCACATATNTTAATAA
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SEQ ID NO: 1757 ACGCGGTTCTACTTCAACAAAGAAAAATTTTGTAGTTATAGGAATAAGGACG
GTAATCTGCATTTTGTCTCTTTGTATCTTCAGTAATTTACTTGGTCTCGTCAGGTTTGAGCAGTCAC
TTTAGGATAAGAATGTGCCTCTCAAGCCTTGACTCCCTGGTATTCTTTTTTGTATTGCACTCAACT
CNNTTACTTGAGCTTCAGCAACTTAAGAACTTCTGAAGTTCTTAAAGNTCTGAAGTTCTTAAACC
CANGGATCCTTTCTNAAAAAANAACGTGAAATCTTTCTGGACAGCCNTGACTGTAGCAAGGCTTT
GATAGCAGAGGNTTGGTGGNTCAGAGTTATATCAACTATCCCGGTTGNTGNNCTCATCCAGGGTTA
CCNTCTTCTGAGTTTGGTNGTATNTTTGCCCTCNCCCCNGANTATTTAAGCNGGTGANTTTNAC
TAAANTGNTGGATAATANTGNANCTNCTGNCCCTTTNTNGCNNTATCCGTACCNATCCCATAT
ATCACTGGNACCTTGGNTACNNCTAGGNTTNTCNTNGNGNCTTANANGGGCCNCGNCCNN
TTNCTATAATGTATATTTTNGTGTAAT

SEQ ID NO: 1758 ACTTTTTTTTTTTTTTTTTTTTTTTTAAAACTTTTAACAATTTATTAGTCTTAT
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ATTAATTCCACATAAATATTTAAAATCTAAAAACCTCANATCAGCANACCGAGTCGAAATGTGATT
CTTCAAAGCAAGTATTGCTTTACCTTGCCTGAATGCAGTCCGTCATATGACCACTAACTTGCATG
TGACCAAATGTTTGCANAGGGTTTTTANATATGCTCTNGGGGAGCCGCATCCGCAATCCAAGAA
NAANATGTTGTTGAAGTGCCTTGCACAAAGTTTCTTGACCTCTTCATTTACTTCAATCAGGTTGCAT
TTTTTTGATTCAAATAACATAGAGCTCCGCGATCAGACTTTTTACACCCAGTAATCACTCATGG
CCTTCACAATGACTCCTATCTCTCACTCTGGAAAGCCTGTGATGCCCCGAGATNTTCNTAATCCGGG
GCCGGAAGTGGCGAACCTGGNGTCTATNGGACTGGCTTTTTCGGGAGATATG

SEQ ID NO: 1759 ACTAGGCCATGAAGTGGGGCACTGGAAGTTGGGACATNCAGNCAAAAAATATC
ATTATTANCCAAATNAATNCTTNCCNGGGTTTTTTTTNATTGGCNGAATNAATGGGCCAAANGGAN
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TAACAAAGATAACTTGGGATCCCTGTTCTGCTGGTTGTCTCATGNGCAATTATCTATCCTCACTGTA
GAANACTCAGCCTTGAAGCTATGNAGCAANCTGNATNCCAGATCTGGACTGAANAATTTCTGATT
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SEQ ID NO: 1760 ACCTGTGTTTCATATCCTGAAGTGCACCAAGGAATAGCTCCATGCTAAACTGTC
TTGGCTAAAAATACAACCAAGTCCCATCATCTCTAATCAGACTAATAAACAGAAATGTCTTTAAGGTA
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AAACATATTTAAAAGAGTCTATAGCATCTGTCCAAAAAGATTATATNCTATACAACATCAANTANT
ACAAAACCATTTTCATTGCTTCACTGAGAANATCTATCACACCTTCTCCTCTGAGNGGTCTATCTG
ACAAGCTTGTTCAGTTTTATNTCTAAACTNANATTCTTCTTTCGCCAGTNTAGCNANCANTTT
TTTGGTTTNTGAGNCACTCTAAGGAGNTTAAAAATCCAACC

SEQ ID NO: 1761 ACATAGTGTGCGANCTCAAATCGGCATTTAGATAGATCCAGTGGTTTTAAAC
GACACGTTTTTGCTTATAAAAAAAGTGCAAAAAAGATGTGGTTTACAAGTTAAAGCTACAGAATC
CCTTTTTGCTGTAATTGCACCAAGTTTAAAGCCTCTGGACAGAGCAGTATTTCTGTTAAACTTTGT
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TGGCCACTGGTGGCAGGTTAANGGGATCTGCNCTTTAAGAAGCCCNAAAATTGAAGNGNACTTG
NAGAAATTNNGGGCCGNTTTTTAACCTGGNNGAGANNTAACCANCCNCTNTTTAAAAATAGGAATC
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SEQ ID NO: 1762 ACTAAGTAGGTGAGAANCTGAAGTCTCAAGTGTTCATCTTCCAACCTTTTCCC
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TCTGTAGCTCTCTGAGCTCCTCTATGTGCAGCAATCGCAGAAATTTGAGCAGCTTCATTAANAACCTG
CATCTCCTGNGTCAAACCCAANAATATGTTNGTCTAAANACAGGAAAGCCCTNTTTGGTTNNATT
TGCCTNANCAACTGNATCCTGTGTCAGGCCCTNTGAACCAAAATCCNAAATNGCNTTATGCATTAC
NANGTAATNANCNTNACCCTGAATNTGAANCTGGTTACCAAANCNTCCNCCAGCCTAAAAATCAGG

SEQ ID NO: 1763 ACGCGGGCTAGGTGGCTTTGACCCCTGGGGGATTAATGGCAGTGTCACAAG
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ACGTCTACGATGTGCAGGACATGTCCCAACAGCACAGAACTATCTGGCCCCACGTGTCAATAAG
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CCTNTTTCCGGGCTGCACTGGTTTGTGATCCATNTTANTTACTNCCGTGCAAAAAGAGANTGAG
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SEQ ID NO: 1764 ACTCTTTGGAAGCATTGGACTTGGCTTGATCGTAGGAGAATCCGGTGTCCAG
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AGGCAATCCAC

SEQ ID NO: 1765 ACGCGGGTGTGGAGAAAAGAAAGACCTCTATAAAGAAATGAAGAACCTTGC
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AGCATGGTGGATGCGGGACAGAGATAGGACATGGGATTTGAACTGAAAGACATCATTTTGGCCA
GGTGGCTTACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGTGGGAGTATCGCTACAGCCCCAGG
AGTTCAAGACCAGCCTGGGCAACATAGTAAGACCCTGTCTCTACATTTTTTTTTTAATTAGCTGGC
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SEQ ID NO: 1766 ACCAAGAACCGCTTTATCCAGATTAATATAAGTGAAAGCCTTTAAATGCAGG
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GGCCCCAACTACAACATAGTGATCTGGTTCTACAAAGCCTTTAATAACTCCAAAGATGTTAAGAAT
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ATGTAGAGCTGTTTCANAGAGGAGCTTCTTCATATCCCAACAGTTTNTGCANAGTTTGAAN
TGCNCGACGGTTTTTGNATCCTGTGACCAAATGNNGAAGTANTGNATGANGAAGGGANCAAG
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SEQ ID NO: 1767 ACGCGGGGCTCTAATCTTCCATTTTCTGTCCCTGAGTGAGTCTCTGGCGTCCC
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CATGGAGTCCACAGCCACTGCCCGCTCGCCGCGGAGCTGGTTTCTGCCGACAAAATTGAAGATG
TTCTGCTCCTTCTACATCTGCANATAAAGTGGAGAGTCTGGATGTGGATAGTGAAGCTAANAAAC
TATTGGGTTTAGGACANAAACATCTGGTGATGGGGGATATCCAGCANTGCAATGCATTNCAGNA
ACAGNTTATCCTTTTAATTAAGATGGAAGACAGCTAAANGAGNGTGGAGAACCTTCTTTTTCT
NATGGAAANCACTTTGNAGTG

SEQ ID NO: 1768 ACTTTTTTTTTTTTTTTTTTTTTTNGGCCATTTGCTATGTTTTATTTTGCTAGTA
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ANAAATAGCCTCCTTCTNTTTNTTAAAAANANTGTTCAAACCTCCCNAAATTAATCTNGANNATN
AACGNTAAATTTGGTCTTGAATCCCT

SEQ ID NO: 1769 ACTGCAAGACCCATTTCCCTCCAGTTAATACACTNCCAGGATGGNCGCAG
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ATGAATAAAGGACCCAGTTGTGCTTTCCTTCCAAAATCTCAACAAAGTGGTTNGTGCTCCAGAA
AAATGTGGGAATAAAAAAAATCATGTCCCAAGGCATCTTTGTGTGTNCGGGGGTGGCGGTGG
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GCTGAGCCGGAATCCGGACAATTATTGNCGGGAAACCAAGTTGGACTACANAGAGTCCAAGAAAC
TATGATCCNCTTTACTCNNTTGAGGCCACNNAATANGGAAAACCTTTAAATGCTACCAACNGGAC
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ACNGNTCTGCCTTTGGGCGGONAGGAAGGAAAATTTGGATCACNACGGGATG

SEQ ID NO: 1770 ACATAGAACAGCCACAGCTGATGACAAAAAGCTTCAGAGTTCTCTAAAAAAA
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TTCATTTCAACAATCCCAAAGTCCAAGCTTCCCTTTCTGCTAATACCTTTGCAATTACTGCTCNTGC
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NCTACTAAAAGTTGGTTTTTGGANCTGCATGGCTANTTAACAATCANTTTGGGTNCAAGTTTCAGAC
NTGANACTCCCTGTCTATCAGGATNAAAAATTTTGGTTTTAATATGCTGGTGTGANATTTTCGC

SEQ ID NO: 1771 ACGCGGGGCTTTTTCTCTCTTCAGCGTGGGGCGCCACAAATTTGCGCGCTC
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TGCCGGCCTCCAGTGCTCAACGATTACCTGGCGGACAAAGAGTACATCGAGGGGTATGTGCCAT
CACAAGCAGATGTGGCAGTNTTTGAAGCCGTGTCCAGCCACCGCTGCCGACTTGTGTCTATGCCT
TACGTTGGTATAATCAANTCAANTCTTACNAAAAGGAAAAGCCACCTGCCAGGAGTGAATAAAGC

TTTGGCAAATATGGTCCTGCCNANGTGGAAAACACTACAGGAAGNGAANCTCAGATATAAAAAATG
ATGATACTT

SEQ ID NO: 1772 GGCACCTACGATGGTCACATTCATATTGGGCATTGGATCTATTTAAGCCTAGA
AGTATAACAGATAATCAGTTCCTTAAGTGTAATATGTTCTTAAATGTTTGGCCTTTTATCTGTTA
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AAA

SEQ ID NO: 1773 ACTACCAGCTTTCACATCAAATTTGGAACGTGGAGGTGTGGAAAAGCTATTG
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CAGCTGCTCCTCCAGACAGTTTGATGCATCTCAATTCAGCCAAGGCCCTGTGCCTGGCACTTGTG
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SEQ ID NO: 1774 ACCCCTTTATTCAGTGTGGAACTCATCTCAAAGTAGAAGATGTGAGTG
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TGCAATACTTTCCCGGCATTTAAAGTTAGAGAATTTCCGTACAGATGCAGNTCCTTTTCCAAT
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TCTGATCCCCAAGGAGTCCATATCCAGAAGCAAAAAATTAGCCGCTTTGTAGTTCCANAAATGTT
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SEQ ID NO: 1775 ACCCATCCAATGAGTCCCCNGAGCCTCCANAAGCTGTTGTCTCCTCTCTGGGG
ACAGCAGCTCCTGCCCTTGGAGGCCAAAGCCCCAGATCTCTCCAGCCCCAGAGCTGAAAAACACCA
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SEQ ID NO: 1776 CANGTTTCCCAGCCCAGTCATTGCTTCATTCTTGTCTGATCAGATGGTAG
TTAGAAAAGAAGCTCTCCTACATCCATCTTCTATACCAGGAAAGAGGAAGAGTGCCAAAAGCAGA
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AAATCTCCTTGGTTTAGTAACTCTTGTGGATTACTGCAGTTAANACAGAACTTCATATGATTGC
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ACCCTTTAGCAANACCTCGTCATCAACTCCCAAGATAGAAATNGGTATNTNGGTAGGGTTCAAN
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SEQ ID NO: 1777 ACGCGGGGACGGCAGGCGTCCGCGTCTAGCTAGTCTGTTCTGAAGCGGGG
CCAGAGAAGAGTCAAGGGCACGAGCATCGGGTAGCCATGCCTTTCTTGGACATCCAGAAAAGGTT
CGGCCTTAACATAGATCGATGGTTGACAATCCAGAGTGGTGAACAGCCCTACAAGATGGCTGGTC
GATGCCATGCTTTTGA AAAAGAATGGATAGAATGTGCACATGGAATCGGTTATACTCGGGCAGAG
AAAGAGTGCAAGATAGAATATGATGATTCGTAGAGTGTTCCTTCGGCAGAAAACGATGAGACG
TGCAGGTACCTGCCCGGGCGGCCGCTCGAAAAGGGCG

SEQ ID NO: 1778 ACCACTGAAACCTGACCCAGAAAAGTGGCTTGCTTGGACACCCAGCTGCCT
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CTGGCTTTTAAATTTTGGCANCCTAAGGGACATTAAANACNTAAATTTAAACNAACAAATAACCAA
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SEQ ID NO: 1779 ACTATTTTCATGGTCCAAACCTGTTGCCATAGTTGGTAAGGCTTTCCTTTAAGT
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CAGGTTTATCTGGGCTCTATCATATAAGACAGGCTTCTGATAGTTTGAACCTGTAAGCAGAAACCT
ACATATAGTTAAAAATCCTGGTCTTTCTGGTAAACAGATTTTAAATGTCTGATATAAACATGCCA
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TGATTTTTTACCATTTCGACTTACATAATGAAAACCAANTTCATTTTTAA

SEQ ID NO: 1780 ACGCGGGGGAGGCGGCACTGGTCTCGACGTGGGGCGGCCAGCGATGAAGCC
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TCTCCAGGTTGTAAATTTAAAGATGTTAGAAGAAATGTCCAAAAGATACAGAAGAACTAAAGA
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AACCTTCTGGATCTCTACCAGCAATGTGGAATTATNACCCATCATCATCCAATCGCAGATGGAGGG
ACTCCTGACATAGCCAGCTGCTGTGAAATAATGGAAGAGCTTACAACCTGCCTTAAAAATTACCC
GAAAAACCTTAATACACTGCTATGGAGGACTTGGGGAGATCTGTCTTGNAGCTGCTGTCTNCTA
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SEQ ID NO: 1781 ACTTTTTTCTTAATTTCACTGACTTCAGAGACGATTGCAGACTTGCAGTTTAA
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ACACTTGAGTTGTGAAGGTTTTGGGCATCCACCCAGAAAGTGGAATTTGATTTTTATCCTTCCGA
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TCTTTAANGGTGGNTCATTTTCTCTGACCTTTGTACTCAAAAGNAAAAGTACCCTGCCCGGGCG
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SEQ ID NO: 1782 ACGTCTGCATCGATTATCTTACGTGGGGCAAATGATTTTCATGTGTGATGAGAT
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CTCGGAACAGCTTGCGATTGCAGAGTTTGCAAGATCACTTCTTGTATTCCCAATACACTAGCAG
TTAATGCTGCCCAGGACTCCACAGATCTGGTTGCAAAATTAAGAGCTTTTCATAATGAGGCCAGG
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SEQ ID NO: 1783 ACTCTGGATCCCAAGGTGACTGGTTGTTAATCGTGTGCATAGAACCAGCCA
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SEQ ID NO: 1784 ACCTCATAGCCCTGTGTCAATTAAGTTTTCAGCACTTTTGGGAACATCAGTTGG
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SEQ ID NO: 1785 ACTTTTTTTTTTTTTTTTTTTTTTGTAGTCAACAACTTCTATTTTTATTGACA
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CGTAGCCCTCTATATCATGTGGAATGTGAGAGAATGCCAATTATGACCAAGATANGTAAAAATA
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SEQ ID NO: 1786 ACTATGAACACCAGAACAGAAGAGATTTTTACTATTATGACACAAACACAG
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SEQ ID NO: 1787 ACGCGGGATAACCATGCACACTACTATAACCACCTAACCTTAACCTTCCCTA
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SEQ ID NO: 1788 ACAAAGAAGCAGCTCAGGAGGCTGTAACTGTATAATAATCATGAAATTC
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SEQ ID NO: 1789 ACCAAAACAGACATATAGACCAATGGAACAGAACAGAGCCCTCAGAAATAA
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GATTATAAATCATTCTACTATAAAGACACACACGATGTTTATTGCGGCACTGTTAACAATAGC
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ACACCATGGAATACTAAGCAGCCATAAAAAAGGATGAGTTTATGTCATTTGCAGGAGCATGGATG
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SEQ ID NO: 1790 ACTTGCTCATAGCTGGTGAAGGATTCTTCTGAACCCCCACCTACCCCTAA
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GAGACTTGTGTGTGGCCCCAACCCATAAGGAAACCAGGCTTTAGGCCAGGGGAGCAGTGG

AGGTAAGGGCTCCACCCCATCTTAAGCTCTGTCTCCGNGGCACAAATTCCAAGTTCTTTGACGTT
AGTAATTGTTAAAGGAATGGCAAAGTGTGTTTGAANGATCTTTCTACAGTCTGGTCNTACC
CATGTTTCCTTAGCAACCCTGAGATGATTTTCTTCCATTTTACCAAAAGC

SEQ ID NO: 1791 ACTATTAAGAAAAAGAAGATTGATTCTTAACCTACTGAATTGTGCAGATACA
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GGACAAGTGCAATTCTCTGAGAGCCATCCGGTCAATACAATTGAATGTGAAATTCATGCATGCAA
GGGTAATTGCCTGAGCTGTTTCCAAGTTACCATAGTCACTAAATACCAAAACACCTACAGATTTTA
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SEQ ID NO: 1792 AAAAAATTGCCACCAAAACGATGTTGATGTCCAAATTGACCAGGAGTCCTA
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ACACCCTGGAAAGCCGGCTGGATCTCATAGCCAGCAGATGATGCCAGAAGTCCGGGGAGCCTTG
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CTGCCCCAGTATTGCTCTGTATTTATCAGCGATGCCCTCTGTCACTCATGCCTTGCCTAATTGTTT
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SEQ ID NO: 1793 ACCCACAGAGACTGAGAGTTGGTGCTGGTGGTTGTGGTGGCAGATGATATTA
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SEQ ID NO: 1794 ACTTGAGTCAAAGACGACATTTAGATTCTTCAGCTTTGAAGCATTTAGTAACA
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TCCCCAGATAATGACATTCTTTACATCATTAGCAGTCACACCAAGTT

SEQ ID NO: 1795 ACATTTCAATAGCACGTTTCATCCTCCTCATTAAACTCGTCTTCATGATCCTCCA
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SEQ ID NO: 1796 ACTTTTTTTTTTTTTTTTTTTTTTGTGAAAACTTTTATTGCTCTTTTGGAT
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SEQ ID NO: 1797 ACGGGGAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGACCC
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GCTCCTCAGTTCCAGCCTGACCCCTCCCATCTTTGGCCTCTGACCCCTTTTCCACAGGGGACCTA
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AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCAAAAAAAAAA

SEQ ID NO: 1798 ACAAAGGAATGTTTCCTTTATAAATCACAGAAAGAAAATGACAATATCTGTT
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CATAATGCAGAGTTTAACTTTGATTCTTCAACAGAGTCCAGATTTAAATGTCTACTTGAATTA
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SEQ ID NO: 1799 ACGGATCTTACTTCTGGCTCCACGCGTCTGCTGGTATCCTGCCGGGGGA
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SEQ ID NO: 1800 ACTTCAACCAGGCACTCCAGGCCGGGACCGTGTGGGTAAACACCTACAACAT
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SEQ ID NO: 1801 ACTTTTATATATACTATCTATGAAGAATTCATAAAGCATGAATCACCTTATA
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CAGGTGGCTGAGGAAACCTTAACTTCCAAAGGCTCAAAGTGGTCTCCAGAGACTGTTACTCTCC
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SEQ ID NO: 1802 ACCCATGGATCTCTAGCATCAAGAACTTGAACACAACATCTGATGAATCTA
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SEQ ID NO: 1803 ACGCGGATTGCAGCATTATTTCAAGTTCAAAAATGAACATATGCCTGGCACC
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SEQ ID NO: 1804 ACTCAGTCTGAAAAGCTAACAAATACTGCATCTAACCACTCAATGGACCTTA
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SEQ ID NO: 1805 ACAGAGTCGCATCCATTCTTTTTGAACAACATGTAGCATGTCTGCAACAGTGG
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GCACTATTCTTGGCCCTTATAATTGTGGTGGTTATATNATNCACTAAGTCCTTACGACTTATAGAT
TTGATATTTTCAGTTGGNNCCAAAATTGGTCCGTCCAAGTGCAGTATTTTGA

SEQ ID NO: 1806 ACCTGTTGTACGCGTCTGTGTTGCCCTGAGCCGCTGGCTGTAGAGAAGGGC
TACATCCCTGAACCCAGGTGGGACCCGTTCCCGCTACTCACTGCGGTGGTGTGGGGGCTGGTGCTG
TGGCTCTTTGAGTATCACCGATCCACCCTGCAGCCCTCGCTGCAGTCTCCATGACCTACCTCTATG
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SEQ ID NO: 1807 ACGCGGGGCTTCAAGCAACAGCGACGCAAGATGGCAGCCACCACGGGCTCG
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GAGATGGCAGAGTTAGCTGGGGTCTAGAAGATGACGAAGACATGACGCTTACAAGATGGACAGG
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SEQ ID NO: 1808 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGGNGGCCACCACATCTTTATTGCATACT
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AGGAATTTGAAGTGAGAATGATCTACAAATCTCTGACAAGGAGCAACCGGGCTTGCTGCTANTG
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SEQ ID NO: 1809 ACCAAGTCCAGGTATAACATTCCTATTGGAAGCCATACTTATATTTTCTTGTA
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SEQ ID NO: 1810 AAACATGATTTTGGCCTAAAGAACAGCTGAACTGTTGAGAGAAGCAAGGGCT
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SEQ ID NO: 1811 ACTTTCCTTCATCGAATGATTATTTGCCTGGAGGAAGAAGTCTTCCGTTTCAT
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CNNTTGAATATTCATATCCAATTTGTCAGAAAACNTGTTTATCATCTCTCAAAGTTGGNAGAACT
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CTACACCTTTAAACAAACCTTTGCTGGCNGATCACAAACAGTTTGGCTTTTTTGA

SEQ ID NO: 1812 ACACAGTTTCAGAAAAACNAGGAATGAATACTATTGATGNCTGGTGGCTTT
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SEQ ID NO: 1813 ACCAACAGAAAGCAGGCCAGGCTCCCACTCTCATCTATGGTGCGTCCAC
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GGGAGGCCAAAGTNCCTTGCCGGGCGGNCGNTTNAAGGGT

SEQ ID NO: 1814 ACGCGGGGGTTTATCGTGTGAGCACACCATATATTTACAGTAGGAATAGACG
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SEQ ID NO: 1815 ACAGGCCCTTTGATGGCTTGGGTTACAGACAACCTCATAGCTGGTGCACCAC
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SEQ ID NO: 1816 ACTTCAAGTTAAAGTGAATAACCACTTAAAAATGTCCATGATGGAATATTC
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SEQ ID NO: 1817 ACTTNTTTTTTTTTTTTTTTTTTTTTCTGGACAGGAAGTANAATTTATTGGTGA
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GCCACGACTGGGGATGTACTACATTCATTGTGCACATATTTACGGCCCTCATACACCCCTTTTAA
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AAAAAAATTTTATATTAGCACATAGAATACCCTTAGATATATNTGNTNTGTTCTAAAGAGTTTGN
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GCTTTTAACTTCTTTTGATACTCCAGTGGCAACCATTTTNTTTGCCCATGCAANATCTTTTTTA
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SEQ ID NO: 1818 ACTTTTTTTTTTTTTTTTTTTTTTCCGGAATTTCTTTATTTTTTACAAA
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AATGCAGCCTGANCTGAAAATCAAGAACTAGAAAAAGAAAGNGGTAGANATAACTNTNTTAAAA
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GGCATTCTNGGCACTGTTTCTAAAGAAAACTCCNTTTTCCCAGCAAAAANCACANAAAGNGGA
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AGTTAACAGGGTTAACAGGAAGGAAGTGCCTTTATTAANTTCTCAAGCCAGAGGCTGGAGGCAG
CAGCTNATTNAGAGGACAGCATCCTCAGGTGAAAGGNGCCATTGGGGTGGCATGCACTCCANGA
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SEQ ID NO: 1819 ACGCGGGGACTCTGCGCTTCACCATGGCTTTCATTGCCAAGTCCTTCTATGAC
CTCANTGCCATCAGCCTGGATGGGGAGAAGGTANATTTCAATACGTTCCGGGGCAGGGCCGTGCT
GATTGAGAAATGTGGCTTCNCTCTGAGGCACAACCAACCGGGACTTCACCCAGCTCAACGAGCTGC
AATGCCGCTTTCCANGCGCTGGCGGNCNTGGCTTCCCTTGCAACCAATTTGGACATCAGGAGA
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CTTCAACCTTGTCCAAAAATGTGNGGTGAATGGNAGAACGAGCATCCTGCTTCCCTACCTGAAGG
ACAANCTCCNTACCTTATGATGACCATTTTCCCTCATGACCGATCCCAAGCTCATCATTTGGA
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ANNCGACNTTCTACATTAATTNGCTGGCTAACCTCTANAGTG

SEQ ID NO: 1820 ACTTTTTTTTTTTTTTTTTTTTTTCTATGNAACTGTCCCTCATCCTTCACCA
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TTTGGTTGTGAACACACACTTTTGCTTAATTNGTCTATTTAAATTAGAAAGGGAGGGGAAAAATAAT
CTAAAAATCCCAATAAGTCTGGAATCAATATTGAACTCCCCANATCAAAAGATTCTTAGAATC
TGCTCATAGNGAATCACTACAGCTTTGCTTTNNCTTGCAATGGCACCCAANG

SEQ ID NO: 1821 CGATCGAAGGGACTATGTCTTCATTGAATTTTGTGTTGAAGACAGTAAGGAT
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CATAATTGAGAGAATCCTGAGTTGATAGCTCTAANGCAGATTCTGATTTC

SEQ ID NO: 1822 ACCTTTGAATCTCTGTTACCTGAGGAAACAGCATTCTCAGCTTCTTGGTGCTC
GTCTGGTGGAGAAAGAACTTTTGCAGTAGCTCTGAGATCCTGGCTTTCCTGCTTTTCATGATTCTGG
AATTCAGTGGGATTACTTATTTTATCTCTGAATGATTCTGCTGTGAGTCAGGGTCCACACGGACA
GTCTTGACCTTCTCCTTGTGTTGTTGATGGCCAAAGTGGCTGTCTCTCAGCTTCTTCTGGTGC
TGATCTGAATCTCAGTCTCATCACAAAGAGGATGCAGAAGTTTGACTTTCATCCTGATTCTCATTTC
TTTTCTTGCTCATGTTAATGTAGCCTNTCAAGGCTTTTAACTTGTCTGCCTNGGTTGGCCCG
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SEQ ID NO: 1823 ACAGTTATGCTCAGATGAACACTGGACCCATGTGACAGGGTCAAGCACTAG
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SEQ ID NO: 1824 ACTTTATGTTCTTTGCAACTGTTTCCATTATGAGAACGCTGTGCTATTTACAAG
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CTAAAAATACAAAAATTAGCCGGGTGAAATTAGCCGGCGTGGTGGTGTGCTTGTATATCCCG
CTACTCGGAGGCTGAGCAGGAGAATCGCTTGAATCCCGGAGGCAGANGTTGCAGTGAGCCAA
GATCANGCCACTTGCACTCCAACCTNNGGGTAANAGCGAAACTCTGCTCAACANAAA

SEQ ID NO: 1825 ACTGTTTACCAAACCTGAAGGTGCAGTGCTTGCAATATTTTGTCTTGGGTGTCA
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CAGGTGTTCCAAAAGCTCCAATTCTCGAACCCACAGCTGCTGTTCCCAATCATACAGCCAGCAT
GGGCAACCAACTGTATAAACTGGTCAAATGGGACGTGTTAACTGCACGAAAAGTTGGGATGATGC
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AATGTCAGTGGCACAGGGTGTGTAGTGCAACAATGTAATCTTTAGATTTTACATCATCACCTAGC
CCATGCGAATGATGCTCATGTAGTCTTTGTCTTGACTGAGAGAAGTTTGCATANGAAGGCACCTGC
CAAAGGATGCGATCATGGTCCTCACACATGGATATCAAGTGCTGTCTGA

SEQ ID NO: 1826 ACACAAAGGATGTATGAAATGTGGGTTTTGTTGCTGAGGATAACAGGGTATT
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AATGTGATTTGACTGCAGGGGTGGCGTGTTTAGGAGGGACAGGAGTTACAAAAGACAGTTTG
TGACCTGAAGGCTTCAACAATATAATTCTATTCAAGCTTCCAGGACTGACAGAGGAAAACTGGA
TTCAGACAGAGAAAGCTGATNAAAATCTTACCTAGCTATTGTTCTTCTTTAAATAAAAAATAAA
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SEQ ID NO: 1827 ACCTGTCTTTTCTTTTCTTTTCTTTTAAATCATAGTTTGTGTTTACCTGAAAGTTG
AGAAAAGATGCAGTATAAATATAGCTTTTCTCTACACGGGAGCAGGGGGAACAGAACCAATCCCC
AGCTTAGCCACACCCAACATCATGGAATTACTGTGAACCTGTTGTCTCTTGAGGACAACTAAAC
CAAAACGAAATCCCTAACATTATTAATAATGTTAGGAACTTTTCAGGTAATTGCTGTAACCTGTTG
AAAATACAGAAAAGATTACATTCATCTATAATAAAAAATCAAGTGTGCCACGCCATCTGCAAAGGG
AACTTGCACCATCTTGGTTTCACTCGCATTTGTTAACAGTGCCTTAAAGTATACACCTTTTTCAGGA
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SEQ ID NO: 1828 ACCCGGCTCTGCATCGCGTCGCCATGATGGGCCATCGTCCAGTGCTCGTGCTC
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GCGGCCAAGTCCATGATCGAAATTAGCCGGACCCAGGATGAAGAGGTTGGAGATGGGACCACATC
AGTAATTATTCTTGCAGGGGAAATGCTGTCTGTAGCTGAGCACTTCTGGAGCAGCAGATGCACCCA
ACAGTGGTGATCAGTGCTTACCGCAAGGCATTGGATGATATGATCAGCACCTTAAAGAAAATAAG
TATCCCAGTCGACATCAGTGACAGTGATGATGCTGAACATCATCAACAGCTCTTTACTACCAA
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SEQ ID NO: 1829 ACACTTTTGTACAGTTACATATATGAATAGTTAGCAGAGGAGAACTCCTCC
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TATCACAAAATATTGATAAAATTGGAATTGTATCAATTATGTTATGGAGCTTAACATTTTAGCCG
AAATATTAAGATAATATAAATAAGGCTTTTAGCTTCATATCAAGACCTATTTGAACACTTCTAGAA
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TGGCNAAGATATTNAGTCCAAAACCTCAAATNACACCCCAAATATGTTTGTGGCTTAATCTAT
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SEQ ID NO: 1830 ACTTTATTTTTTTGTTTGTGTTTTTCTTTTGGATCTTGATTGATAACTGCCAT
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AGTATGCAAATATTGAAGTATGATGGTTTACTGTATGGCAGTGTGTAGCAGCCTCTGTTTTTTT
CCCCATTGCCTCTTTTTTAAAAAACTTATAAAGTCACTTTTTATTTTTCTCAGCTTCAATGACGA
GAGCAATATTAAAGAACATTGCTATCTAATTTTAAATCTTTTTAAATGAAAAAATCCTATGTTT
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CAACTTGCCTGCGTGGCAGCGGAAGACGATTCCCATATTCTACATTGCTACTGTTTTGTATAAAAT
AAATTGGTAAGATTGCGGCTAAAAAAGTCTCGCCGCGACAC
NCTANGGCG

SEQ ID NO: 1831 ACGTGGGTGAGGGGATGGAGGAAGGCGAGTTTTCAGAGGCCCGTGAGGACA
TGGCTGCCCTTGAGAAGGATTATGAGGAGGTTGGAGCAGATAGTGCTGACGGAGAGGATGAGGGT

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 GTACTCNTTTGGANNACCTNCTATGANNGAAAAAGTCTTTAATTTTGCCACTGAAAAGCATTCTGGTT
 TGNTGCTTTTTATATTTTTTATGCATATGAACATTTTAAAAAGTAGAATCGGTAATATATAGACTT
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 CTCGATGTATCCCGNGTACCTNCNNGCGGCCGCTNTAAAGNCGNATTCCTNACACTGGCNGTCGT
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SEQ ID NO: 1832 ACAAGCTTTTGTCCAAAAATGGCACAGCGAGCACAAATGAGTTCCTGTGTGAT
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 TGGCTACCATGGGGCTGCAGCTGAACATCACTCAGGATAAGGTTGCTTCAGTTATTAACATCAACC
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 CCATTAAGTATCTANACTTTGTCTTTGCTGTGAAAAATGAAAACCCGTTTATCTGAAGGAAGTGA
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 NATCCTTTGTTCTAANGGCTCACCTTTNATGTGACCAANGAAAGTTTCTA

SEQ ID NO: 1833 ACTGCCGACTTCCTCATCTTACTGGGTCCAGCATAAAGCAGATGTCCACTGT
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 TCATCATTTTCTCAAGTTGTGAACAAGTGCTAATTCCTCGGGGGCAATCGGGCTTTATCTTCTCT
 TTTCAGAGTGGTTCTTCCCAAAGAGCATGATTCCATCCACGGCCACTAGGAGGTGAAACATACC
 CAAAGAACTTTGCTCTTACTCTTTCAGCACAAATCCAACCTGATCTGTGC

SEQ ID NO: 1834 ACTATGCTATGTTGGCTAAACTGGTGTCCATCACTACAGTGGCAATAATATT
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 TTCACCTGCAAACCTTAAACCTGCAAAATTTTCTTTAATAAAATTTGCTTGTTTAAAAAANA
 AAAC

SEQ ID NO: 1835 ACTCAATCTGAAAGATGTAGAAGAAGGAGATGAGAAATTTGAATGACACCC
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 CTTTCTACATAAGTATAATAATGTGGGAATGATTTGGTTTAAATTAAAACTGGGGTCTAAATCC
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SEQ ID NO: 1836 ACTACGACATTTCTGCCAAAAGTAACTACAACCTTTGAAAAGCCCTTCTCTGG
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SEQ ID NO: 1837 ACTGTGTGGCGCCTTATTCTAGGCACTTGTGGGCAGAATGTACACCTGCCG
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SEQ ID NO: 1838 ACTTTTTTTTTTTTTTTTTTTTTTANAACCTNTGCAATTATTAGTTTATTA
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CGCTATTTTAAATACTGGCACTTTAANAAAACGATAATCTCGAAAACCAAAAATTGCCAAATT
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TATAAAGGGGCAAACCGTAATATANGAAAAATATACCCTATTTTGAATGTGGCATCTTTGTTGAAA
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SEQ ID NO: 1839 ACAGAAGTTTTTCATCTATGAACATGGCCTCATCATCACCTGCAGCCTTGGCCT
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CTTCATCCCCAGGGCTTTCTCAAGCTCTTCTACCATGTTGATTCCCGGAAGGTGGGGTGAAGTCA
ACATCGTAGCTTGGCCCTCTGGGCCATCTGGGTGGAGGTGACCTGTAACTGCCTGTAATATGCTT
CACCATCCCTGAAACCATCTTCTCCGTGATTTTCATGAGTCGTGATAGTC

SEQ ID NO: 1840 GCCCTTTACATCGCTGAGAGCCGCTGTCTTGTTAGATGGCTCTGGATTAGG
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AGGGGGACATCCCTACATTTTACACCTATGAAGAAGGATTATCCCTCTAACAGCAGAAGGCCAAG
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SEQ ID NO: 1841 ACGTGCACCTCCTGTTTCAAAAACGCAAGCAGAAAATAGGTCTGGACAAGGG
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CGGTGTCTCTTCAAACCTATTCCTTCCATTTTATTTCTCCAGTTTGTTCTTGAGGTTCCGAAGTCTCA
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TCCAAACATGGAGATAAGGAAATAGCTCGCCAACATGACCACCATAACGAACGTNGTGGGGTAGC
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CACCAAGATTCTCCAGGATCATGTTGAAGGGACTCAGAAAACCCCAATGGAAATCATNATGGC
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SEQ ID NO: 1842 ACGCGGGGCTTTTCTCTCTTCAGCGTGGGGCGCCACAATTTGCGCGCTCT
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ACAAGCAGATGTGGCAGTATTTGAAGCCGTGTCCAGCCCACCGCTGCCGACTTGTGTCATGCCCT
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GCTTTGGGCAAATATGCTCTGCGGATGTGGAAGACACTACANGGAAGTGGAGCTACAGATAGTA
AAAGATGATGATTACATTGACCTCTTTGATCTGATGATGAGGAGGAAAGTGAANAANCAAGAG
CTAAGGGAAGAAGCTTTGCACAATATGAATCAAAGAAAGCCAAAAAACCTGCACTTGTGCCAA
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SEQ ID NO: 1843 ACTACCAGGTATTGGTTCGTTTACAATTATTGATGGAAATCAGGTCAGCGGA
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ACCTTCTAGACAAATGATCCCTCATTTTCTGTAGGTTTACTGTTGTAGTTGCAACTCAGCTTCTGTA
AAGCACTTCACTACGCTTAGCAGATGTCTCTGGAATTTCCAGATTCTCTTTTGTATCTGTAGGAC
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TATGATTTGGATCATATGGAAAAAAGGCCACAGTCATACTCCATGGATTGNGATCATAGCTAAA
TATTTAGCACAGTGTTAGTGGAAACAAATGGACGAAT

SEQ ID NO: 1844 ACATCCTACCCCTCTCCCATTTCCAGAGCCACCTAAGAGAAGTAAAAAATA
TTGGATGTTGTCACTGGGAGATTTTGTGTAATCAAAACAACAAAACAGAAACATGTTGGAGACT

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AGGGATCCATGGTCAGCTTTGACTCTACCAAATGCCAGGTGTGGACCGATGGTTGGGCTGGTTG
TATTGATGCTTTGGTAAAATCCTTTCTCGCTCTGGGCTTATTCCTCTCTACCCAGTGGTCCCTG
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CCATATCTCCCCATCAAGGTGACACGGTGACAGTTCCTGT

SEQ ID NO: 1845 ACTTTTTTTTTTTTTTTTTTTTTTAATTTTGANATGGAATTTTGCTCTGTGTCAC
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SEQ ID NO: 1846 GCGTGNITTGTTGCCGAGGTACAGGTAGAAGCTTGATTGCTAGGCCCAGGCC
CACCCAGACCTCCAATCCTAACAGGTATTTAGGCTTGAGGTTCACTCCCTCCTCAGCTGCACACG
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TTATTTATAAAATAAGAATTACATTTATATAACATGGCCAGAAGGAGCTCTAGTCCCCCAGGAAA
GCTGCCGGGGACAGCATTTGAGCCTCTCTTTGCACAGGCATAACTTAACTATACAGCTAATTCCT
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GCTTAAATACAAAAATAAATTTTGTAAAAAACGTTTAAATATTTTCTTTTAAATTTAGACACA
CGCATTCATACTTCTCCCAAAGAGGCTGGGCGTGACAGCAAGGCGCTTGGGCTGGGGTATGTGG
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SEQ ID NO: 1847 TTCGCCCTTTTTCTTTGCCCCGGGCAGGTACTGNAATTGAGCATCCGGAATA
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GACTGGCTAAGGACGANCAGCTGAAGGTTTCATGGGTTTAAAGTGCTTGTGGCTCACTGAAGCNTA
ANNAGGATTTCTNGCAATGAAGTAGAATNACCCCTTCNCTCCCTTGTCACANGGNTAAAAACC
NCACAGCTTGTATAATGTAACCATNTTGGGGTCCCGCATTTNTAACTTNGACAANTGNAACTCCNT
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SEQ ID NO: 1848 GCGNGNTTGTGTTTCGAGGNACCTCGTTTTTCAGGTTTCATCCATCTCCAGTGGA
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SEQ ID NO: 1850 ACCAGCAGTGTGTCAGGNGCTGCAGAGCGTTCCTTGAGAAAGGCCCACTGAGG
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SEQ ID NO: 1851 ACCGCGGGGGCGTGGCGGCGGTGGCGGCTGCGGCAACAGCGGGGCCGATGT
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SEQ ID NO: 1853 ACCTGAGGAAGCGGTTTGGAGGCCAGCGGATCCAGGTCTACCTTTCCCTTCTG
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SEQ ID NO: 1857 ACAAGTTCGGCTTTGAGCTTCTCAGGGGCTCTGGGAACATCCTTCAAAGG
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SEQ ID NO: 1858 ACGCGGGACACTTGGCCAACCATATTTATTTTTATTTTTATTTTTATTTGA
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SEQ ID NO: 1860 ACTGTTTTTCAGTATTTGGGGAGGGTGGTTTGAGCAGCATTTATTGACAATTT
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SEQ ID NO: 1861 ACGCGGGGAGGAAAGCCGTGCGTTGCGTTCCAAGGCATCTGTGAGCCCGGG
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SEQ ID NO: 1864 ACAAGTTCACACTCGCCCCACGGGCAAGTATATCATAGAGGGAGGAAGCCAC
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SEQ ID NO: 1865 ACCCAAATATAAAATACTTGTTTAAATGTAGAGTTTCATATCCTTTAAACCTC
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SEQ ID NO: 1866 ACACCTTGAAGGCGAGGTTAATTAATCCTGTTGTGGAGTTTGAGGGCCGGA
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SEQ ID NO: 1867 ACAGCCAACGGTTTCCCTTGGGGGCTTTGAAATAACACCACAGTGGTCTTA
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SEQ ID NO: 1868 ACGCGGTATTGAAGGTGGAGTAGCAACCGGGCATTATATTATCTCTTGAA
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SEQ ID NO: 1870 ACGCGGGGCTAAGTGTTCGGTGGATTCCCAGGGACTGTGCGAGGTGTGGA
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SEQ ID NO: 1871 AACAGTTGGAGTCTGTGTGTTTTCTTGAATGTTTGAGACAGCTTCACCTTGAA
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SEQ ID NO: 1872 ACTTTTTTTTTTTTTTTTTTTGGTAGTTCTCACAGTTTAATAGAAAGAATGCA
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SEQ ID NO: 1873 ACGCGGGATCCAACCCTGAAGATATTTAGAGATGGTGAAGAAGCAGGTGCTT
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SEQ ID NO: 1874 ACGCGGGGACCGCGGGGCGGACGGGAGCGAGTATGTCCGCTCTGACTCGGCT
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SEQ ID NO: 1875 ACGCGGGAGGAACTGCTCAGTTAGGACCCAGACGGAACCATGGAAGCCCCA
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SEQ ID NO: 1877 ACGTTGAAGGACTTTGCTGGGTTCTGAGTGTTTGTCCCTCACATAGGATTCCA
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SEQ ID NO: 1878 ACAGATGGTGATTACAGAAGCCAGAAAGGTTGATACCAGAGCCAAGAACGC
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SEQ ID NO: 1879 ACGCGGGGTTGCAGTGAGCCGAGATCATGCCACTGCACTCCAGCCTGGCGAG
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SEQ ID NO: 1880 ACATCCATAAGCCAATTCTTCACTAATTAACAAGCATCAAAAGTTCCAAGT
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SEQ ID NO: 1881 ACTTGTAGAGATTGACTTCTAAGCTACTTAAGACAACCTGCACCACTAAGA
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SEQ ID NO: 1883 ACTTTTTTTTTTTTTTTTTTTTTTTTGCATTCTCTTTAGAATGTTTGGTCATTAAC
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SEQ ID NO: 1884 ACACAAAGAGGGGGTGGGTGTCGGATGCAGAGTGTGTGGCCTGATGCTCCAC
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SEQ ID NO: 1885 ACACTGTTGGTGTATATGGGGATGGGGTTCTCGGTAATTTTGTATTATTATA
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SEQ ID NO: 1886 ACGCGGGGGAACACCTGGCGAGTCTCGGTGTGGTGGCCGGCAGTCATCTC
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SEQ ID NO: 1901 ACCGCGGGGGGCGACTGAGCGGNCAACGGAAGTGTTNGGTTNCGGTCTGA
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SEQ ID NO: 1938 ACGANAACAGAACCAATCTAAAAATGGCTGATGTTACTTTANGAGCCTGAAA
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SEQ ID NO: 1944 ACTAAATGCACAATTTAAACATCAGTTATACACTGTCATTAGTTTTCTCTTA
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SEQ ID NO: 1945 ACTTGGCAGGGTCTTGCCACAGACACATTTGGCTCCAGGCTGCAGTTCACAG
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 CCTNTTGC

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SEQ ID NO: 1952 ACCATCGCACACACTATTGACGTCATTGGAAAGAAGGAAGACGACTTTGTCT
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SEQ ID NO: 1956 ACAGTATTCATTTATGCTTGAAATTCAGTCTAGACCAAGCTTGTGGCCACC
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SEQ ID NO: 1957 ACGCGGGGAGGCATTGAGGCAGCCAGCGCAGGGGGCTTNTGCTGAGGGGGCA
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SEQ ID NO: 1958 ACACATACACCTAAAGAGTCATGGCCTTCTTAAACAGCTTTCTTAATCCTT
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SEQ ID NO: 1970 ACAAATGTGGATCACAATAAGACTCTGAGCCACAGTCTCCTGGCATTGGA
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SEQ ID NO: 1971 ACTTCTGATAGCTCATCACTTTCTGTGTCAGAACTTTGAAAAGCAAAGACAGG
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SEQ ID NO: 1972 ACGAGAAAAGGGTCCGAGCACAAGCCAAGAAAGTTTGGCGCCTCATAAGCAG
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SEQ ID NO: 1973 ACACGAGAAGCTCCGAGGATGGCTGAAGTCCAACGCTCTGATGCGGTGGCT
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SEQ ID NO: 1976 ACGCGGGATGTGAGCTCCTGAAAAATCTGGCCTTGTCTGGTTTTAGACAGATT
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SEQ ID NO: 1978 ACTTCATTCCACATTCAATCAAAGCAAGTGCAACCAGCACAGGTGCCCTTC
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SEQ ID NO: 1980 ACAAGGTGAATATCTTAACCAGACTTGCCGCAGAAATGAACAAATTTATGCT
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SEQ ID NO: 1992 ACTGGTCCAGGAGTTATCCAGGATAGATTTTACCCACCATGGGACGTCATC
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SEQ ID NO: 2032 ACGGCTCCATGGGATTAAGGAAGCAATGACATCCTGATCTGTTCTCTGATCT
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AGATGAGAAAAATCTACGAGCTTCTTATTTACAACACTGCTGCCCTTCTCTCCAGACTCTGAC
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CACTGCCTGAAATTTTTANTNTTINAGGGAGTACATTGGTGGTGGGGGAAATTTGTTACTACCTTN
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SEQ ID NO: 2033 GCCGTAGGTCCGCGCCGANGTACTTTTTTTTTTTTTTTTTTTTGTAAAACAAGC
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CAGGGTGCACACTCTGTAGTATATTCNCATACTGTCCCANNTCAATATNANTGCNACTGNAATNA
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SEQ ID NO: 2034 CCCTTAGCGTGGCGCGCGGAGGTACAGATCCGAAGTTTCAAGGGCAAACGT
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NGGAAAAATCCAAAGGGCCCCCTGGCCAAACNTATTCCAATTGNACCTGGTGNGGTNGCTGNAATTG
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SEQ ID NO: 2035 ACCTCTCCCAAGAAGTTCATTATATATCAGAAATTAATAAGCA
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CAAAACACTGAGTATTAAGTAATTTTCATCTGCCCTTTTGTATCTACAATCATTTTTCAAATTTAG
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SEQ ID NO: 2036 ACGCGGGGCTCTTCCTGCTCTCCATCATGGCGCAGGATCAAGGTGAAAAGGA
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SEQ ID NO: 2037 ACCAAAGAACAGATAAAAAGGAGGAACAGGAGACGAAAAGAAAGCGAAAGA
GAAAATTGAAAAGAAAGGAGAGAGAAGGAGAAAAAACAGCAATCAATAGCTGGAAGTGCCGA
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CCCTGATGCAGATTCTTTGTATGTGGAAGAAGTTNATGTGCGGAGAAATANCCCCAAGGACAGTTG
TCAGTGGCNTGTTGAATNATNTTCTGTTGAACNGNAC

SEQ ID NO: 2038 ACCTGGAGTGATGGATGGCGTTCCCTCGGCTAATAACTATCAGGGTGGATTT
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SEQ ID NO: 2039 ACCAAAGAACAGATAAAAAGGAGGAACAGGAGACGAAAAGAAAGCGAAAGA
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CAGTNGCCTNGTGAATCATGTTCTNTNTTGAACANATGCAAAATCGGTTGGGNNTTNTCTNGTANC
TGAANCTGCAA

SEQ ID NO: 2040 CCCTTAGCCGTGGCGCGGCCGAGGTGGACCTTCAGGGGATCAAAGCAAAGTT
CCAAGAGAAGTATCAGAAGTCTCTCTGACATGGTTGCTCAGATACCTCCGGGACTTCCGGAA
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GCATTTNATGGGCACAATTTAGAAG

SEQ ID NO: 2041 ACGCGGGCGCTGTGGAAATTTGGTCTTGGGCTGGGTGGCATCTGGCAGTCAT
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TTCTTT

SEQ ID NO: 2042 ACGCGGGACTACTGGAANTGCACAACTGGCCACTGACAAAAATGACCCCC
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CAAGCACACCCTGGGAGACAGTGATAATGAAAGCTAAGCCTCGGGCTAATTTCCCCATAGCCGTG
GGGTGACTTCCTGGTCACCAAGGCAGTGCATGCATGTTGGGGTTTCCTTTACCTTTCTATAAGTT
GTACC

SEQ ID NO: 2043 ACGCGGGGAGTCCGCTGGTCCCGAGCAGAGCTGTGAGGGGATTCACTTGTG
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AAAGTTTTAATTGATATGTCAAGGGTTCAAATGATGAAATTGGTGATGGCACTACCTNTGGTACC
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SEQ ID NO: 2044 GCGTGCGCGGCCGAGGTACCCCTTTCCATAGAAGGGGGAAGCCCTCTTTTC
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SEQ ID NO: 2045 ACAGAGTGACATCGGCAGTTGCAGCAGCAGCAGTAGCGGCAGGAGGAGGGC
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AAAGGAAAGGGCCTCCATCACTTTCACATTAAGTTCTGANAGTTCTGAATGTTTCTATCAATATC
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SEQ ID NO: 2046 ACGCGGGGGCAGTGAGTTGACACACCATGCCGACTGTCAGCGTGAAGCGTG
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CCATTTGNT

SEQ ID NO: 2047 ACGCGGGGGTAGCCGGAGCCGGCGACGTGAGGCGGGCGTTGCTCGCGCGAC
AAGTAGTTGCTGGGACAGCGAAATGGAGGGGTGTGTGCTAACCTAATGGTCTGCAACCTGCCTA
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SEQ ID NO: 2048 GCCGTGCGCGCGCCGAGGTACTTTGGCCTCTCTGGGATAGAAGTTATTCAAG
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AATGCCCANTAAAAATGAGCAGTTTAAAGGAGGNTGCCTGGCTTTCTGCTGATACCAANCCTAAGTA
NTTNTTATTGGTTGGAAGGNTNTANTAAAAANACTTTGGCTGGGACNTGCATTTGATNGTGCCTCT
CNCCCAGATANAC

SEQ ID NO: 2049 ACAAGTTTGAAGTGGATACCTCTGAAAGAAAGATTGAATTTGACTCTGCCTGT
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ACTCCAAACAGGAAATTCAGCACCTGTTCCGCGAGCCTGAGAAGAGGCCCCCACCGGTGGTGT
CCAATACCTTCACTGCCCTGATCCTCTCGCCGTTGCTTCTGCTCTNCGCTCTGNGGATCCGGATTGG
TGCCAATGTCTCAAATTTAACTTTTGTCTTAAGCACGATTNTATTTACCTGGGGACATTGTCTGC
TATGCTGGGGACTCATGTATGGTCTACTGGGACTCACTTANCAATGTTCAGACCTTGAANTTCC
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SEQ ID NO: 2050 ACTGAAAAATGAAAAACAGCAAAATCCAAGGGTGAACTTTGACCTANATTG
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GACCATCCTGGCCAACATGGTAAACCATGTCTCTACTAAAAATACAAAAAATTAGCCGGCATGG
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GGTGGAGGTTGCAGTGAGCTGAGATTGTGCCACTGCACTCCAGCCTGGCAACAGAATGAGACTCT
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SEQ ID NO: 2051 ACTGCAAGACCCATCTTCCCTCCAGTTAATACACTCCCAGGATGGGCTGCAG
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AATGTGGGAATAAAAAAATCATGTCCAGGTCATCTTTGTGTGTGTCGGGGGAGGTGGCATGGGA
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GTNTGTAAACAATGCCGNTTTTITAGGTTATTTGGCACTCCCCCTATATACNTAGCCCANATCT
TTTNTNAAGTCAAGTGCTTNTTTTCCAAAAATAATCCTNTGAAATC

SEQ ID NO: 2052 ACCTTCTTTTCAGAAGTAAAGCCTGCAGGCCCTACTGTTGAGCAGCAGGGAG
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TCAAAATTGAACAGCCTGCCATCGGTCTTGCNACAGATCGCAANCCTCCTCCANNACAACGTGG
GGACCTGTTTTTGGCCCCACCCCAATCGCCAAAAACTTGGAACGGAAACAAAGTACTGTCCA
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CTCTGACCCNANAAGNTNTTTTATCCATGGGGTNAAGGAGGGCCNGCCACTTGGTTNAATACC
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TTTCCANN

SEQ ID NO: 2053 ACACATTAAGCATCCCCAGTTCCCTCGCACACCCCTTTTCCAGCCACTAGT
AACCATCCTTCTACTCTCTATATCCATGAGTTCAATTGTTTGAATTTTAGATCCCCGCAATAATT
GAGAACATGCAATGGTTGGCTGGTTCTGGCTTAATGTACTTAATATAGTGACCTCTANTTTCAATC
ATGANTTCTTAACTGGCCCTGGATTTTTGACCTTTATTTTTAAAGATTTTGGAAAACCTCNAACTGGT
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SEQ ID NO: 2054 ACTCCAGATGGCGCCAAAGAATAAATAGGCAGGTCTCTATGATAAAAGAAACA
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NTTA

SEQ ID NO: 2055 ACTAAAGATGATGATTNNTTNGTGGNATGCCTGAAGGGGCGNGCNCATTCA
AAAAAGTATTGGAAAAACATTAAACCAAGAAAAAGGCTCCTTGCCCTCCTAATCCATATCCANATA
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CNCTTTT

SEQ ID NO: 2056 ACTTNNTTTTTTTTTTTTTTTTTTTTTTTTTGGGTAAGGGCCGCAAACTGCTGCAA
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ACTC
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AAN

SEQ ID NO: 2057 ACTGTAATCCAACACTTCTTTGTTAGCACAGCCACCCAGTTCACACCCCGG
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SEQ ID NO: 2058 ACAAACATGGGTGAGCAAAAGTTCAACTCAGGTAATAAGTGATTAAAAACA
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SEQ ID NO: 2059 ACCATTTTATTAGTGTGTAGGAAATGTTGGGTTACTTCTTAAAAACGAAAC
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ACCATAAGGAGATACGGAGTTAAGTTTGGTGGATACTAGGAATTAAGTTCTCCACCTAAGGCAATT
AATTTTTCAGCCTTGAGAGATAATTAGTAGTTCTAGAAAAAGAAAAAGTTGACTGGGANAAGGG
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GANAT

SEQ ID NO: 2060 ACCCATCATTACTCCCACTNAGAAAGAAAGAGTAAATGAATGTGGTGAAAGT
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NAAA

SEQ ID NO: 2061 ACAAGATCTACCCCGGANTTTGGAGGCGCTACGCCAGGACCGACGGGAAGG
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SEQ ID NO: 2062 ACCTGTCTTTTCTTTTCTTTTCTTTTAAATCATAGTTTGTTTTACCTGAAAGTTG
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AGCTTAGCCACACCAACATCATGGAAATTAAGTGTGAACCTGTTGTCTCTTGAGGACAACATAAAAC
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N

SEQ ID NO: 2063 ACTGGCTCCACCCCTTGGTGCTGGCAGTGTTGGGGACATTATGCTGGAAAG
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GATTTTCTTAAGTGTCTTGTGCAATCGACAATGTGCTAACCTGCTTTTCTTTTGTAAACGTTTT
TGCAATACAGGCTGCATTCTTGCTTACTGTATAGAAAAAGAAAAAGGCTGGGTTACTATTGCA
CATTTTAAAGCNTTAATACCTTTATCTTCTTGGAAATGGGCAANAATTCTGAAGTGAACAGTCA
AAACNACAGGNTTGNTTGTAAANGGAATTTTAAATTNGNCCATTTTNAACCCCTNNAGGNNAANN
ACTTAANAATATNCCNTGTGNITNACAGNNGTGAGGGGCTGTTATNTNATGTTGCATAAAATTN
NTTGTNAAANGGAAAGTGNTTCTTATGGG

SEQ ID NO: 2064 ACATATAGGTGGAATGAATTCTATCCTTGACATACTGAGGCCAAATTACAGC
CTTTCAATAGCTCCAATCTCAATTAGACAGTCCCAAGCCATAGTAGCACAATGCTCCAAGACCAAC
AGCAGCCCCCTCCAGCAACAAACCATCTTCCATCTGATCAAAATTTAAATATTTTTTATTCGATGG
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GNGGCTATTTCTGGCTAGGGTTTAAACAGCCNNTTNGATCTTTNGGAATGGAATCTTTACAACA
AGGGAGGCTTTGTGAAAGCTTGGTGAAAAACCTNAAAAGNANTGNNCCGGAAACACNCCAC
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SEQ ID NO: 2065 ACTAAGTAAATGTCTGCTATTATTTTTTAATTATTTTTTAAACATCTCATT
CCTCCTTGTGCACCTCTTGTTCCTTTCTGAATTATGTTGACACTGAAGACCAATGGGGTTCTGCCA
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GTACTACCAATNCTTTTTATAAANATAATGGTTNGAAACCTGGGGATAAANGTTAAGGANCAAAA
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CTTGTNTNAGTTCCCTGGAGCCTNTTTTNAAGTCANATTTCANACCCCCCCCCGTTCTGCCNG
GCGGGCCGTNNAAANGGCCAATTCACNACTGGCGGNCGTTCTANTGGATCCGANCTCGGACCA
AACTTGGCGTNATATGGGCANAGCTNNTTCTTNGGGAAATTTGGTATNCCGTTACAATTCANAA
NATTCCAANCCGGAAGCATTAAGTGNTAAAGCTGGGGGGGCTTATGAAGGGACCTACNTACATT
NATTGCGTTGCCCACTGGCCNTTTCAA

SEQ ID NO: 2066 ACGAAGAAAGCATTTCCCAAGCAATGAGTCTCTTAATGGAAAAAATAAAAGA
GCAATGTAATTAACCTTCTTCAAAGAAAGGAAAGAAACCTAAATCTGTTATGGCAAATTTGGA
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CAGTGGGGAACACCTTCTGGAATTGCANGTGCAGATGCTGCCTCATCCAAATAAGAACTGCTTCAT
CANCCAGAAGCTCATACCTAGTGCATCCAACTCTGCTTCTAAATCATCTTCATCCAGTTCTGGGG
TGCCATAACTGCGACTCAGTGCCTCTTGATTTCATTTGCATCTTCCATCATATCCTCTACTGGTCT
TGNAATCCCTAATCTGGTGCATCTTCACTTTGCTTTGTATGCCTTCTTCATTTCTTAACTCCAA
GTTTCTAGCATCAACCGNGGTCTTTGGTGTNCCTTCAAAAGACTGGATNGTATAAATTGGCTTGNTC
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A

SEQ ID NO: 2067 ACCAGCTACTGAATACACCGGATCTAGATATGCCAGTTCTACAAATCAGAC
AGCAGCAATGGACACTCTTAATGTTTCTATGTCACTGCCATGGCAGGCCTTAACACACACACCTC
TGCTGTTCCGCAGACTGCAGTGAAACAATTCCAGGGCATGCCCTTGACATACACAATGCCAA
GTCAGTTTCTTCCACAACAGGCCACTTACTTTCCCGTCACCACCAAGCTCAGAGCCTGGAAGTC
CAGATAGACAAGCAGAGATGCTCCAGAAATTAACCCACCTCCATCTATGCTGCTACAATTGCTT
CTAAACTGGCAATTCACAATCCAAATTTACCCACCACCTGCCAGTTAACTCACAAAACATCCAAC
CTGTGAGATACAATAGAGGAGTAACCCGATTGGAGAAACGACGCATCCACTACTGCGATTAC
CATGGTTGCACAAAAGTTTATACCAAGTCTTCTCATTTAAAGCTCACCTGAGGACTCACACTGGT
GAAAAGCCATACAAGTGTACCTGCGGGCGGCCGTCGAAAGGGCG

SEQ ID NO: 2068 ACTGCACGGCAATTGAAGCATAGCTACTACAGAATAACTCACCTTCCAACAA
TTCCTGAAATGGGTCCCTTACTGGGATTATTACAGCACCAAAAACTTCTCTGAAGCCTTTCTCCA
CAACCTTGTCTATGGGATTCCATAATGGTACCAATGGGATTAAAGCTATGAACCTCAAANCATC
ACGAGAATAACCATGATGGGTCTAAGACTTGGGAAAACTGGCCTAAATTATGNTGGAAGGGAATT
ATGTTAAATTTGAATTCATCTGGGAAGCATTCAAATCAANCTTAAAGNCTAATCTGAAATGCTATG
ACAGCCTGAAAGGNACTGGGAATCTCATTTCTATCATTTGACTAACTTTAAATGTTGGATCAATAT
ATTTAAGNGNATTGAAAATGCTTTGGAGGGAGTCACACTTATCTATCAACTATTAGTCTTCCAC
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SEQ ID NO: 2069 ACTTNTTTTTTTTTTTTTTTTTTACCATGCAACGAAACCTTTATTAACATT
TTGACAGGTTCACTATTACTGAAACTTGTAATTTCTAACTTAAGTTGGGGCAATGGCTATAG
TGCAGAATAATGCCATCACTGGGCACTGCGAATGCCATGACTGAAAAATTAACAGCCACCCNTNA
GGCGCAGGACCAGGTGCAGGTCCACTCTTCTGGATGTTGTATCAAAAAAGANTGCGGNCATTN
TTTCAAGCTTNTTTGCCCTGAAAAANAACCTNTGCTGGTGGGGGGGATCCTTTTTTTATNTTGG
ATCTTGGCCTTTACATTTTCGATGGGTCTGCTGGCTCCACTCCAAANTGATGGTCTTGGCGGCA
AGGTCTTCACNAAAACTTNATTCACCTTTTAAACGCANGACCAGGTGCANGGGTCACTCTTTTN
GATNTTGGAAATCAAAAAANTGCGGCCNNTTCACTGNTGCTGCAANATAACCTTTGTTGGTCC
GGGAAGGGATGCCTTTTTTTTCTGAGNNTTNGCCTTTAAATTTTCTNATGGGGNNTAACTGGGCT
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SEQ ID NO: 2070 ACAAATCCCAATTGCACCATTAATTATGGGGTCACATCCAGTTGACAATAA
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AAATTTCCCGCAGCAATCCAGTATCTAGAGCATTGTGCAAACTGCANAACTGCACAGGAATT
CATTGTGAAACTCAACCACTTATGCCCCGTGATGAACTGATCACTCANTTTGAGCTATCAAAG
GACCTGACCCCATACCTTTGAATCACAACATGAGATTTTATGCTGNTCTTCTGGCAAGAACT
GCTATTTCTCAACAAGGATGCTCCTCTTCCAGATGGCCGAAGTCTACAGGGAACCTTGTAGCA
AAATCACCTTTACAGACCTTGCCGAGTCTCTTATCTAAATCTGATCAAAACCAAGTGGGNTA
TAACACCCCTCATTTGGAAGCTGGGTNAAAAAACTATTCTGAAANAAAAATTTTCTGGGCTTTT
CCAAATTTGAANTGNCCCTTTTCAAAGTCTCGTTAACNTATTTTNTNANNACCCCTGNTGAATG
ACTCC

SEQ ID NO: 2071 ACTTGTGGGCCAGCTTAAGCAGCTGAGTAGCTGTTGGCGGTCCAGGGCCTG
GGTGAACCTGGTTAATCGCAGGAAGCACTTTCACCCGCTTATAGAGGATGGGCTCTGCCCCGTG
AAACCTGATATAGCGGGGCCATTTTACAAAGCNGGTGAAGGGTCTTTTTTGGCTGGAATGGTCC
TTGCCAAATGCCAAATNTTAAAGGCTTTTTTNAAAAAAGGGGAATTCAACCACTTTTTTAANCCTC
CTGNTTTTTTAACNAAAAGCTTGGGCCCGGAACCCACCTTTTTTCTTTGGGCTTTTTTCTTTNC
GCATTTCTTGGGCCGCGGGAAGAAAAAAACCCCNNTCCNTNGGCCGNAACACCTTAAGGG
CNAATTTCAANACACTTGGGGCCGTAANTGANTCCNAACCTTNGGNANCA

SEQ ID NO: 2072 CACTACAGAGCAGTTGGGGTATGATGGGCATGTTAGCCAGCCAGCAGAACCA
GTCANGCCCATCGGGTAATAACCAAAACCAANGGCAACATGCAGAGGGAGCCAAACAGGCTT
CGGTTCTGAAATAACTCTTATAGTGGCTCAATTCTGGTGCAGCAATTGGTTGGGGATCAGCAT
CCAATGCAGGGTCCGNCAGTNGGTTTTAATGGAGGCTTGGCTTCAAGCATGGTTTTTAATCTTIN

TGCTGGGGAAATGTAACAGGGGGGGTTGTGGNT

SEQ ID NO: 2073 ACCCTTCNCNTTACCTATGCCCATGTGCCTGCCCTTCCGGCGGGCCAAAGGTGT
TTTTCCGGCNTCGAGCCCGGGGAATGGACCGTCACAGGCTTGGCGATGATCAGCCCATCTTTTGAT
GANCTTNCGGATCTGCTGACGGTAAGTTGGCATTGGGCGATTANATTGGTNTCATTGGTNGTCTA
NCCACACCTTTNTTTTTTGNAC

SEQ ID NO: 2074 ACTTTTTTTTTTTTTTTTTTTTTTCTGGCCATTCTTGGCACTGTTTCTAAAG
AAAACTCCATTATCCCAAGCAAAAAGCACAGAAGGTGGAGTTTGGCTTCAAGAGATGTTAACTC
AAAACTTTAGGCCTAGCAGANAATCACCAATTTATGGAGAAGTTAAAAGGGGTTTAAACAGGGAA
GGAAGTGCTTTATTAAGTTCTAAACNANAGGCTGGGAGNCACANNTTAATCAAAAGGAANNCTT
CCTCAGNGAAAGGTGAACCCATTGGGGGTGGCATGTACCTCAAGAATTAACCCCACTTAAAAA
CAAATGATTTCTAGGATANACNNNGCCTGGTGCCTGTGAACCCCTGAGGCNCTTTGTAAACTTG
GCNCTGGTTNTGAATNNGGANACCCAAATTTTNCNCTGGTATGAACTTTATGGCTCNATCC
TTTTACCTTAACTTTGTAAANCANCNTAAAACCNACCCNTCCAANATTACCTTTTTGGGGGA
ACNTTTNTTNGGCANCCCAAANGAAAGGACCTNNTATTCCCATTTAGACTTNCCC

SEQ ID NO: 2075 ACCCTTCNCNTTACCTATGCCCATGTGCCTGCCCTTCCGGCGGGCCAAAGGTGT
TTTTCCGGCNTCGAGCCCGGGGAATGGACCGTCACAGGCTTGGCGATGATCAGCCCATCTTTTGAT
GANCTTNCGGATCTGCTGACGGTAAGTNGGCATTGGGCGATTNNATTGGTNTCATTGGGNGTCTA
NCCAAACCTTTGTTTTTGNCA

SEQ ID NO: 2076 ACCCTCTCTTGTCTCTTCAGGAATCAAGGGTCTGTATGCGGCAAAGGATGA
AGTTTTAGGAAGCTCTGGGTCACAACGCTCTGCCCCCTGGCATTANAGATANTTGCCAGTGGGC
TTTGCCATACACTGGCACCAGTGTGNTNAACTGTGANGCCCANCTATNCACANGTCTTCTGCCNG
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SEQ ID NO: 2077 ACTTTTTTTTTTTTTTTTTTTTTTNNCTGGGAAAAATGTTTTATTCCTCTTTG
CACAGANCAGTTNATGAAGNGGTTTTCTCCTGACTCCATGCATCTTTNACACAAAGATGCCCCCT
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ATGCTTAAGTCTCANGANGGTTTTTAANGGCATTTTGGCGAGAGNAATTG

SEQ ID NO: 2078 ACACAATGATATAACCAGCTATAAGTTTAAAAGCTTAAAGCACTGTGTGAGT
GCTGGAGAACCAATTACCCCTGACGTGACTGAAAAATGGAGAAACAAGACGGGCTGGATATCTA
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TCCTCCTGGACAAGAAGGGAGATATTGGCATTCAAGTCTACCCACCGCCATTTTGGCCCTTTACTC
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GATATATGGATAAAGNNGGTTTTCTGTTTGTGCAANANACAGATGATTGCATATTATCCTTGGCT
ATCGANTTGNACCATTNAGGNANAAATGCCCTGATGACTCCTNAGTTGAGAGTCACTGTGTACN
NCCNAACCCATNGAGGAGAGGAGAAAGCTTTGCGTTAATTCTGNT

SEQ ID NO: 2079 ACAAACACGGATCTGTGTCAGAAACACATGTTGAGACTCCTCCATTCTTC
CAGAAATTTTCAGAGATGGGGTAGACCCACCTCAATCATCCTCAGCATCAGTTTGCTAAATTGCCAG
GCTCAATGACAAGCTCTCCTGCCATCTCCAAGCCCACTTTTCATAGTTCCGCTCTGTCTTTGGCTGC
AGCACTTTAGGCACTATTCTAAGTCTGGAGTATATCACTCTTGTTCAGAGCTAAATAAACATTA
ATGAACACACTTACTCANACAAGTCTGGATAGCTGCCATTGCAAGTACATACTCAGGAGATGAA
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AAGCAGAAGATTGTTGAGCAGATTAAAAACCGCTGGNAAC

SEQ ID NO: 2080 ACAAGCACTTAATTAAGCAGAAAGAGCCCAAGAAGAAGGAAAAAGTGG
AAGTGAGAGCCATTAATTTGGGGACAGATTATGAATATGGGGTNTTAAATATGCATCNGACTGCA
TATGATATGACCCTGGCAGANAGTTATGCCAGTNTGGTCAANCCCTCTGCNACTATCTNTTNT
ANANGNCNAGGAANGGNTTTCNATGNCACCCAGNANCNTATATGGTGTAGTTNGT

SEQ ID NO: 2081 ACGCGGGGGTCTCTGGTTTCTGGCCCTTGTCTGCAGAGATGGCTCCCAATGC
TTCCTGCCTCTGTGTGCAATGTCGTTCCGAGGAATGGGATTAAATGACCTTTGATGCCAACCCATAT
GACAGCGTGAAAAAATCAAAGAACATGTCCGGTCTAAGACCAANGTTCCTGTGCAGGACCAGGT
TCTTTTGTCTGGGCTCCAAGATCTTAAAGCCNCGGAAAAGCCTCTCATCTTATGGCATTGACAAAN

AAAAAGACCATCCACNTTACCCTGANAGTGNTGNAAGCCCAGTGATGAGGAACTGCCTTGTNT
TGGGNANTNTGGT

SEQ ID NO: 2082 ACGCGGGGAGAGCGCCGAGGAGCCGGTCTAGGACGCAGCAGATTGGTTATC
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AGGCCTCTTAAAAGTCCACCTCCTTACAGGCCTGATGAATTCAAACCGAATCATTATGCACCAAGC
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CCAAAAAGATGAAATTTCTCACTTNTACAAATGGACCTNTTCTCAGGAGTGATTCCGATCTGGCT
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SEQ ID NO: 2083 ACGCGGGGAGAGCGCCGAGGAGCCGGTCTAGGACGCAGCAGATTGGTTATC
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NAAANGNTTNGGTTNGTNTGGGTATGGTTGCTACGNGGGCTTACAAACCCAAATCATAAAGGC
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SEQ ID NO: 2084 ACGCGGGGACGCTCGACCCAGGATCCCCCGGCTCGCCTGCCCGCCATGGC
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CCTGCNNAATTTCTCTGATNTTCCNTTCCANTGGGGGAAATAA

SEQ ID NO: 2085 ACAAACAATGTTTATTTGTTTGTAAAGTGCCAGGTTTATATTTAAGTAAACAT
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ACGGACTGGTTGTGAGGNANCTCACAAGTTTAAAGATGCTTGTNANGAACATTACGGACAATTN
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SEQ ID NO: 2086 ACCGGGGACAGGTGCAGTCCCTCACCTGTGAAGTGGAATGCCCTTAAAGGAAC
CAATGAGTCCCTGGAACGCCAGATGCGTGAAATGGAAGAGAACTTTGCCGTTGAAGCTGCTAACT
ACCAAGACACTATTGGCCGCTGCAGGATGAGATTCAGAATATGAAGGAGGAAATGGCTCGTCAC
CTTCGTAATACCAAGACCTGCTCAATGTTAAGATGGCCCTTGACATTGAGATTGCCACCTACAGG
AAGCTGNTGGAAGGCGAGGAGAGCAGGATTCTTTGCTCTTCCAACTTTTCTCCCTGAACCTGA
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SEQ ID NO: 2087 ACTCCACAGAGAGATGCAGACAAAGTAAACAATGAAGGTTGTTTTATAAAGG
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SEQ ID NO: 2088 ACCATTGAGGACATAGGCACGGGCAAGGACTTCATGTCTAAAATACCAAAAG
CAATGGTAACAAAAGCCAAAATTGACAAATGGGATCTAATTAAGTAAAGAGCTTCTGCACAGCA
AANGAACTACCATCAGAGTGAACAGACAACCTACAAAATGGGAGAAAAATTTTGAATCTACTN
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NGNCTTTNAAACNANTGGCAATNGGTTGNACATATTCTNTTGAAANGAANACNTTTTCTCNCN
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SEQ ID NO: 2089 ACTTTTTTTTTTTTTTTTTTTTTTATCCTCCAAACAGATTATTGAATACAG
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SEQ ID NO: 2090 ACTGGTCCAGGAGTTATCCAGGATAGATTTTACCCACCATGGGACGTCATC
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SEQ ID NO: 2091 ACCCCTTAACCCCTCTCCTTACCCCTTAGCAGCAAGTCCCACTTTTCTAGGG
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CCTAATCCAACCCAAGCGTGCTGAGTGGTATATTNTTTTCNANAACCCATTGACTNTCCTTCTTTC
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SEQ ID NO: 2092 ACTTTTTTTTTTTTTTTTTNTTTTGGCCAGAAAAATAATCCGTTTAATTGA
AAAACCTGGAGGATACTATTCCACTCCCCAGATGAGGAGGCTGAGGAGACCAGACCCCTACATC
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NTTACACAGNCTCCTTATGGGATTGCCTTCTCGTANAAT

SEQ ID NO: 2093 ACGAGGACTGGATGGAAAGGTGATTTGTGGCTCCCGAGTGAGGGTTGAACCTA
TCNACAGGCATGCCCGAGATCACGTTTGATANACCACCTGCCCGACGTNCCCTNGATCCAAAT
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SEQ ID NO: 2094 ACATTGACAGACTTTTTCAGTATTGTAAGACCAAGAAGACTTCTCTACATGGCA
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SEQ ID NO: 2095 ACTGGCCTGCTGCTGGCCCGCAGGCTTCTCAATAGGTTTGGCATGGACAAGA
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SEQ ID NO: 2096 ACTCCCTACGGCACTAGTCTACAGGGGGAAGGACGCTCTGTGCTGGCAGCGG
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AAGACAGGTCTGATGTTTGGCCAATCCAGTCCTTACAGCCCTGCTGAACTTGTATCTTACGTGA
ACTTAAAGAATAAAATGCATTTCTACCCGATCTCGCCCCAGGA

SEQ ID NO: 2097 ACAGGGAAGTGTGAGGAGAGCAGCACCCAGGAACCCGAGCCAGCATG
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SEQ ID NO: 2098 ACGCGGGGACGTCGCTTTTGTATCCTTCGATGTCGGCTCTTCTATCATTGTG
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SEQ ID NO: 2099 ACGCGGGGAGGCATTGAGGCAGCCAGCGCAGGGGCTTCTGCTGAGGGGGCA
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NGAAGGCNNCCTTTNAANAANANATTAACCCGAAGGGTGNTTAAANAACCTTGAATCNAATTG
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SEQ ID NO: 2100 ACTCTCTGTCCACGATCATGGNAACCATCCAGTCCTTGAAGCGGCCAGTGAA
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TTGCTGTACACAATGAGGGTAGGAGGAGTTCGTGTGGAACCCATGGATCCCTTGGGGGCTTCT
NTTACCTTGTCCCAT

SEQ ID NO: 2101 ACATTCCACATTTTAAATAAATTAACCACAAGAAAATAATCCACATATACAA
GGTCAGGGGTGGGGAAGAGTATTAATGGTATCTTAATTATACCCAGTCTGGTTTTTTTTTAAAT
GGGGGTAAAAATCAAATGCAACCCCATCTTGTTTTANNAATTTGAAAACTAATAAATGCCCTTA
ATGNCAGNGTTTCTTCAACATGTGAGTCTTTAACAATAAAGTAAACCCNGGTGTCTGNG
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CNAT

SEQ ID NO: 2102 ACTTCAAGGAGAATTCACCACTGGAGCTGGGCTGTGCAGTGGCTACAGAA
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SEQ ID NO: 2103 ACGCGGGGCTTTTCCCGGTTGCTGCTTGTGAGTGTCTCTAGGGTGATA
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SEQ ID NO: 2104 ACTTACATATCTACATTTGACTACATTATTTCCAAACCAAGTATTCATCCA
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SEQ ID NO: 2105 ACAAGTCTTGATAGATCTCTGCAGGAGCGGGTGAAGACTCATGTCTGTCTCC
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SEQ ID NO: 2106 ACGCGGGTAAAGATGTCTTTTTTATTTTACTTTTTTTAAGCACCAAATTTTG
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CANTGGGGAAATTGAAGTGGTCCATAACATTGCCAAAATAGNGTGCCACTANAAATGGNAAAA
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SEQ ID NO: 2107 ACCATCTCAAAGCTAGATGCTCGAATCCAGCAAAAGAGAGAGGAGCAGCGT
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SEQ ID NO: 2108 ACGCGGGGAGCTGGAGTGCCTTCTGCCGAAGCTTGTGGTTGCACGCCCATCG
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ACATNGNAAAACCTGATNAATTTGNANGTGCTAAACTTTTTTAATAAN

SEQ ID NO: 2109 ACCTAACCCAGCTAGTGTGTTTTCCCAATTTCAAAGCTACTCATTACTGTTC
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SEQ ID NO: 2110 ACCCAAGGATGTCCTGGAGTATGTTGTATTGAAAAAGCAGTTGACAAACCCC
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TCANGC

SEQ ID NO: 2111 CCGGCCGAGGTACAAGCAGCTTTCGTTGAAGTTTGAAGATAAGAAACATGT
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SEQ ID NO: 2112 ACGCAGGGGTATTTGAAAACCTCAAGGTTATCCAGATGTTCCAGGTCCTCTGA
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SEQ ID NO: 2113 ACCGCCAGCTCTCTGCTCTCCACAGGGCTCCCCGCCCCACCCGGCCTGATAAA
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CA

SEQ ID NO: 2114 ACAGTTCTTTCCAATCTGTGCTTGAACCTCTGACAGTATTGTCTCGAAAATCA
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GCAAANTTCAA

SEQ ID NO: 2115 ACTCAGTAGTGCCTGCTTCTAGGGCTCTGAATACGGGCTTAAAGTCATCTTG
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SEQ ID NO: 2116 ACATTGACAAACACATAACTGAGGCATTAATACCTCTTTATAATAATGCAAG
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SEQ ID NO: 2117 ACTAGAAGTATACACCACCCAGCCCGGGTCCAGTTTACACGGGCAACTTC
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- SEQ ID NO: 2118 ACACCTTTTCAGGGTCGTTAAAGACCACCTCAAAAGACTTGATCTTCTTGAAC
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- SEQ ID NO: 2119 ACAAATTTACATTCATGAGGAATGTTAAAAAAATTCAACTAAAAAACCAC
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- SEQ ID NO: 2120 ACCTAGAAGAGAGGGCGGTCAAAGAAGTAGTGAAGAAGCATTCTCAGTTTCAT
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- SEQ ID NO: 2121 ACTTTTTTTTTTTTTTTTTTTTNGGAATGGAGTTTCACTCCTGTTGCCAGG
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- SEQ ID NO: 2122 ACCAAGGGATGGAAGAAGTAAATATAGCTCAGGTAGCACTTTATACTCAGGC
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- SEQ ID NO: 2123 GTACAATTCATCTAACTTCCGAAAGCACTTTTCACTCCAAATGCANAAACCG
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- SEQ ID NO: 2124 ACGCGGTGGCTCAGAGCACCCGTATCATTTATGGAGGCTCTGTGACTGGGG
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- SEQ ID NO: 2125 ACAGACAGTCCATCTCTGTTCTGGCCGGGTCCACCGTGAAGATGTCCTGAA
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SEQ ID NO: 2126 ACGCGGGGAGCGACAATATTGACTCAGCCTACTCCAGAGTGGTCTGAGAG
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SEQ ID NO: 2127 ACCGCAAGGGAAAGATGAAAAATTATAACCAAGCATAATATAGCAAGGGAC
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SEQ ID NO: 2129 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNCGGGAGGCAANAGGACCAACCC
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SEQ ID NO: 2130 ACGCGGGAAGAAGTGTTCCGAGAGATGGAAGACCATGCCTGCAAAGGAGAA
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SEQ ID NO: 2131 ACCTGGATGAAGCATACCCAGGGAAGAAGCTGTTGCCGGATGACCCCTATGA
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NCAA

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SEQ ID NO: 2136 GTGGGTGCGGCGAGGTACCGGGGAGCACTTCTTCTGAGTGGGCTTCTCT
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SEQ ID NO: 2137 ACGCGGGGGGCGAGAAGAGGAAGATTTCTGAAGAGTGCAGCTGCCTGAACCG
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SEQ ID NO: 2138 ACTCTAGTTCTATGAGGTTCTCTATAATTGTAAGGCACATGGAAAAGCAGAT
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SEQ ID NO: 2139 ACAGGTGGAACAATCCAAAGTTTAAATCAAAGAAGGTGGTGTTCAGTTGCTG
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SEQ ID NO: 2141 GTCGCGGCGAGGTAAGTGGCCCTTCCCCAGAAAAGCGGGACTTGCTGCTAAG
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SEQ ID NO: 2142 ACAAGACTCTTGACAGTTGTGCTTCTTAGGAGGTTGGGTTTTTTAAAAAA
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SEQ ID NO: 2143 CGGCCGCGGGCAGGACGCGGGGGAGATGATCAGAAATCCTTCACTGTCA
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SEQ ID NO: 2144 ACCTAGAAGAGAGGGCGGTCAAAGAAGTAGTGAAGAAGCATTTCTCAGTTCAT
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SEQ ID NO: 2145 GTCGCGGCGAGGTACCGCTTCTTAGAACTTCTACAGAAGCCAAGCTCCCTG
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SEQ ID NO: 2146 ACTACGACATTTCTGCCAAAAGTAACTACAACCTTTGAAAAGCCCTTCTCTGG
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SEQ ID NO: 2150 ACCAAAAACATTTATGACCTTATAATTTTATAGTGCAAGAAAAAGGACAAAGA
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SEQ ID NO: 2152 ACGCGGGGACTGTGAGGTGACGCTTCCGGCGCAGAAAAATGGCAGCCGCGG
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SEQ ID NO: 2153 ACGCGGGGGGGCTCTGCGTTCTGTAGTGGCGCTGCTTGGGCCGCTGGCGGA
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SEQ ID NO: 2156 ACGCGGGGGCTGCCGTCGCCGCCGCCATTTTGTATGGCAGGAAGAGTCCGGTT
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SEQ ID NO: 2157 ACCTTGAAAAGACACTGAAAGCATTTTTGGGGTGTGAAGTAAGGGTGGGCAGA
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SEQ ID NO: 2160 GGAAGCCGGCGCCGGGCAGGTACTCTTGATGAAAGACCGTGAAACCAACAA
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SEQ ID NO: 2161 ACTTTTTTTTTTTTTTTTTTTTTTGGACACACCTGCCCTTTATTGGTCTNTTCT
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SEQ ID NO: 2163 ACAGAGAGGTGGGCCTTGAAGCCAATAAATACAAAGCTTCTCTGCCTTGTA
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SEQ ID NO: 2164 ACATTTTGTACAGACAGAAGGCTGATTTTGAAAGAAAGAAACAATAGGA
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SEQ ID NO: 2166 ACATCTTGACCTTCTTGGTCTCTGAAGTATTCAGCCACAGTCAGCCCAGTCAG
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TGGCATCTNATAAGTTGATAACACCAGATTCAATCATTTTATGGTATAAATNATGCTTTCACGNG
GTCCNTTTCACCAACACCAGCATAACACATAGTAACCCCTTNGCCTTTGGCAANATTNTATAT

SEQ ID NO: 2167 ACCAGCTGTGGGATTTCTGCTTCGGATTCATTTGTTGCTTAACTTGGGCTTTT
CCTCTGCCACGTTTTTCTTCCCATGCTCTGGGTCTGTTCTTCTTGAATTCAGGTTTCTTCACTGT
AGTATCACCACCTTTCAGGTGCCACATCATCTTTACTAANAAGTATGAGTCTTCTAGCCTGCTG
CCTCTTCTTCTTCTCTCTCTTTTGTGTTTTCAAAATTTCTTCTCCTGCTTTTCTCCTTGCCTCTTTTTC
TTCTTATTAAGCAAAAAGATCTTTTGGTGGCTTCATCCCAATTGCTGANAAACGAGGAAAGANT
GGGAANGTGCANCCNATTTCTCANTNTTAAAAAAGGGAGTTTACGCTCTTCCCACTTCTCTT
GGCAATNTTTNTGAAAANTCTTNGGGGAAAAANCAANAATGNTT

SEQ ID NO: 2168 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTCGGAACTTTTATTTATATTNNGGT
CTTACAAATGATCACTTTTAAATGGACTTTTCTGTAAAAATGTAAAACTCAAAAAATTTGCCAAGTN
TGTATNTGATCCACACAAATCCCTAAAAAGGTTTCTGTGTAGTCTTCAATTAACNCAATCTTNGN
GAATGTTCACTCTTACTGTAGGATCTTGAATATGTTTTACAATAATGAAGTCAAAAGTTTATGCA
GGGCATTAATGTAAGTATAAATAACATTTGTTTTAAAAAANAANCTGGGTAATANAAAAATNGG
AAANACTCTNAGGAGCNGGCANTCTGTTGNGGCTCAANATATNTTATTTGCTTTGGAGCCNGCTG
NCATCCTTTNAAAGAGCACACNNGGACANGGCTNNGGAATCCTGNTTGAANCTTCTAATTT
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SEQ ID NO: 2169 ACTCCATGGCAGACTTCACAGGGCCTTGTCATTGGAAATAGAACGCATCAA
AATCGAGAGTCTTCTACAGAAATGCCTCATTTTGAAGTGAAGAAATATGTGCAAGCTGATGA
AGATTTTAGACATGTGCTGGGAGAAGGACTGGCCAAGGGAGAAGATGCCTTTGGGGCAGTGTCTT
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GAGTCCCTGAATGGGATGGTAACAAAGGATTTGACAAGACTAAAAACAATCTCTCAGAAACAG
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GTCTCCTTTGGGGGCCANGGCTTATCTTNTGTCCCTATTGGACAANAACCTGGTNTTTATNACCTG
NCTCTGGANACCANATGGGAAAAATGAATTGAAAAATTTANTTTTTAACNCTTTTGGCTACTAAA
AAANGAAAT

SEQ ID NO: 2170 ACCGTAAGATGGGAGAACCGGACCATGAACTGTATTGTCAACGTTTTTGCCA
TTGCTATTGTTCTTAACTGACTAAAAATGTTGGGCTAAAGCCATTAACTTAAGAAATTTGTCAAGTGT
ATCCTTTCCAAAAAGAGTAATAGTTGTTTACTAGTGTCTANATGAAAGCGTGCAATATGCTTTA
AAGCTTCAACAAAAAACTGAATATTATAAGCAAGCATTATCNTAGTAATTGGCAGATTAGCTCA
TATTCTNNTCANCATCNTNAAATAGGAAAAATTTANTGCTANCANAAAAATAAANTTNAAAAAATAT
GGNNTGACTTGAAAAATNCCATCTTATNTTGACACCANTTTTTACTANTNTTTTGTACCTGCCCN

GGGCGGGCGNTCNAAAGGGGCGAATTTC

SEQ ID NO: 2171 ACTGTCTCTTTGGAAAAGTTCTTGATCCCCAATGCTTCACAAGCAGAGAGCA
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ACAAGAAAAGGGATTGTGATCAGTCACAACAAGCATACCAAGAAAGCTTTTGAAATCAGCAAAAA
GGAAATACAACCAACNCATCTATCAGACTGGGTCTGGCCCTTAACCTTCTGTGTTCTATTATGA
GATTCTGACTCCCCAGAGAAAAGCCTGCTCTCTTTGCAAAGACAGCTTTTGATGAAGCCATTGCTGA
ACTTTGATACATTAAAGTGAAAGAGTCATACAAAAGACAGCACGCTNTTAATGCANTTACTGAGAG
ACAACTTGACATTGTGGACATCGGATACCAAGGAGACNAANCTGAAGCCTGGANAAGGAGGGG
GAANTTTAAACCGCCTTCCACITTTGNTGCTCATTTCTTAAATTTACACAGTNACCTTTGTCATCC
NTGCTGCCCCANAAATAGNTTTTGTTCATTATGANNNGGTTNTGTACCTTTNTTTNAAATTCNT
ATTTCCNATNTGGTTTTTANGTTAATATTNAGGGGAGTAGA

SEQ ID NO: 2172 ACTTTTTTTTTTTTTTTTTTTTTTTTNAACAAAAGCAACAATTTTTATTATCTTG
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GTAGTTGCAGATCTTTAATAACATTTTCAATTTCAATTTATGAGCTGCTCATTATAAATGANATGCTC
TAAAAATAATAATCGCTTTTGTGTTGTTGTTATAAAACAATGAAAAATCCTGTTCGGAAACACAAGT
TGCTNTTTATATTTGCTTGCTCTTAAATANTATTGANAAGGTAANGNGGANCTTGCGNGAA
AGCCCCCTC

SEQ ID NO: 2173 ACGAGTCTGAGGCGGAGGGAGTAATGGCAGGACAAGCGTTTAGAAAAGTTTCT
TCCACTCTTTGACCGAGTATTGGTTGAAAGGAGTGCTGCTGAACTGTAAACCAAAGGAGGCATTAT
GCTTCANAAAAATCTCAATNGAAAAGTATTGCANGCAACANTAGTCTCTGTTNGGATCGNGG
TNNTAAAGGAAAGGGGTNGANAGATT

SEQ ID NO: 2174 ACAGCTTTTAGCAAACTGCTTTCCAGAAAAGCAAAATAAAAATAATGCAAT
CAGCAGATCAAGGAGACTACAGCTAGACATCAGAGCTACAACTTCTCATATCTGTGTGAGAAAAAT
CCTATTTACCCAGAATAGACTAAAATTTAGGACAAAACAGGGACTTTTAACTTTCTTACTTTA
CCCATTTTAAAGTTCTTTTATCTCCCCACCCCCAAGCCACTAATTCAGCAAGATCCAGGAGAAA
GAGGGCTACTTTTGAATTTGGCTACTTTATTTTCTTTCTATGGCAAGACTGCTGGAGCCTGGATA
TTTCAGGCTCATATGCATCCATGACCAAGTGCTCACTGTGGCAAAAAACTTAGCAATGGACTTTGTG
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AANACTGGAGGACAGCTGCCAAATTCATCAGGATCCCATTTGCGANGACTTTCTTTTGCANAATA
TTCCAANAATTTTTTACANTGGACCATCCNCTTGNNAATTTTTTCAGGCTTATCATTTTTTNCNTTT
ATCNACAGCCCGTACGGGCTTTCTGNCCG

SEQ ID NO: 2175 ACGCGGGTGAAGATAAGAAGTTTCTTGACAAATACATGCCCCAGTTCATGAA
ACATCTTCATTATAGAATAATTGATGTGAGCACTGTTAAAGAACTGTGCNGACGCTGGTATCCAGA
AGAATATGAATTTGCACCAAAAGAAGGCTTGCTTCTCATAGGGGCACTTGATGACATTNATTGAA
AGCATCAAANGAGCTTTCANTTTTACCGAAATAACATCTTCAAGAAAAAAATGNTGATAAGAN
GNAGGAAAAATTATNGAAAAATGGGGNAANATGAAAAACCGGTGAGTTNNTGCCANNTTTTATG
GCTGCCNCTTCNATTTGTATTNTGGAGGCACTTNTGGGTGGTTTTTTTTTTCTNNCNCCTGATG
GCTTTGGCAAAGCACCTTCGGGTATCCTTGATCTNAA

SEQ ID NO: 2176 ACTGAGAATGCCGTTTCGGGGGCTTTATGGCGACGTAAGAACGGGCTTGGAC
TTGGTCTGTGAATCCAGAATCCAGAGGTGCAGGTAGCACTATGGATCAGGGTTAGCCTCGGGGG
CCAAAAACAGGCTTCAGTTTCTCCCCACTCTCACTTAGTGTTAAAGAGTGGCAGAGGTGGGGTGT
GGGAGCTTCCCNAAAGACCTGCT

SEQ ID NO: 2177 ACTTTTTTTTTTTTTTTTTTTTTTAAAAAGTTAACGCATATTTGTTTTATTTA
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GCATACTACGGCTAAGGAGAAACAATGTTCTACATATTATGGGTAGTGAGAACATTATCTGTATA
ACAGGGAACGTGATTATTTAAAAATATGCAGAACTTATTTTCATCTGTGCTTTANAATAACTGTT
TCAGTGTATAAGTTGAAAAGAACTCAAAATACTAATACCAAAATNTACACCTTGTNTTANAATTCA
AAAAAGCTGCTTTCTGTGAAGTCAATCAGCTTTATTTAAAAATGACACAAATCCAAAAACAAGATG
CATGTTNTATATAAAGGGGACATTGTAAGTTCCTTGCTGCANTTAAACCCATGGTTAAATCCATGA
AATTCCTTTTAAATATCATTTAAACAGAANTGCCAATAGTCTCAGGATCTCTTAAAAACCTTTCC
CAATCCCACTNNTTCACTCCCCCTTTTNAAGAACTAAACAGGTATTTCGGGTANCTGNTTCTCTTNT
CATAANTTNGNTTGTNTAATTTTNTCAAGGGTTNGGGCAAACCGNGCCCATTTCTTATTGNGGGG

SEQ ID NO: 2178 GTACAAACAGCACTTTTACCTTTGCCATAACCTCAGGATCAGGATCTTCTATA
GGATCAGCCCATTCACAGTTTCCAACATTCCCCANACCTTGACTTTACCACTCATTAACTACGC

CTTGCTGGGCAGCTGTTTTGTGATCTTCATATTCAGAAAGCAAAGCCTNTGTTTTTTCTTGT
CATCCGGTGGTGGGTATAAAATGACGTCTGGAAAGAACCTCTGTTACTTTGCTAAANTCTTTAA
GANTCTGTNCCTTGGTTTNCCTNTTAGGAANTAGAAGCCACAAAAAG

SEQ ID NO: 2179 ACTTTTTTTTTTTTTTTTTTTTGGGTTTGGNATGCNCTATTTTGCCTTAAAAAT
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TNATTTCTCANTTAATTTTGGGAAAAANNTCCANAAAGATGTGTTCTNTNANTAAAAANNTTAAANA
AAATAAGCTTTTTGANCCCTNCCAANCCCCATCCCCA

SEQ ID NO: 2180 ACGCGGGTGCATGCCTGTAATCCCAGCTACTCAGGACACTGAGGCANGAGAA
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AAATGATGAACCATATCATGTCCGTGGGTCAAAAGCATTGACATGAAATGACACCCACTGTGTT
ATTTCAATTTCTAAATGCCTTAGAAAAAAGACCAGAAAGAAATCTGCCAGGATNTCCACAAGGG
TTGCCTTTAATGGTGAGATTATNGGAAATACTGTTGGTINTANACTTTGCCAAATTCANGAAANCT
NTGCAAACTCCTTTTNGCACNATTNCANCTCCAGNAAAAAAAAAANAATNAANCCNGAAAGGAAA
AAGNACCGCTCTT

SEQ ID NO: 2181 ACCCCCTTTCCATAGAAGGGGGAAGCCCTCTTTCTGTCTGCCAACCEGATCG
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CGTGAGCTGCTGTAATCATCATAGCGACTGCTTCCACCATAAGATGGCGGGGGCCCTCGTGTAGGT
GGAGCACTACGTNAGTACCATAACTCTTATATGAATCTCTGTAGGAACCTCCACTTGGATGAATCT
GAATAGTCNCGATCACGACCATATCCATCTTATCCGCTATATNCTCTTGAATGGATAGNCATNAC
CGTGAACTGGGAANTGACCATTAAATNACGGTAAAGTATNAATCTCGNNGGNGGTGGNGCATAATC
CTCTANTTTTACGAAGAACCTTNGGNAATCTTTNGATTGAATNGCTGTNTTTATAANAATAACC
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SEQ ID NO: 2182 ACTTCAGTTGGTGCACAAAATACTGTCAATTTGCTCAAAGCTGGTTGCCAAATG
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CTCCAGACAATGATGGGCTTTATGATCCTGCTGCGATGNAGAGCCGGCTNTTTTAAAGCCAAAGCA
GTGCACGGCCCTTCATTGTGCTGGTGTGTGAACACTGCTGGGGTCAAGAAACATACAAAGNCCC
TGGANNTAACCTGCTCTGAGCGAGTGAAAACCTCTGGATCATCATTGAACTAAACACAAANCAN
GAGAAAAACCTTTTGATAGTNAAGGTTTGCNGACTGNACTTCANAAGGAGTCNCAACCCNTNTT
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TCNTCCCAAAAACCTNAAATNATGTGGACATTNCTGATGTGGGCTTATNTTTTNAANAANATNTTAA
AGGGGAATCCTTGTTNNTTCTAAAAAATGNNCCTGACATTNNTTGGGNGACACCTGGNTCCTGG
ATCCTGNCAAACTTTTAATTTAATTTNTT

SEQ ID NO: 2183 ACTGGTCCAGGAGTTATCCAGGATAGATTTTACCCACCATGGGACGTCATC
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AGATGGGAGGCAAGTTTATGAAAAAGCCAGGGGCTAAGCCANCTCTACCATAACCAAGAGTCAA
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AGCTTAATGCANATGAAATTAGCCTGNGCCTGCTCAATCCGTCCTAATGAATAAAAAATCAAGTGC
CAAAAGCTTCAGCCCCAGATAACTATGATTCCTTCTAGTGCCACAACCCACGCACTTAAACACCA
CCTTTTGGGACAGACACTCAACTTGGTCTNAAACTTATCCACCATTANTCNAGGAAAAACCTGGC
AAGACCCAGAAAAAGCCCCACCGNCNAANGGAAAAACTCCTTAACTAACTGAACCTTNTNGA
CTNNATTTCTAANTANNGGAAATNCNAATGAAGCTTGTAAATGGNTGTAAAGAAANTONAGGCTCT
AAAACTTTCTTCTGATATNNTAACCAAGGTATNATNCNGNCCNNGATANAANCCATAANATAAA
NAAAAAGCANNTTNTT

SEQ ID NO: 2184 ACAGACATGAGATGCTTCCAGCCAGCCTNATCCAGGCTCATCGGGATTACTT
CNGGGCTCACACCTATGAACTCTTGGCCAAACCAAGGGCAGTTTATCCACACCAACTGGACAGGGC
CATGGTGGCACCGNGTTATCCTCATACATAAAATGCCTGATCATGCTGCTCCTGTCAACCTCCACG
ATTTCCACANAACCAGGACATTCCATGTGCCTCATGGCNCCTGCCANCTGGCCCTTTGNCCTNTTT
TNTGTTCAGTNTTTTAAANCGGTTGGTAAGANACTTCTTGNAGAAAAACACACAATTTNTT

SEQ ID NO: 2185 ACGCGGGCACTTGATTTAGAAGAATGACACCAAAACACATCGCTGAAAAAAT
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TTATTTCTATGCTGATTCTGGAGGGAGTTAACTCCTCGCAAAAAAAGGCATCTTGTCCCTACATCTT
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CTGCCTTTCCANCTTTTGGNTTTCATTNNGGCGCTGGGCTTTACCAAAAACCACAACTTATATTA
AAATACCNNTTCATTTTGACANAGTTTTAATGAGNGATTNATNCCCTNNGTATTTGGTATGNTTA
AGAA

SEQ ID NO: 2186 ACGCGGGATGGCAATGTGGAGAAGGTGAAATTCATGAAAAGCAAGCCGGGG
GCCGCCATGGTGGAGATGGCTGATGGCTACGCTGTAGACCGGGCCATTACCCACCTCAACAACAA
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GCCCTNTGGAAGTGACCCGANGAAAACCTTNTTNAATCTGCNATGAGCTGGGAATTAACCCGC
CNTNTTCINTGAAAATATTCTNANGCCAAAATGAGCGCAANTCCTTTTGANTNCTTNAATGGGNA
TCNAAANCCAATGCCCT

SEQ ID NO: 2187 ACGCGGGGATTTTCTCCCGAACCTCTGCTCAGCCTGGTGAACCAACACAGGC
CAGCCGCTCTGACATGCAGAAGGTGACCCCTGGGCGCTGCTGTGTCTGGCAGGCTTTTCTGTCC
TGGACGCCAATGACCTANAAGATAAAAAACAGTCCTTTTACTATGACNNGGCACANCCNTCAGTTT
GGCAGGCTNATNTGCGCTGGGCTTCTGTGCGCCATNGGCATCATNTTTCNTNATGATTGCTAAAT
GCAAAATGCANTTTTNGCCANAANCTTCGNTAACCATNNAGGGNNAATNGTAAATTTNAT

SEQ ID NO: 2188 AATAAAGAACCTCTATCAGTGAGACTTCTCATTTTATAGCAAATACATTTTGC
AGCTTAAATTTTCTNGAATTCATATACGCTTCTGTCAATTTAAACAACTTCCAGAGAAAACCTGGNC
TCTATATATTTAAATTACAAATTTGGCCAAATACATATTTNCCATATTTAGATCTTTAATTATAAA
TATTAATTTGAAAAATCAAANGTGAAAGCANAACTGNTNTTCAAGTTTGTGGANAATATTT
ATTTTATNATTAAGTTTGTGTTGAATATNCCCTCAATAGGNTTCTAANAAACACCNATTATCTG
NNTCTTATGNAATTGGGGANNTTNTGNAAGNATGGTGAANCAGGGGTTAACTTTAACTCTGGG
NT

SEQ ID NO: 2189 ACGCGGGGCTCTTCTGCTCTCCATCATGGCGCAGGATCAAGGTGAAAAGGA
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ACAGACTGACGCCNAGCAGCCAAANGTGTGGAGCACTCACANGGCNTACCCCTGTNTTTTCAA
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SEQ ID NO: 2190 ACTTTTTTTTTTTTTTTTTTTTTTNGGCTTCTATGTTTCTCTGTGCTGATTCT
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SEQ ID NO: 2191 ACCTGCATCAGCATTAGTAATCAACCTGTTAATCCAAGGTCTTTAGAAAACT
TGAAATTTCTGCAAGCCAATTTTGTCCACGTGTTGAGATCATTGCTACAATGAAAAAGAAAGGG
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NTTTCCAGGTNCCT

SEQ ID NO: 2192 ACCCATGATTTGGACACTTTGTGCGGCCCATTTACTTATACTGCAAAGCGTCC
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GACCAGGATGTATTTAAATCAGAAAGTCATAGGTGATGGGAATCAGATTGAGATTGAAATCCCTC
CAACCAGAGCTGCATTATCCATGCATGTGATATTGTAGAAGATGCANCTATTGGCTTATGGATATA
ACAACATTC

SEQ ID NO: 2193 ACTGGATGGCCCCACAAGATGCTGCCACTTTAATAAGGCTGCAATACACTGT
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TCTGGTTCCAGGATCAAGAGTAGGGATACCACACTGTTTCATCACACTTTCAACATCTTTATCATCC
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TTCTCTTCTGAAATCTCAGCTCCTTTAGATTTAGATAAGCAGAAAGCTCAGCAGCTGATCTTCTT
CACTGATGTCGATGAAGGCCGGGACGCTCATGGTGCAGGCCNGGCACAGCGGACACTCCACTCG
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SEQ ID NO: 2194 ACAGTTTAAACAACAGCTGAAAGAACTAAAGAAGCAATGTGGTCTTCAAGCT
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ACCTATGAAGAGGACGCCATTGGTCCAGGCAAAAGCGGAAGAAAAAGGCCTATTGCCCTCAAATT
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ACCAAGCAGCTACCTCTACCCCACTGTCTGTTGAGAGCAGTGTGACCCAGCAGTTAGGGAGT
GCTGCATAGCATCTGTTGGGGGTAAAAGTGTGCTTTATGTGTGCTTGAAAAATTTTTCAAA
GTTTCACAAACAGAAAAATGCCATTCATATTGTTTATTTTAAAGTGTCTATAATGTAAAAATAAACCT
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SEQ ID NO: 2195 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAAACAAGTNTCACAATGTTT
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CTT

SEQ ID NO: 2196 ACGCGGGGTATTTATATACTTGGTTTTAAATAGGTTCATATGTTACATGGTT
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GAGTTGTAATATATNCATGCATACACNCACACACACNCACACTCNCNCACACTCACACACACC
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NGAAGACANGGNAATTAAGNGAAGGAAAGANNATTATAAACCTAAANNNTNACCATTTTCAATT
TNGCNGGAGTAAGTNTTTAATTATCATTTNGNTAGCNTTCGANTATAANTGGACTAAACTTTTCNATC
AAAAGAAACAGACTGNCTGAATA

SEQ ID NO: 2197 ACGAAGAAAGCAATTTCCCAAGCAATGAGTCTCTTAATGGAAAAATAAAAGA
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AAGATAAATATTTCTAGTCCCATATATGTGTTTGTGTTTACAAGATATGCTTGAATGATGCAAT
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AGCCAGAAAGCTCATCACCTAGTGCATCCAACTCTGCTTCTAAATCATCTTCATCCAGTTCTGGGGT
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TGTAATCCTCAATCTGGTCNGATCTTCACTTGTGATGCCTTCTTCACTTCTTACTCCAGTT
TCATAGCATCAACCCGTGGTCTTGGTGCCTTCAAAGACTGGATGGTATAATTGGGCTTGTTCAT
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A

SEQ ID NO: 2198 ACTTTAGATACTTGGCATATCTGGGTCTTTCCAGTAAAGCAAGTATTTAAGA
TAATTAACAAAAGCTTTGTCTTTGAAGTAACCTCTTTGGGCAAGAAAAATTAAGGNAATTTGGGTTG
GCTAAACATTGCACAAATTCAACTCCAAGTGAACCGAAGTCGATTNCCAGCATCATCTGACTCC
ATAGCAACAGCATCNGGCCATAACAAACNAAGACNCCAAATCGCCGCCANCTGACAGAGCAAA

ACCCANAAACGCCNGCCCCNAGTTTCAANATAAACCTGACTNACTTANAATGAAACATANTAATT
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SEQ ID NO: 2199 ACAAACCTGGTGGGTCANATCGTCTCCTCTAACATGACGCTACACTGTCGCTGA
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CATAGGTGGGTTTCATANCTCTTAACCTATNCAGGAACAAATTTTGATNCTTACNTATTAACNACNT
TAATNCNTTCAATGTTGNAAT

SEQ ID NO: 2200 ACGCGGGATCAGACACTGGATCAGACACTAAACGAACTTAACTGTATATAAG
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GCACCAGNTTTT

SEQ ID NO: 2201 ACCCCTTAACCCCTTCTCCTTACCCTTAGCAGCAAGTCCCACTTTTCTAGGG
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ACTATGGGCAACCTTCCATCCTCCAATCCTCCTTCTCCCTTANCTGTGTCTCAANAACTTAAAC
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CAATACAAACTTGACAAATGGCTCTAAATGGCCANAAATGGCACTNTCNATTTCTCCATCTTACAA
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SEQ ID NO: 2202 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTTCANAACTTTCCTCAGCATCAGAT
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CATATGCTCCATTTCTTACTCTTTTATCCTCTGAANAGTCACAACTATCTCCCTTCCCTGTGACTTC
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TCCATCAGTTGNCCATTTCTAATTTGTTTATGCCCTTAGGAAATGACAAATTNCTTCTCNCTCA
GGTAACITTTTCAGTGCCATCAGATTGAAAGATTCACTAGNNGGTTCATTTTAATTAATTTTNT
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SEQ ID NO: 2203 ACTCCACAGAGAGATGCAGACAAAGTAAACAATGAAGGTTGTTTTATAAAGG
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AACTGATTGGAATCTTNTCGCCTACTGCCTCTCTCGTGCCCTTANCAATAACCTGTNTGAAAAAG
NGTAACCCAATGTATCTGTGNGCCTATTCCTCTNTACCTTT

SEQ ID NO: 2204 ACCTTCATCTTTACTTCCAAGTAAACCCGTGGATGATTTGATGAGGGATAAAT
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SEQ ID NO: 2205 ACATAGTGTGCGGAACCTCAAATCGGCATTTAGATAGATCCAGTGGTTTAAAC
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SEQ ID NO: 2206 ACATTCTGGGAGAATATCACTGACGCTCAAACCATTTTTATTTCCAATATGTA
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SEQ ID NO: 2207 ACGCGGGGGTAACGGAGTGGTGACCAACGTGAGAGGAAACCCGTGCGCGG
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SEQ ID NO: 2208 ACTGTCTCTTTTGGAAAAGTTCTTGATCCCAATGCTTCACAAGCAGAGAGCA
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AANNTAAACNGGCCTTCCAACCTTTGANTGNCTAATNCTAAANTTTACCACANTAAACCATTTGGTG
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SEQ ID NO: 2209 ACAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAAGAG
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SEQ ID NO: 2210 ACTACAAGAAAGAACTTTTTATGAAGGATTCTTTATGTAGAGTATCTTTTT
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ACCCANGCTGGTCTCGAACTCCTGCCTCGGCCTCCCAAAGTGTAGGGTTACGGCATGANCCACC
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AACCGTGTNCANTTCNCTGTCTTATTTCCAGTGCTTAACAGNNGGNGGCAAAATAGTTTANTGATC
ANT

SEQ ID NO: 2211 ACGCGGGGGACTTTACCCAGTGTGCACCACAGAGCTTGGCAGAGCTGCAAA
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TGGTCTTCCACCATCCTTGAAAANAANCCAAAAACTTTCCNAAANGGATCTTACCAAAANAGCT
TCCATTTTGGCAANAAATTCCCTCCGTTACACCCCAANCCTTAAATTTCTTTTGGAAAANCTTGGN
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SEQ ID NO: 2212 ACACCGGGTGGCATTAAAGGGTAAAGATGTCCCCCTTACGGAGCAGACCGTG
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CCCN

SEQ ID NO: 2213 ACTCTATGCATTCTATCTATACAGAAACACCTATTTATTATTACAGTTGATTTA
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SEQ ID NO: 2214 ACTTTTTTTTTTTTTTTTTTTTTTTTTTCCACTGCTGCCACCACCATGAAANAN
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GCAANATNAAAGAANTTTCACCCCNAGNANTTTGAAGTGANAATGATCTACAAATNTCTGACA
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SEQ ID NO: 2215 ACCCTGGGATAGGGAGCGATCTCCGAGCGAGGCGGCAAGATGGACGCGGGA
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SEQ ID NO: 2216 ACTTTTTTTTTTTTTTTTTTTTTTTTTTCCAAANAATTGAAAAATTTATTG
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GGAAAGCATTTCCACGCCAGGAACCAACGCTGAAAGCNTTGGGAATCANACANACAGCCTGGAA
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SEQ ID NO: 2217 ACGCGGGGAGGGAAGAATGACAGCCACAGGGAGATGGTGGTGGGCAAGAA
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SEQ ID NO: 2218 ACAACCTGAATTGAGGCTTCTCCTTCACTGGAAGTGCACCTGCCTCTACCTCAT
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SEQ ID NO: 2219 ACTGTGAACATGACTTTCAGATGCTCTTTGCCCTTGTCTGTCATCACTGTGGT
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CCCCTGTCTAATCGTGAGAAAGCCAGAGGCTTGGGAAATACATCTGCCAGAAATGCCATGCTA
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SEQ ID NO: 2220 AC GCGGGCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGAC
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TCTGACCTTTTCCACAGGGGACTAGCCCTATTTGGGTCCTCCAGCTCATCTTACCTCACCCC
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CCCTGTAAAAAANA

SEQ ID NO: 2221 ACCTTTTCTTTTCTTTTCTTTTCTTTTAAAGTCAATATAGTTCCATTCTTTACTGTGC
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SEQ ID NO: 2222 ACAGTTTTCTCAGAAGACTCAAGATTTCGCCACATCCCTTTGAGCTCCCGCT
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SEQ ID NO: 2223 ACTGCCCTTGGGCCTCTCTCTCTCTCTGTTTCTCCTCTCGAATCTTGTTCTT
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SEQ ID NO: 2224 ACCTAATGAAAAGATCTCCAAGAGGTTGTCTCATTCTCCTTGGGCTGTA
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SEQ ID NO: 2225 ACTTTTTTTTTTTTTTTTTTTTNGNATTGAGTTTTTATTGATGATTCIATGTG
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SEQ ID NO: 2227 ACGCGGGGCCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTACGTT
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SEQ ID NO: 2229 ACTCATTAAATATTAATAGGCGCTTGACCCACAGGCTGTCAAAATTCGA
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SEQ ID NO: 2230 ACAGAGATAACAGAGGTAACATAAATACAATCCTTGTCTTGAGGGGCCAAT
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SEQ ID NO: 2231 ACTCCTCAACAGTCACAATCCATCCTAGTATCTTAAATAGTGATTTTTTTTAA
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GANC

SEQ ID NO: 2232 ACGCGGGGGTTTTTAAAAAGGAGAGCCTTTCTGATGCCACTTTTCTGCTTGACA
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SEQ ID NO: 2233 ACTAAATATTGCTGAGAGCATCCACCCAGGAAGGACTTTACCTTCCAGGAG
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NNCATTAGGTATTNTNACAATTTGGNNTCCTTTAATAACATGAAAAGTGNCAATCTCCATNTT
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SEQ ID NO: 2234 ACGAGTCCCCTATGCGCTGCCCTGGGCCGCAAGAAGGGAGCCAAGCTGAC
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NTATTATTTCTTNTAGTAATATATAAAGNTCATGTGNTTCTTNGNTT

SEQ ID NO: 2235 ACCTGCACGTCTCATCGTTTTCTGCCGAAGCAAACACTCTACGAAATCATCAT
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TCAAAAGCATGGCATCGACCAAGCCATCTTGTAGGGCTGTTCACCACTCTGGATTGTCAACCATCGA
TCTATGTTAAGGCCGAACCTTTCTGGATGTCCAAGAAAGGCATGGCCGATGCTCANTGCCCTTGA
CTNTTTTGGCCGCCGNTTCAGAAAGACTNGCTAGCGACNGCTGGACCGCTTGGCCGNAANG
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SEQ ID NO: 2236 ACTTATACCCCTAAATATATAAAACATTTTAAAAAGAAAAAAGGAAGAAA
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SEQ ID NO: 2237 ACTAGGACAGTCAGTAATTAATGCATCATTCAGAGGATTATGGCTGTTCCTTA
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AAAGCGTGGATGANGTACCTGC

SEQ ID NO: 2238 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAATCCACACCTGCCCTTATTG
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SEQ ID NO: 2239 ACCTGCTATTTTTGGTAATGATCTTCAGGCAGATTTGGCCCCATGGAGTTTTT
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SEQ ID NO: 2240 ACTTTGACCTGGAAAGGTATGGGTCTGCTTAAAGAAAGAAGAAACATACA
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NINTTAT

SEQ ID NO: 2241 ACCTCACCCATATGCTGAAGATCTTTGGGGCCGTAGAAGAGGACAGCTCCCT
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TGGGGACTATTGCCTT

SEQ ID NO: 2242 ACGCGGGGGAGTGGTGTGCTGTTGTTGTGAGCCTGTGGCGGGCTTCTG
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SEQ ID NO: 2243 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGTTTCGTTGTTTTCANAGGCTTTTGAAC
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SEQ ID NO: 2244 ACACAAAGAGGGGGTGGGTGTCGGATGCAGAGTGTGTGGCCTGATGCTCCAC
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CAGGTAGGTTTGAGGGGATACATCCTAANACAACACCCATTCCANGGCAGTANGAAAGGAAAGC

SEQ ID NO: 2245 ACGCGGGGAAACAATGAATCAGAAAATTTCAAGTTCTAGTTCACCATGACTT
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CCCCAGTGAGGGCCTTGATTGCTTGGCCTACTGTGGAATTGGAAGATATTTGAAAAAACA
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TAACCTGGCCACGAGTAATGTGATTATTGAAAATCTCANCCCCAAAAATAAAGATGCTGTTAGA
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TGGATTTTCT

SEQ ID NO: 2246 ACTGGGTCCTTCCCAAAGGGAGAGAGTCTCCTGCTGGCTCTGAAGAAGTGAA
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CCAGAGCAGCCTCAGCTGACAGCCAGCAAGAAAACGGGCCCTTCANACCTATGGTTACAGAAAC
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SEQ ID NO: 2247 AACTGTATACATCTTGTCTATGATGGTCTTTACCAATGGCCCAATGTTCTGT
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SEQ ID NO: 2248 ACTTGATGATAACGGTTTTAAAAATCCTTCACTCGTCTTTCTCAAACTTTCCCA
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SEQ ID NO: 2249 ACTTTTTTTTTTTTTTTTTTTTTTTTGGANANACACTTCTTTTATTAGGAAG
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NCA

SEQ ID NO: 2250 ACTTTTTTTTTTTTTTTTTTTTTTTTINACANAAGGGAGGGANATTTAATGTT
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SEQ ID NO: 2251 ACAAGATGTGTTACTATCGCTTTGGACAGGTTTACACAGAAGCCAAGCGTCC
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SEQ ID NO: 2252 ACGCGGGTGTGGATCTAAGGGGAATGCTTTATTATGGCTGCTGTGTCCAACA
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SEQ ID NO: 2253 ACTGGTCCAGGAGTTATCCAGGATAGATTTTACCACCATGGGACGTCATC
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SEQ ID NO: 2254 ACGCGGGTATTATTCATCCAGCATATGGGGACCAACATGTGATGGCCTCGAT
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SEQ ID NO: 2255 ACGCGGGGCTTTTTCTTTTCCGGCGTTCAAGATGTGGAAGCGAGGACGT
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SEQ ID NO: 2256 ACCAAGAGGCCAGTGTGCTCTGTGGACCTCAAAGTTCACCTGACTTGCTTCAG
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SEQ ID NO: 2257 ACGCGGGGACCTAGTGTCTGAGCGGCACAGACGAGATCTCGATCGAAGGCG
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SEQ ID NO: 2258 ACATGTTGAAAGCTTTAAATAAGGATCCTTGGATACAAAATATGGTCCACAT
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TGCTGTTGTCCTTCAAAGTTCATTAAGGTTTCANATGCCTTTTGTNGAAANCCNAANTTTCTTNTC
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SEQ ID NO: 2259 ACGCGGGCTGAACGTGAGAAATTGACCCAGCAGATGATCAAGTATCAGAAA
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SEQ ID NO: 2260 ACTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTAAAAATTTATCGGTTCCGACTTAA
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ACAAACCTGTTTTTGTCTCTCCTTATGCTCCACTTCCTTCAAGTAGACTANAATGCTNCGGCAAT
TCTCATTTATGCCACCATGCACTCTCAATCCATTTAACTTGNCTANATACTAAAATTTTCCACT
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SEQ ID NO: 2261 ACAGAAATTAATAATCAGGAAAAATAAGAAAAAAGCATTACAGTAAGAT
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SEQ ID NO: 2262 ACGCGGGGGGTGTGTTACCTGCCACAGCATAATGCGAGGCAATGTCCAGCC
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SEQ ID NO: 2263 ACATCCTCCCAAGTCTGGAATACAGAATTGATGGAGGACACTTAACTTGCTT
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TCAAACAACAAATGAGTTATAATATTTTCTAATAAGAAAAATACACCTGNGAACTATGAGATA
CTACATCCTTGATCTGGCTGGCCACCATTTTGAAGACCACCACANATCTCAAGGCATGATACTACT
CACCAACAAAAATCTATCCCTGCTATTGCACCTANTGTNATCTCAATNTGTGGCTGACACCAAATGT
TCTNACTTANICTGATAGATGCTCTTATTGCAATTAANNNGGCTAGNTNTGTTCCCTATTANCTTGT
AGC

SEQ ID NO: 2264 ACAAGATCTACCCGGACACGGGAGGCGCTACGCCAGGACCGACGGGAAGG
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SEQ ID NO: 2265 ACTTGGCTTGGAGACTGGCGCGCGCTTCGTGTCCGAGGTCACTANTTTCCCGG
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SEQ ID NO: 2266 CGCNGGGGANACATCACCGNCAACCTGGGCATNNGGGANATGGCCGANACT
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G

SEQ ID NO: 2267 ACTAAATATTGCTGAGAGCATCCACCCAGGAAGGACTTTACCTTCCAGGAG
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CTCTGGG

SEQ ID NO: 2268 ACATATTACATACTCACAACGTTCTTTGAAATGTCAGACTCCTAACCGTATC
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NNCACNTNAT

SEQ ID NO: 2269 ACATGAATTAGAAGCGTGCATCTAGGATTATGGCCAACTGTTTTAAAAATG
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SEQ ID NO: 2270 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAGTAAAAAAGCTGA
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SEQ ID NO: 2272 ACTTTTTTTTTTTTTTTTTTTTTTTTTTGGCTGTCTAAATGTTTATTAAGTATGA
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SEQ ID NO: 2273 ACCTTGATACACATAATCAGCCTTTTCAAAAAATGCCTGACAAGAATTAGTCTT
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CCCTCTGCTGGTCCCACTTCTCATCGTGGCGGGTCNCTGCTGAGTAGAGGAAGAGCTACAGATGG
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GNTAATCATTTTTTGTATCAAAAAATCAAAATNAAGGAACCCCAANTTCTTGCCCGGCGGC

SEQ ID NO: 2274 ACACAGCAGCCAGTTTTCATCGGTGATCATGCACAGCAATGCCATTGCTGCC
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TAAGCCCGAGCCAGATAAAGTGGGTAGGTTTGCAAGCAGACCCAAAAGCATTAAAGGAGAAAAAG
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CAGGATTCCCTGACAAACCGTGGCGCCCTTACTACAACTACAACCCC

SEQ ID NO: 2275 ACTTTTTTTTTTTTTTTTTTTTGGGATTTTAGTAAANACATGGTTTCGCCAT
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GGTCTGTNTCTTCAAAGTGTGGGGCTGCCTATTCTCCANGAACCAAAATGGCCCCCGCTTAAAN
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TANAAACCTN

SEQ ID NO: 2276 ACAAGATCTACCCCGGACACGGGAGGCGCTACGCCAGGACCGACGGGAAGG
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SEQ ID NO: 2277 ACTTTTTTTTTTTTNTTTTTTTTTTTTNGGCTTNGAAATTACTTTAATTTANAAA
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SEQ ID NO: 2278 ACGCGGGGGCTCGGCGATGTGCTGGGTTCAAGCAGCCTCCTTGATCCAGGG
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SEQ ID NO: 2279 ACCAGCTGGCACAGGAGCAGGGGCATGGCACCTCTGTTGTTTATGCCCAT
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TGATCTTCTCTNTCT

SEQ ID NO: 2280 ACTGTTAAATTATTGCTAGCCATATCTTTAAAAATGGTTTCAGGAATATTC
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CTNAAATCCATTTCT

SEQ ID NO: 2281 ACTTGTTTTCTGTATGAATTGAGAACTTTTGAGCAATAAAAGTGCTCTGCATA
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AGCTGCGGCTGGCCAAAGAAATTGACCTGCTCATGCACTGTGTCAAGGGCATTGGCAAAGATCAT
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SEQ ID NO: 2282 ACTGTTAAATTATTGCTAGCCATATCTTTAAAAATGGTTTTTCAGGAATATTTT
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SEQ ID NO: 2283 ACGCGGGATACAAAGATATCCTAGAGACCCATCTGAGAGAGAAAAAACAAG
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SEQ ID NO: 2284 ACTGCTAAGAGGTATTATTAGAAACAAGATTTAAAAATATGTAACAAAATCT
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SEQ ID NO: 2285 ACACCANATCAGAGACATCGTTTCATCTCCCAAATAGTTTTATATTTTATG
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SEQ ID NO: 2286 ACCACACAATACTAACCTTCCCTCCTCTGATGTCTTACATCACCTCCAGG
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SEQ ID NO: 2287 ACTAAATATTGCTGAGAGCATCCACCCAGGAAGGACTTTACCTTCCAGGAG
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ATCCATGAGAGCTTTGGTTCCCGGGCAAAAGCTTTCCATTCAATACCCCAAGGACCACTTCCA
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GCCCATCCAGCCAGCANGTATTGCCAGAAGCCACCAGTGGCTTGGCCAGTCTTGGGCATTCTCATC
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SEQ ID NO: 2288 ACNCGGGGGCAGTGAGTTCGACACACCNTGCCGACTGTCANCGTGAAGCGTG
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SEQ ID NO: 2289 ACGATGTCTAGTGATGAGTTTGCTAATACAATGCCAGTCAGGCCACCTACGG
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SEQ ID NO: 2290 ACTTTTTTTTAAAAAGNGGCCACCACATCTTTATTGCATACTCAGGTGA
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SEQ ID NO: 2291 ACTGTGTAGAATTAAGCAAAACAGNGTGATGTTTCAGAAAGTAACCCATTACTG
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SEQ ID NO: 2292 ACAAANATGGCTATAAACAAGATGCAGCCCTCGGTTTCCATGAACAGCACAC
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NGGGNAA

SEQ ID NO: 2294 ACGCGGGGAGCGCGCTCCAGCCACAGCCTCCCGCGCTCGCTCAGCTCCA
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SEQ ID NO: 2295 ACGCGGGGGCTGCCACCACTCCGCTGCTGAGGTTGCAGATGGCTCTTCCCC
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SEQ ID NO: 2296 ACTTTTTTTTTTTTTTTTTTTTTTTGGGAATGGTAGTGANAAACCAACATTTAT
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TAACCACTCAGGTTCCGGTGGTTTTAACCTTGTGCGGTAGAGGCCAAAATAATGACNAATGAA
NCCNNAAAAAATTTNAAACCNAACCTGACAGGTNTTANGATGAACAAAAGAATTGAAACT
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SEQ ID NO: 2297 ACTTTTTTTTTTTTTTTTTTTTTTAAACANAGCCTGCTCTGTTGCCAGGCT
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TCTTTATGGCATTTATCANAGTTTGAATTTTTGCCATTTATTTGATGTCTTGCCTGTTTNTGNN
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SEQ ID NO: 2298 ACTTTGCCTACGGCAGCAACCTGCTGACAGAGAGGATCCACCTCCGAAACCC
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SEQ ID NO: 2299 ACGCGGGTTATCAGAAAAAATTTCCAGCTCAACCAAGATAAAATGAATTTT
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CACTTGATGGTGAATATAAACTTGGTTTACTGAATAGTGTGCTGTTCATGGAACCGAGGGCTGC
ATCTTGTTTATAGTCATCTTTGTACCTC

SEQ ID NO: 2300 ACTTTTTTTTTTTTTTTTTTTTGGGTTTTTAAANCCAAAATGTGTTTATGAT
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GAATGGGGCTNTGCNCCAAGCGTNNNTNTTGTGTTTCCINTTCTCTTCTGGAANGGATGAA
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SEQ ID NO: 2301 ACACAGTATGTCCCTCATTTAAACCAAAAGTATCCCAAGTTTTGTTGGTCACT
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GAACITTTGGATGAATTTGTATTTTCTGCTTGGGTCTTCTGGGTNA

SEQ ID NO: 2302 ACCTTCAAAAGTGAGATTCTGAAAGCATGAGTAAATTTGGGGGTGGTAATA
TTTTCTCCATTTTCAAGAAATATCTTCAGCATATGTCCAAAGAGCAGGATTCCATTCAAATAGGCA
AGAGCAAAGTCTCGTTTTGTCTAAATAAAAAAGGAAATATTAACCGGTCTTCAAAAAANAA
TCTTGCTTGAGCCTANAACAAAAGGTTGTTGGGATCANNAGGGTTACTGGAAGTTAAAGGGAT
ATCAGGGAGANTTNAANGGATGTTNNGTTAAANGAACTTTTNAAGAAATATTCTTC

SEQ ID NO: 2303 GGGGTACATTAGGATCCCTCGGCCAAGGACTGGACCAGAAGAACAACCTGGG
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GNTGGGCCCTTGGCTATCTGCCAAAAGGGCATCCTGGATCC

SEQ ID NO: 2304 ACTGCGATTAAAAAAAAGCACTTCTGCCAAAGGAACCATGTTCCAACACCG
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CCCCCTCCCAACTTGAGTTGTGTCAATTCGACCAAGTGTCTGGGTGGTAGGGATGTCTACAGCCACCT
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AAGGGTCAGCTTGCTTCTATCTAGAATCTCTGGATGTTCTTCCAGAANGCATCCCCNATGATATC
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SEQ ID NO: 2305 ACGATGACATCTCAAGGAGTCACTGGCCCTAGGTTTCTGCAGTAGGATCTTA
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CTGCAAGGACTTTACAGTGGGGTCCAAAGGATGCCACCATCAGCTCCACCTGGGGCTCAACAAAG
CCTGAAAGAAGAAAGGGATGATGCTTCCAGCAGAAACCTGGAGGCCTGCAGCTCTGCCANCCAN
ACANCAAGCGAGGCCATTGNCATCAGGGGCGNAAAGGAGGGAACCTACCCACCATCTTTCTCTA
CANNGCANTTCCATTATGAGGTTTCCACTTTAAATGCTAAATNATTAATTTTNTTAAAGNAAT

SEQ ID NO: 2306 ACGCGGGGCTTTTCGAGGTAGGAGTGCAGTCTGTGAGGTATGGTGCTGGG
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SEQ ID NO: 2307 ACAGTCTTTCATTAATAAGAATACTTACACATACATTTTCANATATTTCTAC
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GGCATNTGGAANTCCATGAAGTAAAGAGCATNCTTTTAAAGCANATTTGATNGCTNNCTTTN
AANTATGAANATTCNGAGAATCTCTNATTANACCNCANTNCATANAANATTCCTAATACCCCT
AGG

SEQ ID NO: 2308 ACTATTTTCATGGTCCAAACCTGTTGCCATAGTTGGTAAGGCTTTCCTTTAAGT
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AAA

SEQ ID NO: 2309 ACCCTTGGACAAATGTTTCCAGCAAGAAGCTAACTCGACCACTGGTGATGA
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SEQ ID NO: 2310 ACATTGAGAATATGTGTAAGTCATTTTTTAAAAAGGCTTCTTGTGATTAAGA
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GAAGCCACGCTATCTGTGGTTGAGAGCTCACTCCCTTGAAGGCATTGCAGAGAACAAAGAGACATGG
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SEQ ID NO: 2311 ACGCGGGCAACCCCTGTTGAGATAAAGCTGGCTGTTATCTCAACATCTTCATC
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TCTATAGCATGATTCTTCAAGTAAAGGCAAAAGATATAAAATTTTATAATTGACTTGAGTACGGC
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CGCAGATAAGTTTTTCTCTTTGAAAGATAGAGATTAATACAACACTCTTAAAAATATAGTCAAT
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SEQ ID NO: 2312 ACAGAAAGAGCAGGGCCAGCTCAGCCTGCCCTGGCCATCTAGACTCAGCCT
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SEQ ID NO: 2313 CGNCGAGGTACTAGAAGTATACACCACCCAGCCCGGGTCCAGTTTTACAGG
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SEQ ID NO: 2314 ACACCAACCTGAACAGATTTTGTGCCACAATTTCAATCAAAGGGTTTGTCAAT
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AGTGTCTCTAAATTACAAATTTGGCTCCTGTAGGAGTCTCAGAAAAATAACAGAAAGAAAAACCC
CCCTCCCAAAAGAGTATGACACACATTTTGAAGAAACCCCAATGTTTCATGCAATGGTAGG
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SEQ ID NO: 2315 ACTGTGGCGCTCCGTGAAATTAGACGTTATCAGAAGTCCACTGAACCTTCTGAT
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GCCGCATACGTGGAGAACGTGCTTAAGAATCCACTATGATGGGAAACATTTCAATCTCAAAAAA
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SEQ ID NO: 2316 ACTATTAAGCCATGGTCAACCCACCGTGTCTTCGACATTGCCGTGACGGN
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TTTTT

SEQ ID NO: 2317 ACTTGATTTTGAACACAGCAGCAAAACATTTTGAGCTGGTGAAATCAGCG
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SEQ ID NO: 2318 ACTTTTTTTTTTTTTTTTTTTTTTTTTTGTGCTGCCNCCACCATGAAAGAGTGG
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AGCAACCGGGCTTGNCTANTGAGGTCTGAANAATTTCTGGNANAGCGTAGGGGAGATTANAT
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SEQ ID NO: 2319 ACACAAAGAGGGGGTGGGTGTGCGATGCAGAGTGTGTGGCCTGATGCTCCAC
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AAGGCTGTGTGGCAGGTGAACCTCCACGATTTTCTCTGCTCATAGGTCCACTGCTGCCCTACTGC
TTCCACATCTTGATCCANCGGTATCCCANCCACTCGGAGGCCCAACAGGTGAATTGGGANGAAG
CGTTTCTACCANAAATCANAAATGTAANTAAAGAAACCTCCAGGGCTGATCATTCATCTGTGC
CTTANC

SEQ ID NO: 2320 ACTGTGGAGGCTGAGGCAATTTTCTTCAGGCTAACCCAGATTTTCTAAAGCCC
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TTCTCCAAGCTGCCGGCGAGAGCCACCATAGGTGGNGGACTTGNCGCTTTCAAAGGCCGGGT
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SEQ ID NO: 2321 ACACCTAGGACCTCTAGTAAACCTCATAAACATCTGCCTCCTGCAGCCCTACA
CCTCATTGCATACTACAAAGAAAACAAAGACAGGGAGGACAAGAGGAGCGCCCTGTCTGTGTTA
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TTAAGTGGCAAAAACCTTCCACATTGAGATTGGTGGATACCCCTGAAGGGCTGCCAACACGCTGT
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SEQ ID NO: 2322 ACCTTGTAGCATTCTGAGGACAGGCCTGATTTCTGAGAAGGAAAGTGTAA
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ATGTGTACGGAAGGNA

SEQ ID NO: 2323 ACTGTCTCTTTTGGAAAAGTTCTTGATCCCCAATGCTTCACAAGCAGAGAGCA
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SEQ ID NO: 2324 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGATTATAAATGCATTTTAATACC
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SEQ ID NO: 2325 ACAACTAAAGGCAACTGGCATGGACTCAAATATTTTGGGGAAGAAAAAGACT
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C

SEQ ID NO: 2326 ACGCGGGGCGGGAGAGAGGCGGAGATGGCAGATGAGATTGCCAAGGCTCA
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SEQ ID NO: 2327 GTTGGTGAAGGAGTGCCAGTCCCAGGTGACACTGGACAAGAAAGAGGC
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SEQ ID NO: 2329 ACTACGCAGGCCTTGGCATCCCTGGGGTTACCTGGCTGACTGGGATGTTGA
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SEQ ID NO: 2330 ACATTACGCACCATTAACATGCGTCTTTAAAGCCTTCCCAAAATATTAGTAATCT
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SEQ ID NO: 2331 ACCTTCACTATCACTGGGCGTTTTTGGAGAACATTTCTTCTGGGAGTTACCTG
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SEQ ID NO: 2332 ACTACTTCTCAAGGAGGATTCATGGTCCGTCCTTTGCTCACTACAGATTTCTC
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SEQ ID NO: 2333 ACACATACACACCTAAAGAGTCATGGCCTTCTTAAACAGCTTTCTTAATCCTT
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SEQ ID NO: 2334 ACTATGCCAAACACTTATAACTTGTATAAAAAATCCACATCCCATATTGGCC
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SEQ ID NO: 2335 ACAGCCAACGGTTCCCTTGGGGGCTTTGAAATAACACCACAGTGGTCTTA
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SEQ ID NO: 2336 ACGCGGGGGGAAGGGAGAGAGCTGTGCGAGCGTGGGGGAGAGTTTTCGTT
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SEQ ID NO: 2337 ACGCGGGGAGGAAGAACTAAATCCAAAGATACTAGCTTTGCAGAATGCTCAG
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SEQ ID NO: 2338 ACCACTACGATGCTGGTGACCCAGCTGCTGTTGCCAAACCTTGACCAGCG
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SEQ ID NO: 2339 CGCCGGGCAGGACTTACTTGGAGAGACATATGTCTGAATTTATGGAGTGTA
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SEQ ID NO: 2340 ACGCGGGATTCACTAAACCATGTGTCTGAACTGAAGAAGCTTGGGCTCACT
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SEQ ID NO: 2341 ACTACCTGATGGATGCTGCCTCCTTGTGCTGCTGTTCTGGCCCTCGGCCTGCAG
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SEQ ID NO: 2342 ACATTAGCACCATAACATGCGTCTTTAAAGCCTTCCCAATATTAAGTAATCT
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SEQ ID NO: 2343 ACGCGGGGCTATTTGAAGATATGACTGATTCTGACTGTAGAGATAATGCACCC
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SEQ ID NO: 2344 ACNCGGGTGATCGACCANAGCTAACAGGTGCCAAAGTGGTGTATCTGGTGG
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SEQ ID NO: 2345 ACTAACCTCATTTGTAATGAGGTTTAAAGAGAAGGCCAGCACTAAGCCAGGCT
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CTTGAAGAGGGT

SEQ ID NO: 2346 ACTGTTCAAAAAGGAATGCCCCACAAGTGTTACCATGGCAAACTGGAAGAG
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SEQ ID NO: 2347 AOCTGCATCAGCATTAGTAATCAACCTGTAAATCCAAGGTCTTTAGAAAACT
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SEQ ID NO: 2348 ACGCGGGGCTTGTCCAGTGAAACACCCTCGGCTGGGAAGTCAGTTCTGTTCTCT
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SEQ ID NO: 2350 ACCTTGGCTTGGCTCTTGACGTGGACAGAATTAAGGACCAAGAAAGAGGA
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SEQ ID NO: 2351 ACGAAGAAAGCATTTCCNAAGCAATGAGTCTCTTAATGGAAAAATAAAAG
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SEQ ID NO: 2352 ACAAAAATACAGTTGATGACTTGACAAAATGGCTACACCTAGGGCTTGAAGG
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SEQ ID NO: 2353 ACATAGACAAGTTTCTTGTNAGACAGAAAAACAGAGAAATCCACAGTAACCTCT
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SEQ ID NO: 2354 ACGCGGGGGCGGGGAGAATCGCTTGAGCCGGGAGGTGGAGGTTGCAGTAAG
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SEQ ID NO: 2355 ACCCGACCTCCATCTTCACCAAGAAATGTTATCTCTAATATAAACGAGACCTC
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SEQ ID NO: 2356 ACGCGGGGAGTGTGAAATCTTCAGAGAAGAATTTCTCTTTAGTCTTTGCAAG
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SEQ ID NO: 2357 ACTCTTGATGAAAGACCGTGAAACCAACAAATCAAGAGGATTGCTTTTGTGTC
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SEQ ID NO: 2358 ACGCGGGGCTCTTCTGCTCTCCATCATGGCGCAGGATCAAGGTGAAAAAGGA
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SEQ ID NO: 2359 ACTGGCCCTCAGTGTGGCAAAGGTGTAGTTCCACTGGCCGAGGGAATCAAG
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SEQ ID NO: 2360 ACATCAAGTCAGAATGATGTTGACATGAGTTGGATTCTCAGGAAACATTGA
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SEQ ID NO: 2361 ACCGAAAGGAAGCTCCATTCAAAGGAAATTTATCTTAAGATACTGTAAAT
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CGGGGA

SEQ ID NO: 2363 ACTTGCCCTTCCCCAGAAAAGCGGGACTTGCTGCTAAGGGTGAAGGACCAA
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SEQ ID NO: 2364 ACACCTGAAGGCGAGGTTAATTAATCCTGTTGTGGAGTTTGAGGGCCGGA
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SEQ ID NO: 2365 ACGCGGGGGAGGAGACTATACAACCTACAATAGAAGCATTATATCTGCTAGT
GGAAGAGCTATCCAGGGAGGAACATCACATCATTTAGGGCAGAAATTTTCCAAAATGTTTGAAT
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GATACTTGGAGAAAAGCTGACAGTTGCTTGAATGAGGCANAACTAACTTTCTAGCTTTTTTG
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SEQ ID NO: 2366 AACTAGAGGCTTTGGTAAAACATCTTCTCTCCAGAGGGTGAAGATAAATAA
ACCTTACAGAGATTCAAGACTGGCCACTGCACTGAAGTTTACAGGCTAGTGGTTAGGGGCATC
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SEQ ID NO: 2367 ACCCAAAGGAAGAAAGGTCTGCCCTGCCTTCTATAAACACATGCATGTGGCTC
CGTCTCCCAAGACATCATTTGCAGACAAGAAATTAGTGAGAGTTGCTCAGAGGCTGTTTGCTCAGC
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SEQ ID NO: 2368 ACGCGGGGGTGTGCTGTAAGGGGTCTCCCTGCGCCACACGGGCGTGGCCATG
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SEQ ID NO: 2369 A C A C T A A C T T T T A A G T G T G G C A C A A A T G G A A T A G A G A C A T G A A G T T T A A T
G A G A T C C A A G C T T C C A A C T A A A T G A T T T C A C A T T T G A A A A G C T A T G G A A A G A T A C A A T N A T T T A C T
G T T T T A C A A A T C A A A T G C T T A A A C C A A G T T T A A A A G T T G A G A C C G A A A A A A A T T G A T G A A N A A A A
A A T G G C C A A A A A A T T A A A C A A A A T C N T I G G T T T C C T T T A C A G G T T A C T T T T N T T G C G T T T N A T T N
T T T T T C A A A T T T G C A T T T T A C A N T T A N A A N T G C A N A N C A C T T T G G A T T A G C T A T T G G A T C N A A T A C
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SEQ ID NO: 2370 A C A C T G A A A A C T G G A C A T T N T A A C A T T A A T T T T A T T A G C T C T C T G G A G T G A G
C T A C A T G A T G T T G T G C A C T G A A A A T T A C C C A A A T G T T C G C C T T C T C T T T C T G G A T G A G C T T C A G
A A G G A G T T C A T T A C T A C T T A A C A T G A T G A A G A C A A A T A C T G C T G T C A G A C C A T A C T G T T T C A T T
G A A T T T G T A A C T T C A T T C A G A G G A C C A A G C A G C G A T A T A A T A A T C C C A G G T C T C T T T C A A C A A A G
A T A A A C T C T T T C G A C A T G C A N A C G G G A A T C A A G C T G A A G G C C T C C T A T C N A A T T T C C A N N G C C A A
C N N G G G G T C A C C C A T T G N A N T C N N T C A C C N T T T T T G T T G A C T G A A A A G N G C T G G T A A A A T T T C
T T C T G T C A C C A G C N A C T G G A C C A G C A A C T C T G T C A G G G A T T G T A G G A T T T A T C C T T A G T C T T T T A T G
T G G A G C T C T G A A T T T A A T T C G A G G C T T C A T G C T A T A G A A A G T C T C C T G C A N A G N G A T G G G T G A T G
A T T T T A A T T T A C A T C A T T G C T T T T T T C C T T G G A A C A C A G C C T G C C T T T N C A A G N G G T A T T A C T T
G T C T A C T A C A C C G G C T T G G N G G A A T G G C A A A T N T T T T G A C C T T T N G G C T T A A T C T G C T A T T G C A A
N A T G G

SEQ ID NO: 2371 A C T A G G C T A A C T A G A A G G A T C T C A T C C C C A T A T G T G G T C T C A T T T C A A G T C T A
T G G A T G A C T A C C T T C A T T G C T G T G C G A G A T G G T T T C A C C C C T T G A A A A T A T G G T C A C T T C A G C A
T A A A A T A G T T A A A T C T T T A T A A T G A T C A A T T C A T C C T A C C T C C T T T T A C A T G C A G C T G A A A A A T G A
C A G G C T A G G G A C A T A G A A T A T T G T G A A C T T T A C T G T T A G A A T C A C T G T C C A T T A A A T G A T C A C T
A G C T A A T G G T C A C T A A A T T T A C A A A T T A A G G A A A T T A T A T A G A A T A C T G C A A A A C A C N A G T A A
A A A G A C T G A A G T T C G C C C A T T T C T G C T C A N G G A A G T C T C T C A C T C C T A A G C T T C A T A T T G T T G C
C T T C T G G C T N C A A A A A T T C T G C T A T T A T T A C T G N T T T C C T C C T T T T G A T C T T C C T T T T G G T T C C C C A
G T G C C A G A A C T T C C A N A N C C T T C T G C T C A A A T G C C A T C T T T T G T N T C C A T T T C A A A A C A G C T T C
A A G T G A T G C C T T G T G G A A N A A A A G G A T G C T T C C C T G T C T A A N A T T T N C T N C T T G N T T

SEQ ID NO: 2372 A C G C G G G G C T T A C A A G T C C T T C T T G A T C C T G A A C T G G G T T A G G T G C C G C T G T T
G C T G C T C G T G T T G A A T C T A G A A C C G T A G C C A G A C A T G G G A C T G G A G G A C G A G C A A A A G A T G C T T A
C C G A A T C C G G A G A T C C T G A G G A G G A G A A G A G G A A G A G G A A T T A G T G G A T C C C C T A A C A A C
A G T G A G A G A G C A A T G C G A G C A G T T G G A G A A A T G T G T A A A G G C C G G G A G C G C T A G A G C T C T G T
G A T G A G C G T G A T C C T C T G A T C A C A T C A N A A G A G G A T T G C A C G G A G G A G C T C T T T G A C T T C T T G C
A T G C A A G G G A C C A T T G C G T G G C C C A C A A A C T C T T A C A A C T T G A A A T A A A T G T G T G G A C T T A A T T C
A C C A G T C T T C A T C A T C T G G G C A T C A G A A T A T T C C T T A T G G T T T T G G A T G T

SEQ ID NO: 2373 A C A A T G C C T G C C A T C A T G G G T C A G A A A T T G A A G G A T G A A G A A A T C T A C T G T
T T G A A A T C C T C A C C T T T C A G A C G T A T T T C T T A T T C A C A T C C C A G G A G C A T C C A T T T T A A G G A A C T
A T T C T T T G G A A A A A C A A A A A C A A A A A A C A A C A A A A A A A G C T A A G T T A A A G T G A A C T G T
T T G G T G C A C T G T A T G T C A C T T T T G C T T G T T G C A T G T G A A C T T G G A A C T A A G G T T A C T C G T G C
A T A A A A A T T C T A A A T G A A A G G G T G T G G G T T C C A T C A A T C T G A T G C T G C C C A T C G C T T G C A C T G G G
G T C T T T G T G G A T C G G G C A G A N T T N T C A G T G T G C T G G G G T G T G C T C C T A T G T G T C T T T G A A
T C T G A G G C T G A C A T T T T G C T T G G A A G G C C A A C C C T T G C T C C A T C A N A G A G G G C N A G T G G C N A A A G
G C C A A T G A G G C A G C T G T G A N T T G G A C A G G G T T C A

SEQ ID NO: 2374 A C A G A A A C T G G T A T T T T T G G T G C T A T A C A A G A G A A A T G T A T T T T T A A A T A T C
C C A C A T C C T G G A C T T T T G T T G G G T A T T T A G T A T A T T G A C A T A T A T T T T A A A G G T G A G G T A A C T C A
G A A C T T A A T T T A A A A G T C T T A A A T A T T C T G A T A C A A T T C A G C T G T C T C T C N A C C T T A C C A T A N G C C
A G T T G C T T T C A T T T T A A A C C A A G C A A G T A A C A T A T T N A G T G A C T T G A A T C T T C A T A A G T T T A A A A
G T A A A A C A G C N A A A A A C C T A N T C T T T G T C T T T N A A C N C N G A N C A T T T T C N A G G A A A

SEQ ID NO: 2375 A C C T G T T A T T G A A T C A A C A G A G A C T A T A G A G G C T A A G G C T G C C C T T A A A C A G
T T G C A G G A A A T T T T T G A G A A C T A C A A A A A G A A A A A G C A G A A A A T G A A A A A T A C A A A A T G A A G C
A G C T T G A G A A C T T C A A G A C A A G T T A C A G A T T T G C G A T C A C A A A A T A C C A A A A T T T C T A C C C A G
C T A N A T T T T G C T T C T A A A C G T T A T G A A A T G C T G C A A N G A T A A T T G T T G A A G G A T A T C G T C G A T A A A
T A A C A T C C T T C T T G A N A N G A A A T T A A N A A C T C G C T G C N A C A C T N A A A A G C A N G A A C N G A T T A
T C A A T N C G A T G A C T C A A G A T T T G A N A G G G N C A A A T G

SEQ ID NO: 2376 A C A C T C G A G A T G A A G A T C A C A T T G C A T T G A T C A T A G A A C T T C T G G G G A A G G T
G C C T C G C A A G C T C A T T G T G G C A G G A A A A T T T C C A A G G A A T T T T C A C C A A A A A A G G T G A C C T G A
A A C A T A T C A C N A A T C T G A A A C C T T G G G G C C T T T T T N A N G T T N A G T G G A N A A G N N T G A G T G G T C T

NANGAAGAAGCNATNTGGCTTCACACATTANTG

SEQ ID NO: 2377 ACATTAGCACCATAACATGCGTCTTTAAAGCCTTCCCAAATATTAGTAATCTT
GACCAGCAATGACAAGAAAAAGAGGAGCACCTTTACAAGCAGTTGATATCCAATATTTAAATAA
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SEQ ID NO: 2378 ACATGGCTACACTGTGCTCTAAAATTACTTGCATTAATGAGGACATTAATTTT
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SEQ ID NO: 2379 ACGGATGTGGCAGCGAGAGGACTAGATATTCCTGAAGTCGACTGGATTGTTT
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CAATCCAAGGTTCCATTAAGTGAATTTGACTTTTCTGGTCTAAAATTTCTGACATTCAGTCTCAGC
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CATACGAGCCTATGATTCCCATTCCTGAAACAAGATCTTTANTGTATAAACCTAAATTTGCCCTC
AGGTTGCTCTGNCAT

SEQ ID NO: 2380 ACACAGCTGTACAGGAAAGTCTGATGGCCACAGTGAAAAAGGTCATGGGTG
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SEQ ID NO: 2381 ACGCGGGGAGGCAACCTGAGGTCTCAGAAATGGCGGGCACAGGTTTGGTG
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ANAAAAAT

SEQ ID NO: 2382 ACCATGAAATATCCAGAACATACITATATGTAAAGTATTATTTATTGAACTC
ACAAAAACAACAATAATTTTAAATATAAGGATTITCCTAGATATTGCACGGGAGAATATACA
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GNTTGGCCACCATNTTACCTTACAGTGAATG

SEQ ID NO: 2383 ACGCGGGGAGCTCTACGCTCTACGTTTACCTGTCCATGTCTTACTACTTTG
ACCGGATGATGTGGCTTTGAAGAACTTTGCCAAATACTTTCTTACCAATCTCATGAGGAGGGG
AACATGCTGAGAAACTGATGAAGCTGTANAACCAACGAGGTGGCCGAATCTTCTTCAGGATATC
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SEQ ID NO: 2384 ACTGTTCAAAAAGGAATGCCCCACAAGTGTACCATGGCAAACTGGAAGAG
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CCAAGAGAAATTAATGTGCGTATTGAGCACATTAAGCACTCTAANAGCCGAGATAGCTTCCTGAAA
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AACAGAGACTATTAATTGCACAGGATTCANAAATCATGGAAAAGCAGCTATAAGGAAAAGACCAG
ATGGATGAGAAACITATGGAACTCTGAAATATCTTGAACAACTTCCTGTAGCTTCAGATAATACA
CCAGAAACCGAAGCTGGAAGACTGGCATTCTCTGGGGGGGCTTTTATTCTGGGATTNTGGGG
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NACNTGAATGATGAATGNAAGAATGCATGGAGGGACTNGCAAACCTTGGATAATAATTTTATGT
NTTATNTNTTTAAAAAGNGTGGTNTTTTGGNAINGAATTGGAAANTANGNNTGAGGAATCTA
AANTNNGG

SEQ ID NO: 2385 ACGCGGGGCTCACTCTGCGCTTCAACATGGCTTTTATTGCCAAGTCCTTCTAT
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AGAACTGTCAANAATGAGGAGATCCTGAACAGTCTCAAGTATGTCCGCTCTGGGGGTGGATACCAG
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TCATTTTGNAGCCCTGTGCGCCGNTCAGATGTGGCTGGAACTTTTGAANAANTTCCTCATAGGGCC
GGGAGGGAGAACCCCTTCCGACGCTACAGCCCGCACCTTCNAACCAATTAACATTGGAGGCTGAC
NTCNAACCGCCTNTTNAAGNTTGCCATATAGATGTNACTGCTTAAACACACAAAATCTTCTTAC
TCCATCC

SEQ ID NO: 2386 ACTTCTAATTCCTCTATTACTGTGCAAACTAGAAATTCCTATGTAAAAGACA
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SEQ ID NO: 2387 ACGCGGGCAAACTGTCAAGTGAACCCGCGGTATTAAACGATTGATTAGTGTG
TTAAACAAAAGCACGGGTGAAGTCACAAAGAAAAAGCCTAAGTTTTTGACTAAAGGCCAGAAATGC
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TANTN

SEQ ID NO: 2388 ACCAGGGCAAGAAGCCGGATGTCTGCCCTTCTCAACCCAGCTCCCTCAGGAG
TGTTTGCTTCAAGTATGGCCGGTGAGCTGCGGAGAGCTCATGGAAGGCGAGTGGGAACCCGGCT
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CCATGAAGGCCAGATACACAAAATCCACCCCATGATCAAGAATCCTGCTCCACTAAGAACGGTG
CTAAAGTAAACTAGTTTAATAAAAAAAAAAAAAAGT

SEQ ID NO: 2389 ACACATCCAAGCCTAAAGAAAAATTAGTCTATGCCATTTTCTTAAATGGCCC
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AGCTAACCAATTCATCAGATGCCGTGTAATGGGGCTGGGCTCTAGCCCTGACTAATGTGATCTAAA
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SEQ ID NO: 2390 ACACAAAGAGGGGGTGGGTGCGGATGCAGAGTGTGTGGCTGATGTCTCCAC
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CAGGTTNGTTNAGGGGATACATTCTAAGANCAACACCNNTTCNATTCAATTATTGAAAGGAANGC
ANCCANAGCTGTTTTTNNAAAGATGNCTCAAAATTCATNATNTNTTTTTNTNCCCTNTNTNTAAG
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G

SEQ ID NO: 2391 ACTCATTTACAATAAAATAACCAAGTGAAGTTACAAAGGCATATATTACTG
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SEQ ID NO: 2392 ACAGAGGGGTCTGTTTCTAAGTCTGGAACCTCAACACGAGGCTGGGATGCTT
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TCAGTTGGTANTGTGCTGGCCAAATGGCAACNTCTGGTANGGACAAAANTNGTCATANTNTNTT
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ANAAAAAT

SEQ ID NO: 2393 ACAGAAAACATAAATCATCGAGGTGGATACCATGGTGGAAAGTTCGGTCTCT
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ATCCTGAGTATGAGAGAGAACCAATCACAATAAGTCTTTAGCTGCAAGTGTGTGGGGCTACAC
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SEQ ID NO: 2394 ACAAACCATCGCCATCAAAAAACGCTGTTCTGACAACACTGAAAGTAGAAG
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SEQ ID NO: 2396 ACGCGGGGAAGCCAGCTGCTCGGAAAGCTCTGGACAGATGCAGTGAAGGCT
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ACATTGAGG

SEQ ID NO: 2399 CGGCGGAGGACGCACTGAAGGAGACAAGAAAGCAGCAAAGGTTCAAAAGCT
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SEQ ID NO: 2400 ACGCGGGGATAGGGAGCGATCTCCGAGCGAGGGCGGCAAGATGGACGCGGGA
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ACAGATTGAACAAGAAAACTGGCATCTATGAAAAAGCANGATGAAGACCAT

SEQ ID NO: 2401 ACCCTTGGAGATACTGGAGCGCTTCTGCATTCAAGGCTGGTGTCTACCATTTGAT
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AACTCTTGATAAAACTTGGTTGGTTTGGAAATCTGAAATCTNTGGAAATANCANAATGAANATTTGT
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SEQ ID NO: 2402 ACGGTAAATTCAGTGGCAGATACAAAAGCTTATTTGGGAGACAGCAGATCTC
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ATCAGCAAGAAAAATTAACCTAAAAAATTTAAAGACTAAATAATCTCTTAACAGGTAATACTA
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SEQ ID NO: 2403 ACCCATAAATCTACTTTCCAAAAACAGGAGCTTTTTAAAGAAAAACCACAT
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GNTAATN

SEQ ID NO: 2410 ACGCGGGGAGGCATTGAGGCAGCCAGCGCAGGGGCTTCTGCTGAGGGGGCA
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SEQ ID NO: 2411 ACCTTTGTGACAACTCTAACACATTATCGGGAGCAGTGTCTCCATAATGTAT
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SEQ ID NO: 2412 ACTGCTAAAGATAAAAATACAGGGAGAAAAATAACTTGTAGCAATAGATCCCC
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SEQ ID NO: 2413 ACGCGGGATGAAAAATATAGACATTCTACATAAGCCAGTTCATCACCATT
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SEQ ID NO: 2414 ACTTTGCTACGGCAGCAGCCTGCTGACAGAGAGGATCCACCTCCGAAACCC
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SEQ ID NO: 2415 ACACGTTCTTGTGTCTGGCTCGGCAACAAACACCACTTCTGGCCAGTCTTC
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SEQ ID NO: 2416 ACGCGGGAGAGACCCCGGACCCAGCGCTGTCTCTCCCGCCGCCGAACCA
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AAACCTT

SEQ ID NO: 2417 ACGCGGGGAGGTGCCGCCATTTTCATCTGTCTCTCTGCGCCTTTTCGCA
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SEQ ID NO: 2418 ACGCGGGCATCTGTTACCCAGATCTACCATGCAGTTGCAGCTCTAAGTGGCTT
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SEQ ID NO: 2419 ACCCTCCAGGTATGGTGATATTTACGCCAGTTTCTACAACTCTGGATTGCTT
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SEQ ID NO: 2421 ACGCGGGGAAGATGAAGGTAAGTAGAAACCGTTGATGGGACTGAGAAACCA
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SEQ ID NO: 2423 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGANACANAGTCTTGCTCCATCAC
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SEQ ID NO: 2424 ACAGGCTTAAATCTATGTCATTTACACTCACTGAATCATCAACCTCATCACCA
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SEQ ID NO: 2425 ACAAAAAAATCCCTTGCTTGCAAGTTTTGTACTTTTACTTAAATATTTA
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CC

SEQ ID NO: 2426 TACGGTCTGAGACATCACCGCCAAGCTGGGCATCGGGGAGATGGCCGAGACT
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SEQ ID NO: 2427 ACCTGTGGTATGAAGCCGACAAGCGCCGCTGTTCACACCTGGATTAAGCC
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CTGACCCCAATAATGAAAACATNGTTGGCTATAATAANAANAATGCTGGCCCNANATCCCCAT
TGCCCT

SEQ ID NO: 2428 ACAGGTGGAACAATCCAAAGTTTAAATCAAAGAAGGTGGTGTTCAGTTGCTG
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SEQ ID NO: 2429 CNCGGCCGACGTACTTCCACTCTTNCCTTAAAAANCTTGCCATTTGCTTATCA
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TTGGCTTAAANCANANGGGGNNANTGNCCTTGTNTGAAATGTTTGCAANANCNNATCTAT
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SEQ ID NO: 2430 ACTTCCACTCTTCTTTAAAACTTGCCATTTGCTTATCAGTTCTCTGGGGC
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CCTT

SEQ ID NO: 2431 ACCAATTAAAGTTGAACAAATTGAAGCAGGGACACCAGGCCGACTCAGAGT
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GTTATGCAAAAAATNATCTGTATTACTAAAGACAATGAAGCTGTTTGTGGGNTTTNACGTTCTCTG
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SEQ ID NO: 2432 ACGCGGGCCAGCAGTTACTCATGGAATATATTCTGCGTTTAAAACTAGTTT
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SEQ ID NO: 2433 ACTCTCCCTACTTCCCTTAACTCACTGATTTTCTGAAGAACAGTAATAAC
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SEQ ID NO: 2434 ACATAGTGTGCGGAACCTAAATCGGCATTTAGATAGATCCAGTGGTTTAAAC
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CCTTTTTGCTGTAATTGCACCACTTTTAAAGCCTCTGGACAGAGCAGTATTTCGTTTAAAACTTTGT
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GGAGAAATNAGGGGCTGATTTTTTAACTGTGTGAGATATT

SEQ ID NO: 2435 ACTTGGCTTGGAGACTGGCGCGGCGTTCTGTCCGAGTTCTCTGCAGGTCACT
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ACCGCTATATAAGCAGGCCACTGAAGGACCTTGTAACATGCCCAAACCAAGGTGATTGACTTG
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SEQ ID NO: 2436 ACTTGTATTGATTATGTAGTTCAGTAAGATGTGCCCAAGTCATTTAGAAAA
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CTGANTTNATTGACTTNTGATTNTAAATCTTAATT

SEQ ID NO: 2437 ACAGGATGAATTTAAATGTGTTTTCTGTAGAGACAAGGAAGACTTGGGTAT
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GGC

SEQ ID NO: 2438 ACCTAGAAGAGAGGCGGGTCAAAGAAGTAGTGAAGAAGCATTCTCAGTTTCA
AGGCTATCCCATCACCTTTTATTGGAGAAGGAACGAGAGAAGGAAATTAGTGATGATGAGGCAG
AGGAAGAGAAAGGTGAGAAAGAAGAGGAAGATAAAGATGATGAANAAAAGCCCAAGATCGAAG
ATGTGGGTNA

SEQ ID NO: 2439 ACATTAGCACCATATAACAGGCGTCTTTAAAGCCTTCCCAATATTAGTAATCTT
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AATCAATCTGTGTTTCTGACANTTGAGGTAGTTAAATANGGAGGGCTT

SEQ ID NO: 2440 ACGCGGGGCACAGCCAGAGCCTAAAGGCTAGAGCCGGAGCTGCCGGGCCA
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TGAAAGGAGAAAGCACGGGGTCCGCCAAACCCCTTCTGCTTCTGCCCATCACAAGTGCCACTAC
CGCATGGGCCCTCACTATCTCTCTCTTCTCCGACTATTGGCAAGAAGCAGATGCGCATTTTGAT
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TTGCA

SEQ ID NO: 2441 ACATTTAGAATTTTTGGCCGGGTGCAAGTGGCTCACACCCGTAATCCAGCACT
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GAGGTTG

SEQ ID NO: 2442 ACACAATGTGTAGCTCATATGAAAACCTCATGACAAGTCATTGAGTTCTGTAACTGCCATACAACTTACATGTGTAATATTAATTGCACAAAGTATATCAAGACATATTGAAGAAAACAAAAATTAAGTGCTATTTTAACGGTTCATCTTTCAAGTATGTGAATACGTATACAAATTTAACTGCACAGTTTTGTGAAAAATAAGTTTCAACAATAAGACTTCAGTTGTTAAAAATTAACCCAAAAATATACTTTAATTAATTAACATCACTACAATAATTAATCTTTATCTTTGTTTACATTTTGGTGTGTTGGGACTTTTGTAAAAAAAATCCAANTTCTAGAATTGCAAAAACCTTCATTGTTGCCACTGAGAGAGCAACATATNGTNGCGGGGGGGGAGACCANANATCTANCGACTGAANCANATTTGGCCAAACCGNGTGGGGT

SEQ ID NO: 2443 GATCTACCATGCAGTTGCAGCTCTAAGTGGCTTTGGCCCTTCCCTTGGCATCCCAAGAAGCACTCATTGCCCTTACTGNTGCTCTNAGCAAGGAGGANACTGTGCTGGCAACANTCCANGCTCTGCAAAACAGCATCCCACTTGTCCCAACAGGCTGACCTGATGAGCATCTTGGAGGAAATTGAGGACCTTGTGCTCGGCTNNATGAACTCNGGGGGCGTNTATCTCNNNTTTAAAAAATGACTGGAAACAACATCCCTTTTTTGTGGGCTTGCCACCCTACAAAGCTCATTGNATCATNTTGGGACTTGAACCATCCATTAAANGGNAGGATNAGGTCAATCCAACCTTGATNAACCCNATCTTTAACAAATAANTAANTTTTGAATTCNCTCTTACTAANCNTTTAAACAGGGAGCCCTCTTGCAACNTGGTTTCCTTTGAA

SEQ ID NO: 2444 GTACATACACACACACACANCNCAGAGAGAANACAGAGAGAAANTCCTGTGTCAAAAGATCACATGACCTTACTAGTGTTCCTCCANTGACTGTAATTTATAAACTAAAAATTTTACAAAATCCACTGCTATCTTCTTCTGCTCCTGAGTTTNGGTTNGACTTTAATGGATGCTCCAGCAATAACAGANTCTAGGACATGCAAACTCACTGTGAGCGAGAGGCTAGGGATCTGCCCTAACATAGGAACCTGTTTCTATCAAGCCTGAATGAGGCGAGCTNTGNTAGANTTAATGACAAATCAATGCCAGNGAANTATTCTGCAAAACAGGGTAGCTTTTGTGCTTTCTTTNATTATTTNNTTTGGGGAGATAAAAGTTTTTGANCCATGGGTCTACTAATTTATCACTAAAGGACTGGGACCACATTCTNAGNAANACANCATGGTNTTACTGTCCANGGAGGGAAAAATCCC

SEQ ID NO: 2445 ACCTTAAAGTGTCTCACCTAGAGGCTCTACCTGTAATCACATTAATTTTTCTAAAGACAATTTGGTGTGTTTGAAGATAAATGTCAATAGTCTATGATAAATAGCATCATAGGACAATAGCCATTTTAGACTTGACCATAATTTCTCTTTTAGCATATAGCCATCTTGATATTTAGGTGGGAGACTACTCCAATGGAGCAACAGTTTCATTTTACATGATTGGATTAAANAAATTTACAAATTTTAAACCTCATAAGAAATCTTAATAATTTNAAAAATNGAAACATTNNACCCANAGCTCTANCANCNTAAATAATTTNTAAAAATACCTTCATTG

SEQ ID NO: 2446 ACGGGTATCACTTTCCGGAGCTGGTGAAGATCATCAACGACAATGCCACATACGCGCTCTTGCCCACTTTATTGGAAACCGAAGGGAAGTGAATGAGGACAAGCTGGAGAGCTGGAGAGCTGACAATGGATGGGGCCAAAGGCTAAGGCTATTCTGGATGCCCTACGGTCCCTCCATGGCATGGACATATCTGCCATTGACTTGATAAACATCNNAAGCTTTTCAGTCGTGTGGGNGTCTTTTATCTGAATACCGNCAGANCCTACACACTTACCTGCGCTNCAAGATGAGCCAAGTAGCCCCACCCCTGGGCAACCTAATTGGGGAANNCGGTAGGGCACNTNTNATNGNACATGCTGGANNCTNACCAACCTGNCAAATTATCNACATCCACAGTGCAAACTCTNNGGCTGAAAAAGCCCTGTTNA

SEQ ID NO: 2447 ACCAAAGCTCACTACTGCGGTTTGCTGTGCTGGACAATGAGGCGGAGCCACTGTTGGGGCACCCCTTCCCTCCCGGGTTTGCAAAATAGAGGCTACCGGGTGTGTAATTCAGCAACACCTGTTTACTATTTGTTATTAACATATCATCTCCACCTTCCCTTTGATTAGCAATTTGTACACTGTGAAACAGCTAAGTCGAGCTAATTAATGCACTGCCACACATACCTGTCACTTTTGGGGTGAGACACTTAAATCTACTCTCTTAGTGGTTTATTATTAATTTTGTAGACGGAGTCTGTCTGCCGCCAGCTGGATGCAATCTCGGTTACTGCAACCTCCACCTCCAGT

SEQ ID NO: 2448 ACTTTTACTTTTTAAAAATTTCAAACCTTTTATAGTATTCTGCTAACATATCTCCGTGAGGAACACTTAATACTGAATTTTCCCTCAATAGCCAAGTCAGAAATACCTTATTTTCAATTTTACCCTAAGTCTTTGTTTCTAAACGCAATTATGTAGAATAGATTGATCCGTCACAGCATCTTGAGTAGCTAATGAGGTAGGAGTATCTTAAGTCTTAGGCTTANTGAAGCAAGCAAAAGACAATCAAAATACAAAGATTTTCTTTGNAGTGGGTGNNCTTTNAANNAAAAANNGTAAAAANCACTGGNAANTGANCAATGCTACTAACATTAATAAAN

SEQ ID NO: 2449 ACAGCATCGTAGGGTCCCTAAACCTTGCCCTGTTTTGTTTTTTAGTTTGTATCCCCCTTACTGAGCGGCTCTACTAGTGGCTGTGATTAAATGTCCCAAGCAAGGATAGGGGAAGGGAAATGGGTTGACCTCTGGAGATCATTGTAAACCAATCCTGCCAGACCTGTTTGGGCAGTGGGGAGCAAAACCTAGATAAGGACCTGTTGGGGCACAGGGAGCAAAATCTCTTTAAACAAACCAANCAAGTTCCTATTCACATCAACAGANCGAGGCTGTGATAACTTAAGGAGGCAACATCTTAATAGTCCTTCAGT

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SEQ ID NO: 2450 AAATTTACAAAANAGGTTTATTGGACTTACAGTTCACGTGGCTGGGAAGGC
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SEQ ID NO: 2451 TACGGNCTGAGACATCACCGCCAAGCTGGGCATCGGGGAGATGGCCNAGAC
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SEQ ID NO: 2452 CCGGGCCATCATTTANTNATGGAATATATTCTGCGTTTATAAACTANTTTTT
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SEQ ID NO: 2453 ACTTTTTTTTTTTTTTTTTTTTTTNNNGGAATGCGTTTATTTTAAACAACCAAA
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SEQ ID NO: 2454 ACAGGATGAATTTAAATGNGTTTTCTGAGAGACAAGGAAGACTTGGGTAT
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SEQ ID NO: 2455 ACTGAGGACATGGCTGTGAGCTGGTTTCTTATCTGCTCTGAAGGCATGCTTTG
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SEQ ID NO: 2457 ACGCTGGATAGCGTCCAGGCCAGAAAGAGAGAGTAGCGCGAGCACAGCTAA
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ANGGTC

SEQ ID NO: 2459 ACGCGGGGAAGCTTGGACCGCATCTAGCCGCCGACTCACACAAGGCAGGT
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SEQ ID NO: 2460 ACCITTATGGATTTGACCCACCTCATTTCTGGACAAAGCCTCAGGAGGATCTCTT
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SEQ ID NO: 2461 ACCATCTGTGGCTCCTTAAGGAGGCTTCTCTTTAATTCOCATGAGGCAAT
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SEQ ID NO: 2462 ACAACCCATAATTTCTGTGTCATCAAAAGAAAAGGGATCAGAATCATCTGGT
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SEQ ID NO: 2463 ACGTTCAATCCGGGGAATGATGACATGTTCAATGGCATTACACGCCTGTTGG
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TTCCTCGCTCGAATCTTCACCTTCGCTTTATTGACATTTTGGATAACTGTAGTGTGAAGTCACCTG
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TTTGGACCTGTCTGTGCTCCCTTTAAACGAGCCTTCATGATGGTCTGTGCCATTCCCGAGGGGAAAG
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SEQ ID NO: 2464 ACTACTGCTGTTTCTGAAGACGCGAGGGCAAGTGCAGCCAGCGGTTCTTTT
CCTCTTTAAGCGTTTCTCTCTGTTTCTCCAGCTTCTAGTAATCTCAGCAGCCGCTTCTCTGGC
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GTCNCTCTTCAACTGTCTCGAAGCTTCTCCCGAATACACTNTGGGCACTCANAGAAACAAT
CNATTCGTGAGGCAATACTGCATTNGTTTGCCANTNTATCNGGANATGCGGNCCTTGTATTGCA
NCT

SEQ ID NO: 2465 ACGCGGGGGAACACCACCCAGTGTGGAGCATCCCACTGCTCACTGAGGCA
CCCCTGAACCCCAAGGCCAACCGGGAGAAAATGACTCAAATATGTTTGAGACTTTCAATGTCCC
AGCCATGTATGTGGCTATCCAGGCGGTGCTGTCTCTATGCCTCTGGACGCACAACCTGGCATCGT
GCTGGACTCTGGAGATGTGTGACCCCAATGTCCCATCTATGAGGGCTATGCCCTTGGCCCATGC
CATCATGCGTCTGGATCTGGCTGGCCGAGATCTCACTGACTACCTCATGAAGATCTGACTGAGCG
TGGCTATTCTTCGTTACTACTGCTGAGCGTGAGATTGTCCGGGACATCAAGGAGAACTGTGTTA
TGTAGCTCTGGACTTTGAAAATGAGATGGCCACTGCCGCATCTCATCTCCCTTGAGAAAGAGTTA
CGAGTTGCCGTATGGGCAAGTGATCACCATCGGAAATGAACGTTTCCGCTGCCANAAACCCCTGTT
CCANOCATCCTTATCGGGATGGAGTCTGCTGGCATNCAATGAACACCTTCAACAGCATTATGA
AAGTGTGATATTGACATCAGGAAGGACCTTTTCTAACAATGTCTATCAGGGGGC

SEQ ID NO: 2466 ACTTTTTTTTTTTTTTTTTTTTTTGGCTTTCATTTGAACATTTAATAAAAAAT
GTTTAGGTTGATATCTTAAAGTTGTGAGTGAATCTCANATTTACATAACAGTTTGATCCAGTAG
TTTTTTTGGAGTAACACAAACATCAGTATAGCCAAATGTTAACTCTTATCATCTTTTGTGTTAATAAC
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ATTTGATCCAAAAGGTAATCNAANTGGCTTTTAAATTTAAGCNTGGGGGANAATTAANCCC

SEQ ID NO: 2467 ACTTGTAGGGAAAAAAGTTTGCACCCCAAAAGTCTGTATCTTATG
AAAAAAGGTTGATATCTTAAAGTTGTGAGTGAATCTCANATTTACATAACAGTTTGATCCAGTAG
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CCCTTGCCCTGGANTANCGAATTTTGTGGGAATTTTNCACATGCNCTTTNTTGAANNGGGGT
TTTTCCCTAATCAANCAATTTGGAGACACTTTTGNAAATNNGGACTTTTATGTCAACCATTCGGNC
NGTTCAACAT

SEQ ID NO: 2468 ACTACAGACCTCCACATGTTGGACAGTAGGATTACAGCAGAGAATGAGTCCCA
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ACCGAAATTTTGTCAAGAAGCGGAGGCTCTTAGAACGGAGAGGCTTCTGAGTAAAAAGAACCAA
CCCTTAGCAAGGCGCTAAGTTGCACTCTGAACCTTCAAGAAAGGGGAACTCTACGGTCCGA
TGGCACTTGGAAAGACCCCTTCTTCCCAAAAGAAAGACAGCTGCTTCCAGCAATGGGTACGGAC
AGCCCTGGACAAGAAAGCTGCAGTGTCTTGGTTGACCCCTGCCCTTCAAAAAGGCTGATTCTG

TTGCTGCTAAAGTAGATTGCTGGGGGAGTTCAGAGTGCCCTTCCAAAGATCAATAGCCACCCAA
CCCGTTCTCAAAANAAGAGCTCCCAAAANAATCCTCTAAAAAAGAACCATCCTTANAAGAATGCC
CACANNACTCCACCAAGCTCATTGAGANAATAAATGCCTCCGGAANCTTCAAAANNTTGCC
ACNGGAANAAGGN

SEQ ID NO: 2469 ACITTTTTTTTTTTTTTTTTTTTTTTGGAAAAACITTTAACAATTTATTAGTC
TTATTTTCCAGTAAATATTCAAATAATGTCAAAANAATGAAATGATAGCGATNTAGCCAACTACC
TTAATTAATTCACATAAATATTTAAATNTAAAAACCTNANATCAGCAGACCGANTCGAAATCT
GATTCCTCAAAGCAAGTATTGCTTTACCTTGTCTGAAATGCAGNCCGTATATNACCACTAACTT
GCATGTNACCAATGTTTGNATAGTGTTTTTAAATTTGCTNTCGGGNANCCGNNATCCNTCAAN
CAAGAAAAANAT

SEQ ID NO: 2470 ACTTTTTTTTTTTTTTTTTTCCNAAAGTGGTTTATTGCAATTTACATGGATT
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SEQ ID NO: 2471 ACTTTTTTTTTTTTTTTTTTTTTTTTAGGATAAATACTATGCTTTAATGAN
CCCCTTAAATANAATAATCCACTACAAAAATACANAGGAGATAGGGTGTTCCTGTATCCGCTCAT
TCCCATANAATACTATAAGGGAANAATAANAACCTTGAATTAANACAGCAGCAAGCGGAGGTGA
NAATGCNATTTCTAGGCCATCTTGTGGGACTGATGAACAGCATCTNTGATCTCATGATTTAAACAT
CTGGTTATCCAAAAGGGATGGGATTGGCTAAAAAACCAGATCAATTCNNGATTGGTTTGTGTTT
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AAGCTGANGCTGCAAGTGCAATCAAAAAAANGATTTTACAGACCTCTNTCTACCCCAAT
CCCCCGNNTACCTGCCGGGNGGNCGTTCNAAAGGGC

SEQ ID NO: 2472 ACTTTTTTTTTTTTTTTTTTCTGGGACTCTGGAGATGCCGAAGCACACGCCTT
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CCAGGCGGCTTGTGAACAGTCAAGTGGAATTTGAAGAAAGAAAAACAGATGGAACAACGACGTT
GGGACTTCTCCATCCTGTGGATCCCATTTGTAGGAGAGCCAGGCTACTGCCCTGTGAGACTGGGAAT
GACAACTGGAAGACTTCAGTCTGGAGTGAATACTTTGCAGGGGTTCAAAGAGGATAAAAGGAACA
AAGTCACTCCAGTGTATATTGAATTATGGGCCCTACAGTTCTTATGCACCCGATTATGACTCCAC
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TCCAAGTNGATTTCAGCATCCATGAGTTTTTGGCCAGTGCCAAAGATTATCCCGTATGTGATGGG
AGATAGNTTACTGGATGTTTTAACAAAAGGGGGGNCNTTCCAGGACCTCAAAAGANATGGGAGA
TGTCTNTCTGAA

SEQ ID NO: 2473 ACTGAAGAACATCCCATGGATATCGGTTAACTTGCCCTCCACAGCATGTAA
AATAACTTCTGGAGCAAAATATCCCACTTCTTACAACAGGACTTGCAAAATACATAAGCAGAGG
CTTTGCTTCAATCAGCTGAATAATCTTATTCTGCTCCTCTACTCGCAGCACAGCATCGGGGT
CATAGCAGCAACACAGTCAGTAACCAACTTGTGCTATGGGATCGAGTAGTGTGATAATGTGTTT
CCCAGCAGGACTTCTTTCAGCTGAAACCCAAAGGCGCTAAACCTAAACTCCCAGATTGTCTT
CCCCAACACAGCATCTGGTCTGCTCATAGTTGTAATATGGCTGGTTAATAACTCCTGCTATGGC
TTTTCTTCAAGCAATCCAATAAGAACTGTACATTGTCAAGAAAGACCTCGGTATATTCCTTG
GTTCCATCCAGAGGATCAACCCAGACGAGATCTTCTTTAATAGCACTGT

SEQ ID NO: 2474 ACGCGGGCAACATGACTGTCTTTAACTCCAGTGGCTGGCCAGGCACGGTA
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CAAGACCAACCTGGCCAAACATGGGGAACCTGTCTTTACTAAAAATATAAAATTAGCTGGGTG
TGGTGGCNG

SEQ ID NO: 2475 ACTTTTTTTTTTTTTTTTTTTTNGGTTTTTTTTTTCCACACCTGCCCTTTATT
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GGGACTGATATCAAGGGAATGCTGAGGTCCAGCAGTGTCTCTGAAGGCATGCTGCATCCTAAGG
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SEQ ID NO: 2476 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGNTTCAAAAGGGTGTTTACTATTTGG
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ACCAATCTGCATTTGCTGCTACATGAAAACATTTTTTGGTCTGTGGAAAATGTAATTCCTGANAT
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SEQ ID NO: 2477 ACCGGACCCCTGCAGCCGAGAGATGTTGATGCCTAAGAAGAACCGGATTGCC
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CCCAAGGCTACGTGAAGGAACAGTTCGCCTGNAGACATTNTACTGGTACTATTTTTTTTNTTTA

SEQ ID NO: 2478 ACGGGTATCACTTTCCGGAGCTGGTGAAGATCATCAACGACAATGCCACATA
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AGCCCTAATTGGGGAAGCGGTAGGTGCACGTCTCATCGCACATGCTGGCAGCTCACCAACCTGG
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SEQ ID NO: 2479 ACAGGAGATCTCATTGGGACAACCTAAGGATAAAATGCTGGTCAATCGAGCAG
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TTTCCAGACCT

SEQ ID NO: 2480 ACCATAGGATTTTGAAGATGGTATCATCAATTTCTTAGTTAGTGATGGTGT
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CACTGGGCTTNCATCANATANCCCTCCTNCTCACTGAANGCNCCTACTATANCTCCTNCACCTA
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SEQ ID NO: 2481 ACGCGGGTCTTTCTCGGGACGGGAGAGGCGGTGAGCGTGGCGTTACTC
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SEQ ID NO: 2482 ACGCGGGTCTCCCGAGATGACAACTACTCTCGACACCGAATCACCATCAA
GAAACGCTTCAAGGTGCTCATGACCCAGCAACCGCGCCCTGCTCTGAGGGTCCCTAAACTGAT
GTCTTTTCTGCCACCTGTTACCCCTCGGAGACTCCGTAAACCAACTCTTCGGACTGTGAGCCCTGA
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ACAAGATTATTANAGAT

SEQ ID NO: 2483 ACTTTTTTTTTTTTTTTTTTTTNGGAATCCTAACTCTATTAAATAGTGTGATACA
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ATCANAACGCTCATAGTGTGCAAAAGCTCTTGATAAGCGTTTCTCTNATTTCCAGGAAAGCATC
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TACCTCGG

SEQ ID NO: 2484 ACTTTTTTTTTTTTTTTTTTTTNGCCAAAGACAACTANAGCAATGCCTATGTAA
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TGTTAATTTTAGTAAAAATAATCATATGCCAACAGGGGAATTGAACCACTTTCTAAATCATAGT
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CAAAAAAATCTTTTTACTTTGACATCACAACCAAGGNGCAGTNTAAACCAAGTTGCTGGATT
TGNTGGTTTTATACANATAAAAAAACCACATTTNCCCATACATTTTTATAGGCTNTCCNAANGNT
NTAAAA

SEQ ID NO: 2485 ACCAACCTGGCTACTGGAATCCCGAGTAGTAAAGTGAAATATTCAAGGCTCT
CCAGCACAGACGATGGCTACATTGACCTTCAGTTTAAGAAAAACCCCTCCAAAGATCCCTTATAAG
GCCATCGCGCTTGCCACTGTGCTGTTTTGATTGGCGCCTTTCTCATTTATTAGGCTCCCTCCTGC
TGTCAGGCTACATCAGCAAGGGGGGGCAGACCGGGCGTTCCAGTGTGATCATTGGCAATTCG
GTGTTCTACCCGGATTTTNCACNTGGCCTNNTTACTATGCATCCAAAGGCTTCCNGGT

SEQ ID NO: 2486 GGTACTTATATAAAATCTAGTCCAGTTCTCTCATTTAANAAAAATGAAGACAT
GAAATACAGACTTAAATAGCTCAGATAGCTAATTAGGAAATTTCAAGTTGGCCAAATAATAGCAAT
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TTTTGTATTTACTGCCATGTAATGAAATATATAGATTATTGNAACCTTTCAACCTGAAATCAAG
CAGTATGAGAGTTTAGTTATTTGNATGNGGCACTAGTGGCTAATGAAGCTTTAAAAATCTACCAT
TCTTCTTTAAAAATATTATTAATGNGNATGGGATATNACAATTCACTTAATTTCCCACTTATNT
GGNGGNACCATGTTTCCCAATTTGAANGNGGGGGTTAACTTTAAT

SEQ ID NO: 2487 ACTTTTTTTTTTTTTTTTTTTTGGAGCTGAGACCAGGAGAAATAACTTTAT
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CTGCTGGGGAATGTATTTGCCACTAAATTCCTCAAGTATGCAACATTACAAAAAGATAGGTTTT
TCATCAATAATTGAATTTCCACAAACCTCCCAATCACAAGTATTATAAGTGGAAGTAAAAATCAC
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AATTCATTANCTATATGATCTAACCAAGCAGCAACAAAGATGGCCAGGCCATGGCAATCCTNTTC
CATTTCCCTACCACTNAGGGCTTAACAACANGGTGAGGCTTAAGTNGANGTANGGGGGTGGGGGG
CAAAAGGGTTANTTTNCCCATNCTTGGGCGNACCCCTTAAGGGGAAT

SEQ ID NO: 2488 GGTACTTTTTTTTTTTTTTTTTTTTGGTCCANNGATCCTTACTGAGA
TCCACTTGAAACACTTCGGTCTTAACCTGTTAACTGAGTTGACAGGCTGATGGCTGATCTAGGTA
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GAATATCATCAAGGNCCTGTGCCATCTNTTCAGGGTTCGATTAAAGCTCCTCAAAATTTGGGATCT
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CAATGTAGAAGTCAACCTCTGAGGCTGACTGAAATTCACCATCCAGGGCTGAAAAACCCGCTGGC
CCACGAGGGTCTTATCTGTGTTGAAGACAANAAGCTGGATCCCGAATCTCTGCTGTGAG

SEQ ID NO: 2494 GGTACACTTGAAAACCAATTCTTAAACCTGTGTTTCTTAAAAATAGTTGTGTT
GTAACCTTAAACCAATACCTAATCAGTGTGTTCACTATGCTTCCACACTAGCCAGCTCTTCACAG
TTCCTTCGTTTCAAGTCTCAAGGCGCTGACAGCAGAAGGGCTGGAGATTTTTCCTTACAAT
CAGCTTCAGCAACTGAGAGCTTCTTCTATGTTGTCAGCAACAGAGCTGATCTCGCAGGTTGCT
AGCATAGAGACGATTTGAATATCTTCAGTGAATATCCGGCTCTAAGCTCAGAGATGGGTCAACA
AACATAATCTGGGGACATACTGGCCATCANGAAGAAAGTTGTTTGTCACTGTTTTCATAAAACCG
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GCTTGACTGNGTGGGNCCTACCAAGNATGAATCCCGGTANCTGGCCCGCGGGCGGTTCAAA

AGGGGGAAATCCANCCACTNGGNGCGCTCTAATGGATCCAAACCGGGNCCAACCTTGNGTAA

SEQ ID NO: 2495 ACTTTTTTTTTTTTTTTTTTTTTTTGAGTGTGGGTTAGTAATGGGGTTGT
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CAGGGGTTGAGGTCTTGGTGAAGTTTANTGGGGTTAGCGATGGAGGTAGGATTGGTGCTGTGG
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SEQ ID NO: 2496 ACATTCTAGCTGAGAAGCAATGGGTCACTCATTAAATGAATCACATTTTTTAT
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CTTANGGCAAGAAATTTATGCCAAAGNTCTCATNTGAGNTTTNANGGAGAAAAAACCTTAATG
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CAA

SEQ ID NO: 2497 ACAGCCAGCAAAGGGCGCTATATCTCTCTCATTTAAGGAACCGAGAAGCTA
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AGTTTTGGATCTCGTAGTGATTCAAGAGGGAAGTCTAGCTTCTCAGTGATCGTGGAAAGTGATCA
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GCCAATTCAGTGCAAAACNTTCCATTNCTATTATCAAAAAAANNNNNNAAAAAAGTNCCTTG
GCCGACACCTTANGGCAATTCACAAATGGGGCGCTANNGGNTCCACTNGGNCACACTTGNG
NAACTGGCAAACTGNTCNGGNAATGTTTCTTCAATCCCAATTTNGCGGACTANN

SEQ ID NO: 2498 CGAGGTACTGGCTGGGATGGCTCTGATATAGCAGCCTTGGTGTAGTTTCTGCA
TTTCGGGAAGAGTGACTGGACTGGATTCTCTAGCTCCTTCAATCCCATTTTCTCTGTGGCATCAC
TAAGTATAAGACCTGCTCTCTCTGAAGACCTATAAGCTGGAGGTGACAACTCAATGTAAATTT
CAAGGAAAAACCTCATGCTGAGATGTGGGCCACTCAGAGCTAACCAAAATGTTCAACACCATA
ACTAGAGACACTCAAAATGCCAACAGGACAGAAAGTTGATGACTTTCATGCTGTGGACAGTTTTTC
CCAAGATGTCCCAAGCCTCATCGTGACGAGGCTCTTATCCCACTCCATTTTCTGCTCATGCTGCTG
CTCTTTAATTTGGTAAGATAATGCTGNAACAGAAATTCACAATCAGCGCCTTGTGACAGGTAATTT
GCAGAAATGGTGGATGTGATGNCATCATGTCAACCCCAATTTTGACTAANGGATCCTTATTCTNG
CCAATGNTTACTTTACACATCCTAATACACTGGTTATTCAATCCCGGGGNCCTGGTAAAGTANACC
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NAAANGGNGAATTTGCAATGTGAACCTTTGGTGCCANAANAAACCGGGGCGCNGCCG

SEQ ID NO: 2499 GGTACACTGAAACCAAAATTTCTAAAACTGTTTCTTAAAAAATAGTTGTT
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SEQ ID NO: 2501 ACCTGAAAAATAAGAGAAAAAGCACAGANGCCAGTGAAAGAAGGACAG
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SEQ ID NO: 2502 GGTACTATAGAGACTCAGTTGCAAAAATTAACAAATATGCTGCTTGATTAA
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SEQ ID NO: 2503 ACCCACTGTATTATTTATGTGCAACAAGAAGTGTGCAACTGCACAAAACCTC
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SEQ ID NO: 2504 GGTACTATAGAGACTCAGTTGCAAAAATTAACAAATATGCTGCTTGATTAA
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SEQ ID NO: 2505 NCNAGCGGCGCCGCGCCNNGNCGNACGCGGGCATGTGNCNCTATGGCNCACCC
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SEQ ID NO: 2506 GGTACCTGTTCCTCTGTTTTCAGATCCCCAAATTCCTGCATAAATGTTGATTCA
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SEQ ID NO: 2507 ACTTTTITTAAGCAATGGGTCACGNATTAATGAATCACATTTTTTATGCTC
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SEQ ID NO: 2510 ACGCGGGGACTCAGAAGCTTGGACCGCATCTAGCCGCGACTCACACAAGG
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SEQ ID NO: 2511 ACACITGAAACCAAATTTCTAAAACTGTTTTCTTAAAAAATAGTTGTTGTA
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SEQ ID NO: 2514 ACGCGGGGGTATTCTTCCCCAAGTCTCTATGGTAGCGTCAGCGTCGGAGGC
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SEQ ID NO: 2515 ACCCACTGTATTTATTTATGTGCAACAAGAAGTGCAGCAACTGCACAACTC
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SEQ ID NO: 2516 GGTACATGTGCCACAATTTCTTAATCTGGTCTATCATTTGTTGGACATTTGGGT
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SEQ ID NO: 2517 ACTGTGGTGTGTGAGTCTCAGCAGCCGCCACACGCTCTAACTCTGCTGCAT
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SEQ ID NO: 2521 GGTACAAGATCTACCCCGACACGGGAGGCGCTACGCCAGGACCGACGGGA
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SEQ ID NO: 2524 CGAGGTACGAAACCAACGCCCGAGGGCTGGTCGCGACTACAGTGCAATTA
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SEQ ID NO: 2525 GGACGAGTCAAGCACAACTGCTGCGCCAGGAAAAGACAAGGCTAATTGGG
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CAAAG

SEQ ID NO: 2528 ACTGATGCTGAAAAATCAATAAGATTAACCCAGAAATGGCTCAATAAGAAA
CCAGGGACTCCAAAGGGGGTTTACAATTCAGAAACAGGAAAAAATTAGAAAGTGGTTTATTG
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TAATCACTGCAGAGTATTAATAGTGCTTTCTTATGGCTGATTTCTTGCNNGGAGCAAGATAAGAT
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SEQ ID NO: 2529 GGTACGCGGGGATTCTCCCGAACCTCTGCTCAGCCTGGTGAAACCACACAG
GCCAGCGCTCTGACATGCAGAAAGGTGACCTGGGCTGCTTGTGTCTTGGCAGGCTTTCTGTCC
TGGACGCCAATGACCTAGAGATAAAACAGTCTTCTACTATGACTGGCACAGCCTCCAGGTT
GGCGGGCTCATCTGCGCTGGGGTTCTGTGCGCATGGGCATCATCATGATGAGTGCAAAATGC
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CTCAGCCCAAAGCTGATGAGGACAGACCAGCTGAAATTGGGTGGAGGACCGTTCTCTGTCCCCAG
GTCTCTCTCTGCACAGAACTTGAACTCCAGGATGGAATTTCTCTCTCTGTCTGGGACTCCTTTG
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NGGCGAAAT

SEQ ID NO: 2530 CGAGGTACGCGGGAGCTCAGTGTGATTCAATAGTGATATGTAAGTCCCTCA
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ACAACCGAAAACNAATAATTTCAAGCCCTGNTTATTCAAATTTTACTGGGGCTCTATTTTACCCCTCA
CAAGCCTTANAAGACCTGCCCGCGNCGCGNTCNAAGGCGAAATTCACACNCTAGCGCGGCGTA
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SEQ ID NO: 2531 CGAGGTACTGGTTTTGGATTAGGAATGTTTTCTCACTTACCTTCTTAAAAAG
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TGATTTCCAGGCTCCATATCTTCTACATGGAATAATGTCAAAGAGCANGAGCAGTGACTTCACT
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SEQ ID NO: 2532 ACATATTAGAAGTCTAAGGAGTAGCAAGTCAGTGGGAGGACTTTTTACCCC
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SEQ ID NO: 2533 GGTACTGGTTTTCTGAGAAACAGTCCCTCGTGAAGTACAGTACGCTCAGAG
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AATTAACGAACTAAACACTTTTGGCCCTNACTGATACATTTCAGAAATGGGCTTTTAAAGGCTTG
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SEQ ID NO: 2534 CGAGGTACTTTGACTTACTAGGGTGATTCAAAGTTTCAGGAAAAAGAAAAAT
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TTTTGTGGCATACATTTCCAAATTTTAAATGCTCCCTGACAGGTGAATTTTAAAGGATAAAAAAA
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CTCATATCTCTGGNCAATGGTTAATAGAATGAGTATNTTGAGAAAAAGTNGGAATNANCTAG
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TCCTANTGGGGTTTACCNAANGCCAGGCCNNNGTCCT

SEQ ID NO: 2535 CGAGGTACCTCCAGGTCATGGTGATTTTACGCCAGTTTCTACAACTCTGGA
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GCCACAGTGGATCTGTATATCTTAATCATCTAATGAACCCACCAATGGAAAAACGCTGTGAATTT
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CCAAGGAGCCGTTCTGGCTGTCAAACCACTTAGACTCTTGCTNGGATGGCCAACTCTATAG
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SEQ ID NO: 2536 ACGCGGGGGGAGACGTGCTAGCGCGTGAAGGTAGCTCTATGGTTTCTCTG
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CGCTCCAAATTTAGATCACATTTCTCAAGGTCAAAGTCTAGATCAAAAGTCTAGTTCTCGATCAAG
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SEQ ID NO: 2537 ACATGCAGAGGTAAAGCTGAAGCTGGGCAGGGGATGGCTACAGTTCATGATC
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GGCACACTGTGAGCTGAAGCTGAAGTTTCCAAAGGGTGAGTACATTACACACCAAGTGAATAGTA
ACAGATTGTTAGTATGTTCAAGCTTTGTGTTGATGATGGTAACTATAGAGTTTGGGGTCAAGTTG
TTTGACAGAGGAATCCAGTACAAGAGATAGAAAGACCAAGTCTTGTCTGAAAGCAAAAGTCTGAAT
GCTCCACTTTTCAATTTCTCTCCATTCTTCAGTAAAGTCAACTTCAATGTCNGATGGATGAAACC
CAAACACATAGCAATTCAGGAAATTTGACTTTCCNTCTNTGCTGGATGACGTGAGTAACCTGAAT
NTTGGAGTACCTTGGCCGACCCNCTANGNGAAATTCACACACTGGNGCCGTTCTTTNNGTCCA
GCTTGGTCCAACCTTTGGGTANNNT

SEQ ID NO: 2538 ACCGTCCAGCGAGTTGCAGATCTACACTTGGATGGATGCAACCTTGAAAGAA
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SEQ ID NO: 2539 ACGTGGGCACAACCTCCACCTCCTGGACTCAAGCAATCCTCCACCTCAGCCT
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TCAGCCCTAAATGACCTGCCTGAAGTTATTTTGTGACATGTATCTCCCACTGTGCAAGAGGGG
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AAGCAAGGGCTTGTGAANTGATGGATGCTGTTNGAACAAACAAAGTNTNGCAGGATGGACAGA
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SEQ ID NO: 2540 ACCATTCTTCTGAACTATTCCAATCAATAGAAAAAGAGGGAATCCTCCCT
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GAATCCAGCAGCAGCATCAAAAAGCTTATCCACCATGATCAAGTGGGCTTCATCCCTGGGATGCAA
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CCACATGATTATCTCAATAGATGCAAAAAGGCCTTTGACAAAATCAACAAACGCTTCATGCTAG
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NCCCAGCCATTTATCCCGAATGGGGCAAAAACCTGGAACCTTNCCTTTGAAACAGGGCCAANA
NANGGGGGCCNTTTTACCATCTCTATTTAAATATNGTTGGAAATTTTGGCCGGCCNTTTGCCN
GGAAAGGAATAANGGGTTNCATTGGAAAAAGGACCAANTTGC

SEQ ID NO: 2541 GGTACCCCTAACTGGCAGGACATTTTGAATCACAATTTGCACATAAAG
AATGTCACGAACGCCATGTATCCATATACAGCAATCAATAAGGAATTTATGACCTAAAGCAAA
GGTAAACTTTCTTGAACCTTAACATTCTATACCAACTAGGCAACCTCTGCCAGGATGAGAGTTGG
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CATTGTAAAGNACAATCTTGGNNTCTGCGCTGNTGAACCAATCAACCCCTAANAATTAACNCT
TTGGGTCTTGTCAANNAAAAACCCNANTTACCCTTAACCTTTTNAATGGCCCCACCTTTNA
AGGNTAACNAACTTATTTTTT

SEQ ID NO: 2542 GGTACAGTTTCCCTTCTCCAGGGTGACAGATGAGCCTTTTCCGAAGTTCTCAG
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SEQ ID NO: 2543 ACTGGAAGTGCTATATAATGCAGTGTAAAAAAGAAATAAATGCA
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SEQ ID NO: 2544 GGTACAGGTAGGGGGCGGGGTGGGCCAAGAAAGGCAATCATTTGGGCAGAA
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SEQ ID NO: 2545 CGAGGTACTGATGCTGAAAAATCAATAAGATTAAACCAAGAAATGGCTCAAT
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SEQ ID NO: 2546 ACGAGCAGCTGTCTGGGAAGTAGGGGGTTAGCTTGGGACCTGAACGTCTCT
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NCTAATTTTAAANTTTTTNAAAAACNGGNTTTTNCNGTTNGCCAAAGGTTGTGTTNAAANNTT
GGTTAAANGAACCTTTCCNCNC

SEQ ID NO: 2547 GGTACTGAANGGCTGGAGACAACACTTTATCAGTTTTGACACTGACAGGAG
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SEQ ID NO: 2548 ACTCAAGTTTATAATGTCCCCAAACCTTAAGACTAGAAAAATCATCCCAAGAA
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GTCGAGCTCAAGTGGTGTAAAGACAGNTCTTTCTTCTCTCTTAAACTCTTACTTGTCTTAA
CACGGAAGATGGGGACAGTGATCCCGAAGGTTTACTAAAAATTTGACAGCTTTCAGTANTTATGA
NAGACNCATATATNACTNNAAGAAAGCNATCATTGGAGTNNCTCNGGCCGNCACACGCTA
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SEQ ID NO: 2549 ACGCGGAGCTACGGGCATGCAGTGGACCTATGAGCAGAGGAAAAATCGTGG
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SEQ ID NO: 2550 ACTGGATTTAACTACCTTTGGCTTAATTCCAATCATTTGTTAAAGTAAAAACAA
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SEQ ID NO: 2551 ACGCGGAGGCAATTGAGGCAGCCAGCGCAGGGGCTTCTGCTGAGGGGGCAG
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GGTTTCAAAACATGACGAGGTTGAGATGAAGCTTCTCATGGAGTAAAAATGTATTTAAAAAG

AAAAATTGAGAGAAAGGACTACAGAGCCCGAAATTAATCCAATTTGAANGGCCAATG

SEQ ID NO: 2552 ACGCNGGGAACGCTGGGAACTCCCGCCTCGCCACCATCTTGCTTTCCTTT
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SEQ ID NO: 2553 ACCCATGGAGCTGGGCTAAGTAAATAGGAATTGGTTTCACGCTGAGGCAA
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TNGTNNNTAGTTTTTNGNGGAAAGGGGGGNNAGCNTTAAACTGGTCCNCCCTTTGGTTTTN
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SEQ ID NO: 2554 CGAGGACAAGGCAGCTGGCAACGTTCCCTTCAAGACACAGAGGAGAAATCC
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SEQ ID NO: 2555 GGTACGGATCAOGCTTTCCCGAGGATGACCTCTGCCAGTATATCACATCAGAT
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SEQ ID NO: 2556 GGTACTTTGAAAATTGAAACTGGATCAGTGTGTGACGGGACTGTCAACTGAA
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SEQ ID NO: 2557 GGTACAGTTGATCCCACTTTGGAATAAATGCCAGAGGTAATAAGCATTAT
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SEQ ID NO: 2558 ACCACCAAGCCAGCTGATTTGTATTTTAGTAGAGATGGGATTTCACCATG
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SEQ ID NO: 2559 CGAGGTACTTTTTTTTTTTTTTTTGGTTTATGCAACTTTATTGAAGAAA
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SEQ ID NO: 2560 ACTATCTCTGTATTCTCACAATAGAGAAGACTAATTTGCAGACCTGGTG
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ACACCTGACGTGGAGACTTTCCAAAACCCGTANGAGATTGCTTCGGCATCGCAATGGTTGCATT
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SEQ ID NO: 2561 ACTTTTTTTTTTTTTTTTTTTTTTTTACCAACAAACGATGAAGTCTCA
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SEQ ID NO: 2562 GGTACTTTTTTTTTTTTTTTTTTTTGGAGCAGTTGATTCCAGTTCCAGGC
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GCGTGCAAGAACTAGAGACCCGACAGCGAAACAGGCCCTCTCCCTCACACAGTTTCTCTGTCT
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SEQ ID NO: 2563 GGTACGCGGGGAACANAATCCAGGATGTTCCATCTCTATATAAATGTATTG
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CTATTTTTTTTCTTTCATAGATATGGGGGTCTTGCTATGTTGCCAAGCTGGTCTTAACTCCTGG
CCTCAAGCAATCCTTCTGCCCTGGCCCCCAAGTGTCTGGGATGTGGGCATGANGCTGCTGTGCC
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SEQ ID NO: 2564 GGTACTTCCAACTCTGGGTTGGCCCCAAATCCAACTAATGCCACCACCAAGG
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GGGTCTGGAAGTCCAATGTGGCAAGGAAACAGGCTCTCATTGAATCTACTAATTCACACCTTT
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CTAGATGATGGATGCCAATATTAATCTGCTGGAGTTTCATGT

SEQ ID NO: 2565 ACAGAAAGGGTATGTTAAGTAGTTTCAGCCAGCAGCTCACCACAGGGATTAAAC
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SEQ ID NO: 2566 ACCGCGGGCTTGCCACACCTTGAAGTGATACTGGCGGGAGCTCTTCCCTGC
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SEQ ID NO: 2567 ACCTGGCCATCTTGGCAGTGTGACGTTTCTGGCTGGCAATCGATGCTGGCC
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SEQ ID NO: 2568 ACTATAGAGACTCAGTTGCAAAAATTAACAAATATGCTGCTTGATTAATG
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TAACCATCAGTTTTTAAATCAATTTTCTTCTTGGTCCGGGATCCCTTTANAAANCCCNTTTTT

GTTGTTTGCCCAAGGACTTCNTTT

SEQ ID NO: 2569 ACGCCCTGCTGCTTCTCTGATCTGCTTTAACGTTGGAAGTGGACTTCACTTA
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GCGCGCCTGGATCACCGCCCGGTGGCTCTTCGGGAGGGAGAGGATCTGTCCAAGAAAGATCCAA
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SEQ ID NO: 2570 GGTACTCCAGCAAATCCTCTGAATCTCCACAGACTATGTTACCCAGTCCCA
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SEQ ID NO: 2571 GGTACTTTTTTTTTTTTTTTTTTTTTTTTACAATAGTGTGAGGATTTTTT
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SEQ ID NO: 2572 ACGGAGAGGGTCAACCAAGCGTGGATCGTTGGCAATGTTGGAAAAGGGAACC
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CAAAGAAGGCTGCCTGCATAGTGGTTCCGGCTGCCCTTTCTAGGTGATTGGAATCAGCCCATCTAA
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ANGGCAATTCACCNCTGGCGGCCGTTTTNGACCAACTCGGNCCACTTGNGAANATNGGANAC
TTTTNCTGNGAAATTTCCCTCAAATC

SEQ ID NO: 2573 ACCCGATTAAAGTAGTGACATTGATACTAGTAATTTTGTGACTTGGAAAGAA
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SEQ ID NO: 2574 ACATCAAGTCCATCTGACAAAAATGGGGCAGAAGAGAAAGGACTCAGTGTGT
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SEQ ID NO: 2575 ACTAAAAAAGGAGAAATTATAAAATTAGCCGCTCTGCGGCCCTAGGCC
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SEQ ID NO: 2576 ACCCACTGTATTTATTTATGTGCAACAAGAAGTGTGAGCACTGCACAACTC
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SEQ ID NO: 2577 CGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTGGGTTTTTTTTTTTTTTTT
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SEQ ID NO: 2578 ACTTTTTTTTTTTTTTTTTTTTTTTTCAGNGCCTTCTCANACTGCTGTGGA
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CCNCCA

SEQ ID NO: 2579 GGTACGCGGATGTTTTTCTGATTCCATCCTGTGTCCTTCATCCTTGACTC
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SEQ ID NO: 2580 ACTATGTCGATTGACAGAACATTCAGAAGATTCTCGGCCTTGCCTTCACG
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SEQ ID NO: 2581 ACATGCTTTTATCTTTCCATAGGACATATTTCCAAATAATGATCACAGTATT
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SEQ ID NO: 2582 ACGCGGGGGTGGTGTGTGCGGGTTCGGTTGGAGGACTCGTTGGGGAGGT
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SEQ ID NO: 2583 ACAATGTAGAACTCTGTCCAACACTAATTTATTTGTCTTGAGTTTACTTCAA
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SEQ ID NO: 2584 CGAGGTACAGTGAGGGTGTTCAGAGGGAGGCACAAAGAATAGCTCTGAGAT
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SEQ ID NO: 2585 ACCTGAGCTAAATGACTGAAGCTTTAGGGGTGCATAGAAACCACCATAATT
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SEQ ID NO: 2586 GGTACTTTTTTTTTTTTTTTTTTTTTTCTACAGTNGGACTGAATTTCTAA
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SEQ ID NO: 2587 GGTACTGATACATGCTATAACAGAGATGAACTTCGAAAACATGCTAAGTGAA
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SEQ ID NO: 2588 GGTACTTACTGAAGTTTITTTTTTTTTTTTGAACCAAGTCTCGCTCTGTGCGC
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SEQ ID NO: 2589 ACTTGAAGTGGTAGGAAATGCATCAAAAGACTTAAAGGTAAAGCGTATTACC
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CAACCTGGGGAACATGGCAAACTGGTTCTGGGAATGGTTTCGGTTCAATTCOCCCANATCAACCG
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SEQ ID NO: 2590 GGTACGCGGGGAACCTGGTGGTGGCCACTGCGCAGACCAGACTTCGCTCGTA
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SEQ ID NO: 2591 ACTCTTTTTTTTTTTTTTTTTTGGGTGAGGGGACCTACTCTGTTATCCAAAT
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CTCCTCTCTCTCCTGCTGGATTATTTAAAAAGCATGTGTGGAACCCCACTATTAAATAAAAGT
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CCAAAGGNAAC

SEQ ID NO: 2592 GGTACAGTGGAAAGGTGGATAACGCCCTCCAAATCGGGTAAGTCCAGGAGAGT
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CGCCCTTCA

SEQ ID NO: 2593 GGTACAGTGGGGTGTTCAGAGGGAGGCACAAAGAATAOCTCTGAGATTAG
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SEQ ID NO: 2594 CGAGGTACTGCTCGGAGGTGGGTCTGCTCCGAGGTGCGCCCAACCGAAAT
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SEQ ID NO: 2595 GCGTGGTCGGGCGGAGGTACAGAGAAGCACCTATTGACAAAAAGGGGAATT
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SEQ ID NO: 2596 ACGCGGGATTATTTTAAATGAGACAATCATTTTAAAGTTTAAAGATAACAGAA
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SEQ ID NO: 2597 ACTAGAGCCAGTCATCTTAACAAATCTTTTACATTTTATTTCTTTCATGT
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SEQ ID NO: 2598 GGTACTGATACATGCTATAACAGAGATGAACTTCGAAAAACATGCTAAGTGAA
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SEQ ID NO: 2599 ACTGGAACATACAACACACACACTTTTAGTAGGAGAGTGGGCCACACATTT
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SEQ ID NO: 2600 ACTGGCTGGGATGGCTCTGATATAGCAGCCTGGTGTAGTTTCTGCATTTCCG
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TACT

SEQ ID NO: 2601 ACGCGGGAGATGAATGCCAGAGGACTTGGATCTGAGCTAAAGGACAGTATTC
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SEQ ID NO: 2602 ACTCTTGATAAAAGACCGTGAAACCAACAAATCAAGAGGATTGCTTTTGTG
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SEQ ID NO: 2603 GGTACAATAAAGGAATGGGGAAGGGGGAATGAAGAATAGAGAAAACTAT
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SEQ ID NO: 2604 GGTACGCGGGATGTTTTTCTGATTCCATCTGTGTCCTTCACTCTGACTC
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SEQ ID NO: 2605 ACTTTTTTTTTTTTTTTTTTGGAGGNATTGAAATACAACITTTATCTGAT
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SEQ ID NO: 2606 ACGCGGGGAGCGCGGAGCACCTGCGCCCGCGGCTGACACCTTCGCTCGCAGT
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SEQ ID NO: 2607 GGTACGCGGGCTACAACAGGCAGGCAGGGGAGCAAGATGGTGTGACAGA
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SEQ ID NO: 2608 GGTACAGTCTTTCATTAATAAGAATCTTACACATACATTTTCAGATATTTT
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SEQ ID NO: 2609 GGTACTTTTTTTTTTTTTTTTTTTCGCTAAATGCCCTGTTTATTCTGCAAAACA
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CGAAAGGGCGAAATTTCAACACACTGGGNGGGCCGTTACNTAANGGAATCCGAGCTTCGGGANC
CNAACNTTGGNGGAAANCAANGGGCAAGCTGGGTTNCCGGGGGGGAAATGGGTTTCCCTTC
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SEQ ID NO: 2610 TNTACCAATGGCAACCAAGTCTCTTTCTCGAAATATTCGTGTAATTTCT
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SEQ ID NO: 2611 ACCATGTCCACTGCATCGCGTCGCCATGATGGGCCATCGTCCAGTGTCTGTGC
TCAGCCAGAACACAAAGCGTGAATCCGGAAGAAAGTTCAATCTGGAACATCAATGCTGCCAAG
ACTATTGCAGATATCATCCGAACATGTTTGGGACCCAAGTCCATGATGAAGATGCTTTTGGACCCA
ATGGGAGGCATTGTGTGATGACCAATGATGGCAATGCCATTCTTCGAGAGATTCAAGTCCAGCATCC
AGCGGCCAAGTCCATGATCGAAATTAGCCGGAACCCAGGATGAAGAGGTTGGAGATGGGACCA
TCAGTAATTAATCTTGACGGGGAATGCTGTCTGTAGCTGAGCACTTCTTGAGCAGCAGATGCA
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SEQ ID NO: 2612 GGTACGCGGGCTCGTCTGACTTCTTTATTGGTGCCATCGCCATTGGAGACTT
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SEQ ID NO: 2613 GGTACTATACTGGCAATGTCTGGAGAAGATTTTGAATTTGTTCTCTGATAC
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SEQ ID NO: 2614 GGTACTTGGAAACAGTTACAGCCCTCACCAAGCTAGGTGGGGACATGAAAT
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CGGCCACCTTGGCAGATTACAGGANGTCTCATTNCCATCGGAGGNCAGGGAAGGCCCCCTGCT
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TC

SEQ ID NO: 2615 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAGGACCTTTCTATTTTTAA
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SEQ ID NO: 2616 ACTTCTTTTTTTTTTTTNTTTTTTGGAACTTTTATTNATATTTTGGNCTT
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SEQ ID NO: 2618 ACGCGGGGGCAGAAAGTCTCTCAGTCAGGACACAGCATGGACATGAGGGTC
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SEQ ID NO: 2619 ACTTCACCTTCCAGGAGGTGAAAAGGAATACAAATTCACAGCAGACTCCAG
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SEQ ID NO: 2620 GGNACTTTTTTTTTTTTTTTTTTTTTTTNGGGGCAAAGATTCATTATTIATT
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SEQ ID NO: 2621 ACAGGTTTTATGTGAACATACATTTTCATTTCTGGGATAAATGCTCAAAAG
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SEQ ID NO: 2622 ACTTTGCTACGGCAGCAACCTGCTGACAGAGAGGATCCACCTCCGAAACCC
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GGTTTCTGATTCTNTTGGCCATTATATCAGCAAGANATGCNCCAGTAAATGGCCCTTGGAAATTG
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SEQ ID NO: 2624 GGTACAGGAGATCTCATTTGGGACAACATAAGGATAAAATGCTGGTCATCGAA
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GTATGGAGGAGGGGTGCTGAGATATCCTGTGCCCTGGCAGTTAGCCAAGAGGGCGGATAAGTGCC
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SEQ ID NO: 2625 GGTACGGCTCTACTGCCACCTCTTCCAGCTCCACGGCCGGCGCAGCAGGGA
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SEQ ID NO: 2626 GGTACAAGCTTTGTCCAAAATGGCACAAGTGAACAAAATGAGTTCTGTGT
GATAAAGACAAAACCTCAACAGTGGCACCCACCATACACACCACTGTGCCATCTCCTACTACAAC
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SEQ ID NO: 2627 ACATGCTCATGGCAGCAACAACCCATTGACCACTTCTCAAAGTAGTTCAGTG
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SEQ ID NO: 2628 GGTACTTT
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SEQ ID NO: 2629 GGTACTTTTATATAAGTAATNCTGGATTGACATTCTCATTTAGAGAAACCT
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SEQ ID NO: 2630 ACGATCGAAGGGACTATGCTTCTATGAAATTTGTGTGAAGACAGTAAGGA
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SEQ ID NO: 2631 ACGCGGGGCTCTTTTCCGGCTGGAACCATGGAGGGTGTAAGAGAGAAGAAG
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SEQ ID NO: 2637 ACTTTTCTTTTCTTTTCTTTTCTAAATTATGATCAACTTTTATTGATTTACAT
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SEQ ID NO: 2638 GGTACAGAGGATCAGACCCCTATAACAAAAAGAGTTATGTTTGCCTTATGAAC
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SEQ ID NO: 2639 ACCATGAAATATCCAGAACATACCTATATGTAAAGTATTATTTTGAATCT
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SEQ ID NO: 2640 GGTACATGACCTAAATTTTACATCATAAGTAAAAACAGGCCCTATGGAGAGAGG
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SEQ ID NO: 2641 ACGCGGGAAGACAAAGACCCGCAAAAGATGTATGCCACCATCTATGAGCT
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SEQ ID NO: 2642 ACITTTTTTTTTTTTTTTTTTTTTTCCAAANATTTGTTTATTTTATTATGGC
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SEQ ID NO: 2643 GGTACAGTTGAGTCTGTGTGTTTCTTGAATGTTTGAGACAGCTTCACCTTG
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SEQ ID NO: 2644 ACATATTTTGGTTGAAGACACCAAGTGAAGTAAACAGCTGTGCATCCAATT
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SEQ ID NO: 2645 ACCTTGATACACATAATCAGCCTTTTCAAAAATGCCTGACAAGAATTAGTCTT
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SEQ ID NO: 2646 GGTACTGGAAGCATGCTCCAAAGACCTGTAGAAGCTTTGCTGAGTCGGCTCG
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SEQ ID NO: 2647 ACAGATATCTTCAAAGGAGGAAGAAGAAAGGGAAGCAGATGGTGGAGCTG
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SEQ ID NO: 2648 GGTACGCGGGGAGACGAAGACTGAGCGGTTGTGGCCGCTTGCCGACCTCCA
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SEQ ID NO: 2649 ACATGGTAGTAAACCTATTGATGGCAATTTTGCTGACTGTGGAAGTGACTCAT
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SEQ ID NO: 2650 GCGTGGNCGCGGCCCGANGTACAACATNTGTGCAATAAATTCAAAACTAT
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SEQ ID NO: 2651 ACAAGTATAGGCAGAGTATTTCTGTTTACATTTTTTTGTTTTGGGGAAA
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SEQ ID NO: 2652 CGAGGTACACACACATGGGGAACACACCACAGCTTAGATGTGACAAAGTTCC
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SEQ ID NO: 2653 ACTTTTTTTTTTTTTTTTTTTTTTTTGGCAGTTTCTAAGTCATTACTTTTTAT
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SEQ ID NO: 2654 ACAGATTGCTTCTCTTACAAAAAGAAAAAAATCCTGTGTATTAACAT
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SEQ ID NO: 2655 CGAGGTACAGTGTGATCCTGTTTAAAGTTACATAAATCAATCAGGGTAAAC
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SEQ ID NO: 2656 GGTACCAAAATTAACCTGGCAAACTTTCTATTGCTGTCCCATGTGCATCTTA
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AGGTGGGAGGCTCTGCTTCTGCTGCCGCTCTGCAGCCTGGACCTGTGGACCTGGTTGTAAAGAG
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SEQ ID NO: 2657 GGCCTTGATGCGGTACTATGCCAAACACTTATAACTGTATAAAAAATCCACA
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SEQ ID NO: 2658 ACAGCTTTTAGCAAAACTGCTTTCCAGAAAAGCAAAATAAAAATAATGCAAT
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SEQ ID NO: 2659 ACTTCTCTGGCCAAAGGCTGTTCCACATTCATCATTTAAAAAGGCTTCTCT
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SEQ ID NO: 2660 CGAGGTACAGGCTCCTTTTGAATAAACTGGTTATGACTTGATCCAAGTGTT
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SEQ ID NO: 2661 ACGCGGGGATGCGCAGACACCTCAGGCGACTGGCGGGTTCGCGGCTTCAAG
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SEQ ID NO: 2662 ACTTTTTTTTTTTTTTTTTTTTTTGGAAAAATATACCTTTATTGAGTCAOC
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SEQ ID NO: 2663 GGTACGAGTCAAGCACAACCTGCTGCGCAGGAAAAGACAAGGCTAATTGG
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SEQ ID NO: 2664 ACAGTTGGAGTCTGTGTGTTTTCTTGAATGTTTGAACAGCTTCTTGAACCTT
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SEQ ID NO: 2665 ACTCCTCCAGTTCTACTCAACAAAAATCATGATAATTGTGATAAAATAAGA
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SEQ ID NO: 2666 ACAACATCTACCCCGGACACGGGAGGCGCTACGCCAGGACCGACGGGAAG
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SEQ ID NO: 2667 ACATGGCAATTAGAAGTTGTCATGGCAAAAGAAAAACACAGCTGGCCTGCCA
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SEQ ID NO: 2668 CGAGGTACACAGTTTCTGTGAAATATGATGCTGTATGTGGTGTGATTTTT
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SEQ ID NO: 2669 ACATTTTTTAAAGCCCGTAGCAAGCAAAATGTGACGGCATCCAAAATGTTT
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SEQ ID NO: 2670 ACTCTGGTGAATCACCCTTCAGGGCTTTACTCGTAACAGATTTTGTGGCA
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SEQ ID NO: 2671 ACTGTTTAAAGCCCAAGTAATAGTTTTACAGATCTTTAGTTTCAACTAAG
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SEQ ID NO: 2672 TCTCCATTTAGTTTGTGGTANCAAGCAGCANNGGNGNAATTGAATGANAA
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SEQ ID NO: 2673 ACCANGTTTTGGTGTCAACTAGAAAGAGGTTCTATTGAAGTTAAACAGATGA
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SEQ ID NO: 2674 CGAGGTACGCGGGGTTCTCTTCTGGTCAAAATGGCTGGTAAGCAGGCGGTTT
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SEQ ID NO: 2675 TCGAGCCGGCCCCCGGCCAGGTCCTTCTTGATGGGCCATATGCTTTATCTT
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SEQ ID NO: 2676 ACGCGGGGGGAATCATGGCTGCTCGCAGAGCTCTGCACTTCGTATTCAAAAG
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SEQ ID NO: 2678 ACAGAAAAGAAAATCCCGTTGTTTTTCGATTGCAAGAGGGTTATGATCATA
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SEQ ID NO: 2679 ACTTTTTTTTTTTTTTTTTTTTACAGTTTTTACATTTATTAAACAGAAA
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SEQ ID NO: 2680 ACITTTTTTTTTTTTTTTTTTGGATCTTGTCATTCTTGGCACTGTTTCTAAA
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SEQ ID NO: 2681 GGTACCTAGAAGAGAGGCGGGTCAAAGAAGTAGTGAAGAAGCATTCTCAGT
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SEQ ID NO: 2682 ACAGTATTGGAATGGATCTGTCTTTGGTAAAGATCAGCCTATAATTCTTGTG
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SEQ ID NO: 2683 ACTCACATTCATTGTGCATATTTTCAGGCCCTCATACCCCTTTTAAATGTG
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SEQ ID NO: 2684 GGTACTGGAGATGATTTGATAACCAAGGTTTATAGGTAATTTTACCAGTAT
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SEQ ID NO: 2685 ACAAATAAAATCAAAAAGAGCAGTGTCTGTGTATTCTTTGCGATGTATA
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SEQ ID NO: 2686 GGTACGCGGGGGCGTGCTGTGGGAGTTGCTTGGAGTTGGCGGCGCGGGGC
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SEQ ID NO: 2688 GGTACTTTTGGGATAACTTTGGTTACAGTTCTCTCAAAATGTTCAATGCTGAT
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SEQ ID NO: 2689 ACTATGCCAAACACTTATAACTTGTATAAAAAATCCACATCCCATATTTGGCC
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SEQ ID NO: 2690 GGTACGCTGCTGATCGATTATCTTACGTGGGGCAATGATTTCATGTGTGATGA
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SEQ ID NO: 2691 CGAGGTACAGCATCGTAGGGTCCCTAACTTGCCTGTTTTGTTTTTTA
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SEQ ID NO: 2695 GGNACTTTTTTTTTTTTTTTTTTTTTCGAANCCAACTGTATCCAGCTTT
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SEQ ID NO: 2696 ACGGATACCGAAAGGCTGGATACCTGGTTATTAGAGGATTTGGAGATGG
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ACTGGNCNGTCCCGNGCTCCCAAAAGTTTGAACCNACNGCCTAATGGTGAAAAAGAACTGGC
CTGAAANGTAAANGAAGAAATNGGATTAANTGGCTTNTTGTGAAAATGNTCTATTTTCTAACA
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SEQ ID NO: 2698 GGTACAAAGCTTTGCAAGGGTGTGTTTGGAAATGACGCTAAACTGAAGGTG
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SEQ ID NO: 2699 GGTACAGCCGTTGTCAATGGAGAGTTCAAGACCTAAGCCTTGATGACTTTA
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SEQ ID NO: 2700 ACATGGGAAATGTAAACAAATGTGAAGGAGGACCAGAAAAATAGTTAATA
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ATCCCATATAATCTAGAACTAAATATGGTGTGGCCATTTTAAACACCTGAGAGTCAAGCAGTT
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CTTGNATAATCATNGTCAATACTGGTCCCTGTGTGAANTGTTATCCNTNACNATTTCCCANCAT
CCGANCCGNGAGCATAANANGAAANCTGGGGCTTAANGANGNNTAAC

SEQ ID NO: 2701 ACTTTTTTTTTTTTTTTTTTNTTGGGNCCTCAAAAATCAGTAAACCTTATT
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AGTGAAAAAACCAGGGTCTAANAGCTNNNGGNNCTAGCCGCCCTNNGTTGGCNATCAAT
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SEQ ID NO: 2702 ACTTTTTTTTTTTTTTTTTTTTTTGGCTTNGAAATTTANAACAATTTTTATT
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ATTGCTNTATCATGTTAGAACGTCATNGACTCAAATACAAAAACCATGAAACAAATNACCAT
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CATTAAGNTGAACCTTTNGCCCTAGGAATCAGGGCGTTTTNTCCATNGCTTTNACANTTTTACAA
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SEQ ID NO: 2703 GGTACATTGTGTTTAAAGAGAAAAATGAAACCCACATGCCGCCATTTTCCTGA
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ATGGTCTTGGAACAATTATAGAAACAATGACTTTTGGGAATAGCCCTGTCTTAGGGCAAACTGT
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SEQ ID NO: 2704 ACATAGTGGTGGCCCTGTATAGGACATTGTTAGCATAGAGGCTCTTCTGTATG
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AAGGATGGCTGGAAACAGGGTCTCTGGGCAGCGGAAACGTTTCATTTCCGATGGTGATCACTTGGCC
ATCAGGCAACTCGTAACCTTCTCAAGGGAGGATGAGGATGGCGCAGTGGCCATCTCATTTCAA
AGTCCAGAGCTACATAACACAGTTTCTCCTTGATGTCCCGGACAACTCAACGCTCAGCAGTGTAA
CGAAGGAATAGCCACGCTCAGTCAGGATCTTCAAGAGTAGTCAAGTGAGATCTCNGCCAGCCAN
ATCCATACGCATGATGGCATGGGGCAAGGCATAGCCCTCATAGATGGGGGACATTGTGGGTGACA
CCATCTTCAGAGTCCAGCACNGATGCCNAGTTGTGCGTCCAAGAGCCATANAANAACAACACCCG
CTGGATAGCCACATCATTTGNTGGGACATTGAAAGTCTNAAACATTAATTGAGTCATTTCTCCCGG
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SEQ ID NO: 2705 GGTACTGTATTTCCGCAAAAAGAAATTAACATTTAGTAACACACTAATGAA
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CAGATACCGAAAAACCCCCAGCCTGGCATATCCCAAGTAACGATGGCCTTNACTGACCACTCCC
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AANTACANTAGAAAATTNCCGGGGGATANCCTGNAAAAAATAGANAAAAATGCTCNATGGANNACC
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CTTGGCTTTTAACTNNGATGGNANTGGGTNAATGACACNAAAACTTTTGCAGGGGGCCCTTTAAN
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SEQ ID NO: 2706 ACCTAGAAGAGAGGGGGTCAAGAAGTAGTGAAGAAGCATTCTCAGTTTCAT
AGGCTATCCCATCACCTTTATTTGGAGAAAGAAACGAGAGAAAGGAAATTAAGTGATGATGAGGCA
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CTTGAGGATTGGCCCTGGACATTCTCCNNGAAATGCTTCACCAGAGCAAAATTTTGAA

SEQ ID NO: 2707 GGCNCGGCGGANGTACTCTATGCATTCTATCTATACAGAAACACCTATTTATT
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CATCAACTCTCCATAATGAATCTGAACCTCACAATGATTACCAAAACACTTACTTAAATTAATA
TTAAATAAATGAAAAATGCACCGAGCCAAACAAACTTAACTGGGCTATAAGAAAAAACCCTT
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AGCCTGAAAAAACAGTAAATCTACACAAAATTTTATTGCAATCATACAAAGGGTTACATTAGGT
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CGATTTAATGGGGAACCAATTAATGGGCTTCCATCTCCCTAAGTCATCCATTTTGGTGCATATTTA
TTTTAACGCTTAANGGTAG

SEQ ID NO: 2708 ACOCGGGGGATTTCAAAATCAACACCGATGAGATTATGACTTCACTCAAGTC
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TGGGGTCAAATGAAAGGTGAATTCAGGCTGAAGGAAATAGCAAAATTCACCTACACAGTTCTTGGA
GGATGGTTGCACGAAACACACTGGGGAATGGAGCAAAACAGTCTTTGAATATCGAAACCCCCAAG
GCTGGGAGACTAC

SEQ ID NO: 2709 ACAATGTTGAACAAAAGACCACAGGGGGACCTTTTGTTCAGGTAGCACCAA
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GCATCTGATGCATCTAAGGTTTCTCTCTTGGCATGAGGCCACTTCTCTCTAAGTCATCAATGCT
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SEQ ID NO: 2710 ACACCTTACTGGGCTGGCCTTTTAAATTTTACTCTTTTGCCTTCCCTTCCACC
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ACA

SEQ ID NO: 2711 ACATCAAAGATTACATGAATCAATCAAAGGAAACTTGAAGAACAGAGAC
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SEQ ID NO: 2712 GNACAGNGGAAACAATCCAAAGTTTAAATCAAAAGAGNGGTGNTCANTTG
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SEQ ID NO: 2713 ACTGTACATTCTCTTTTCANATTCCTTTTITTTGGGATAATTTCTCTTCTCTA
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SEQ ID NO: 2714 ACGCCGGAGCTCTTTCCTTTCCGCTGCTCGGCCGAGCCATGAGTATGCTCAG
GCTTCAAAANAGGCTCGCTCTAGTGTCTCCGCTGTGGCAAGAAAAAGGTCTGTTANACCCCA
ATGAAACCAATGAAATCGCCAAATGCCAACTCCCGTCAGCAGATCCGGGAAGCTCATCAAAGATGGG
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SEQ ID NO: 2715 ACGCGGGGGCAGTCCGCTGGTCCGAGCAGAGCTGTGAGGGGATTCACTTG
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SEQ ID NO: 2716 ACTCAAGTCACTTAATGAGGAAGCTGTGAAGAAAGACAATCTGTCCATTGG
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CCTCCACCCAGGACACAGTGGTGGCTCTCCATGCTCTGTCCAAATATGGAGCAGCCACATTTACCA
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SEQ ID NO: 2717 ACAAGTATTACGTAAATATGTAAAGATTCTTCAAGGTAACAAGGTTTGGG
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CTGGCTTTT

SEQ ID NO: 2718 ACCAAACGGGCAAGGACATCTCTACAAATTACTATGGAGTCAGAGAAAAAC
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SEQ ID NO: 2719 ACTGCAGTAATAGGAATCTCTCCACAGAGGCAGCAGAGAAAGTGGTTAGTG
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AGTACCATTTGGTGGCCAAATTGATTGTGTAAGGGAGGGATCGTTGCCCTGTCTTATGTAAAG
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SEQ ID NO: 2720 ACOCAGTAAAAACCAGAATGAOCCATTGCCAGGACGCATCAAAGTTGACTTT
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SEQ ID NO: 2721 ACACCTCTATAAATAAACACATCAATTTTGCTCTATTACTACTCTTCCAAAAAC
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SEQ ID NO: 2722 ACTACTTGGTTCCCGATATGGATGATGAAGAAGGAGAAGGAGAAGAGATG
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AATAGAACTGATGGATTCCAACCTTCTTTTTTTAAATTTCTCCAGTCCCTGGGAGCAAGTTGC
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ACCACCGAGCTCTGTGGGAAAAAGAAAACTGCTCCTTCTGCTCTGCTGGAAGTGGAGGGTGC
TAGGCCCTGTGTAGTAGTGCATANAATCTAGCTTTTTTCTCCTCTTCTGATATTTGGGCTCAN
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SEQ ID NO: 2723 ACCAAGAAATGTGCTGTGACAGGACTTGNCTCTGTGCTGTGGTAGCAAAATGCC
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TAAAAAAGGTTNGAAGAGCATTGTCTGCCATACGTTGCTTCTTGCATAGAGTCTGCCATGA

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SEQ ID NO: 2724 ACAGACAAAACCTACAGACTTAGTCTGGTGGACTGGACTAATTACTTGAAGGA
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CTTCAAACCTGCAATTTGAACCGACCAACATTAAGTCCAGAGAGTAACTTGAATGGAAATAACGA
CATTCCAGAAAGTTAATCATTGAAATCTGAACA CTGGAGAAAAACCGAAAAATGGACGGGGCATG
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AGCCCCAGGCTGCAGCCATTTCGAGGCCACCCGAAAGAACTTCCCAAGTATGGTGGTCTGGAAA
GGACATTTTGAAGTCAACTATATCTTCTGTGCAATTCGATGGAATTCANTTCATCAGATGTTT
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SEQ ID NO: 2725 ACAGACAAAACCTACAGACTTAGTCTGGTGGACTGGACTAATTACTTGAAGGA
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ACATTCAGAAAGGTTANTCATTTGAAATTCGAACACTGGAGAAAAACCGTAAANTGGACGGGNCA
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SEQ ID NO: 2726 ACTGTACAGAACTTTTACATACATTCTCAGTCTAGTTGTGAAAGGCTAAA
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SEQ ID NO: 2727 ACTGTGATTGAACATCCTGAATACGGAGAGGTTATTCAGCTTCAAGGTGACC
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CATGGATTCTAAAAATGAACCTAAATACGTGGAGAATTTCTTGAATAGTTTGTCTCTAAACCCGG
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CAGTAAGATGGTAACAAAACTCATATGTCTTACATGTTTCCAATGGAAAAATGTTTGTAGTGTTT
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SEQ ID NO: 2728 ACAAATACGCAAAATTTTCATAGTGCCTAGAAATAGCACAGATCTATTCTACTC
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TCGCGATCTT

SEQ ID NO: 2729 CAGCTGATGGGAACGGGCTCCAATGGACTGGATTGCATTCAAAATATTATTTT
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GGTCCCGGCTATCTGTGGTATCTGGGCTTGTCTTCAATAGAAATACACAGACACAGCAGCG
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CCCGCT

SEQ ID NO: 2730 GTACCNNGACAGTGCATGTCACATATGATTTCAAAAAAGTTTCATTGTC
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SEQ ID NO: 2731 ACACAAC TGCAACTCTACATAAATGCCACAGATGCAGAATACTGTTTCTTGC
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GAAAGGAAGANA

SEQ ID NO: 2732 ACCTGGGTGTTCCCACTTGGGCATCATGCACCACAACAAACAGGCCACTG
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CTCACCTGCCAAGAGT

SEQ ID NO: 2733 ACTTATTTCAACAATTCTTAGAGATGCTAGCTAGTGTGAAGCTAAAAATAGC
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GTAATATTTTATAATCTGTAATATACCTGCACACAAATGCTTTTCTAATGTTTTAACCTTGAGTA
TTGCAAGTTGCTGCTTGT

SEQ ID NO: 2734 ACTGGTCCAGGAGTTATCCAGGATAGATTTTCAOCCACCATGGGGCGTCATC
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ACTCTTATCCAGCTGCAAGGACAGTCGAAGGATAGCCACCTCGGTTTTCTAAGAAAGGACAGC
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SEQ ID NO: 2735 ACAAATCCCTTTGTTGAAAAATAAGGGGCTTTCTAACTAATAAAAAAGG
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SEQ ID NO: 2736 ACANCCACNNCTCTGGGAGGACNTTATCCNACTGAANCCCGACGNGGACAT
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TGT

SEQ ID NO: 2737 ACATCCAGCAGCTCTGTGAGGACATTATCCAAGTGAAGCCGATGTGGTCAT
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SEQ ID NO: 2738 ACCATGAGAAATGTGGTTTCTGATATTGCTGTGCTAAGGAGACAGCAACGTA
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SEQ ID NO: 2739 ACAGGATGAATTTAAATGTGTTTTCTCTGAGAGACAAGGAAGACTTGGGTAT
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SEQ ID NO: 2740 ACGGTAACTGACTCCAGGGTCACTCATACTGTGTCGGTGGTAACGGTAAAGTCT
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SEQ ID NO: 2741 ACCAGAGTCAAGGTGCCAGGGTCTGGGAGCAACAAATGCATTCCCATGAT
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GAGCATCTTG

SEQ ID NO: 2742 ACTGGGAGATACAGCCATCCACCTTCAGATGTGTCTACGTGGCTCTGCCATT
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AATTTAAAAATACATTA

SEQ ID NO: 2743 ACAGCTTAAACCACAATGGTATAAATCTTCAATTTGTAAATTAATAATTTCTG
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SEQ ID NO: 2744 ACCAGCGATTCTGCGGCAACACGTGCACCTCGAGGAGACAGGTGGCAGTGA
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SEQ ID NO: 2745 ACACTTATAGAAAAGGTAAAGGAAACCCCAACATGCATGCATGCTGCTGGT
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SEQ ID NO: 2746 ACTGGGAGATACAGCCATCCACCTTCAGATGTGTCTACGTGGCTCTGCCATT
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SEQ ID NO: 2747 ACCACTCCAGTTGTCTTCACAAATTAATGCTACAGAAACCTAAATGTTCTAC
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SEQ ID NO: 2748 ACAGGATGAATTTAAATGTGTTTTCTGAGAGACAAGGAAGACTTGGGTAT
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SEQ ID NO: 2749 ACAGCTTAAACCACAAATGGTATAAATCTTCATTTGTAATTATAATTTCTTG
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SEQ ID NO: 2750 ACCAGCGATTCTGCGGCAACAGTGCACCCCTGAGGAGACAGGTGGCACTGA
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CGGCAAGATGAAGTCCATGAGGGGTGATGGAAGGTGCAGAGTTGCANGGGACACAGGGAAAGTC
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SEQ ID NO: 2751 ACACTTATAGAAAAAGGTAAAGGAAACCCCAACATGCATGCACTGCCTTGGT
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G A T G T
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SEQ ID NO: 2780 ACTGCAAGTCAAGGGGACTCTTTCAGGCGTGTCTTTAGAAGGGAGCTGTTT
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GCCGTATACATTTTCTTCTTTGAGAATTACAAAAAATATTCTACACTGACAGGATTTACTAGT
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SEQ ID NO: 2781 AATAAAGAACCTCTATCAGTGAGACTTCTCATTTTATAGCAAAATACATTTTG
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SEQ ID NO: 2782 ACACAGGTATTTTCAAAGGAAACAAGTCATCTTAAAGTAATATTTTCTATAT
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SEQ ID NO: 2783 ACTATAGGAATACATTAAGTAATCAATGGAATATACCTTGCTAATATTATA
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SEQ ID NO: 2784 ACTAAATAAGACCATGGATGTTAGTAACTCTCTGCTGAAAAAGTGGAAAT
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TACCCCTCATGGACGTCTAATCTTCCACACACATCCCTTTTTTGGGAATAAAATTTGAAAAATGG
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SEQ ID NO: 2785 ACCAATATTCACAAGCAAACTATCACTAGTATCCCATTAATTTAAATTCGCC
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SEQ ID NO: 2786 ACGCGGTAAAAACAGGGAAGAACATCATCTGGGTCTTTGCGCAGTAGCAGC
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SEQ ID NO: 2787 ACAGCCAAOOGTTTCCTTGGGGGCTTGAATAACACCCAGGTGGTCTTA
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SEQ ID NO: 2791 ACAAATGAACACAGTTTATATTCTAATTTCTACTGCAGCTCAITTTAATTTTA
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SEQ ID NO: 2792 ACAGATCCACTTAGTCATTTTCTCCTTTTTTAAAGAACATTTTCATCTGATT
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SEQ ID NO: 2793 ACCAGGTCCCTTACCATCTGGGAGAAGGATGGAGGACAGAGGAAAGG
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SEQ ID NO: 2794 ACACTGAAACATAAATCCGCAAGTACCCACACATACAACCCCGCAGGAA
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SEQ ID NO: 2795 ACTTTTTTTTTTTTTTTTTTACATGANAACCAAGGACTTTTTACTTAN
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SEQ ID NO: 2796 ACAAGGGCATATTTAACGATTCTCAGTTACACTTAAAGAGGATGGTGTG
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SEQ ID NO: 2797 ACTGCCACCAGATTTTTTATTACATCATTTGAAAAATTAGCAGTATGCTTAATG
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SEQ ID NO: 2798 ACAGTTGCCTGAAGTTACTATAAATGAAGAACTGCTTTAGCAGAAAGTTAAT
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SEQ ID NO: 2799 ACAAGCTTTTGTCCAAATGGCACAGTGAGCACAAATGAGTTCTGTGTGAT
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SEQ ID NO: 2800 ACGCGGGGAGGCATTGAGGCAGCCAGCGCAGGGGCTTCTGCTGAGGGGCA
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SEQ ID NO: 2801 ACCATGACCTACATAAGGCTGGATGGCACCTCAGGCTGAGGGCCCAATGT
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SEQ ID NO: 2802 ACGCATACTAGCAAGGTAATGGTGATCTAGCAACAAATTTGGTTCTGCA
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SEQ ID NO: 2806 ACTGTTATTAAGCATATTTGATTATAGAGCTATTCAGATATTTAAATATA
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SEQ ID NO: 2807 ACATTTACAAAGATGGGTTCAAATAGTGCTCTAAGAGTTTGTTCAGTGGCTC
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SEQ ID NO: 2808 ACCATCGCACACACTGTTGACGTCAATTGGAAGAAGGAAGACGACTTTGTCT
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SEQ ID NO: 2809 ACCTAGAAGAGAGGGCGGTCAAAGAAAGTGTGAAGAAGCACTTCAOTTCAT
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SEQ ID NO: 2810 ACAACAATTATGACATTTGATTAGGCTGGACTCTAACTTGCTTGGATGAGATT
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SEQ ID NO: 2811 ACCCCAATCTGAAGTCAGTAAATGAATACTACAAGCCTGTTATGGCAA
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SEQ ID NO: 2812 ACNNINTATNTANCAGATNTNAAGAGTCCATTTTAAAAAGTGAGCAAT
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SEQ ID NO: 2814 ACGCGGAGTTTATATGAACATCTACAATCTGTGTTTACACATCTGTT
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AA

SEQ ID NO: 2815 ACAAAATCCAGTGTGCAGACCACANCTCAAAACAAAAAGATCTATTTCTA
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SEQ ID NO: 2817 ACATGAATTAGAAGCGTGCATCTAGGATTATGGCCAACTGTTTAAAAATG
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SEQ ID NO: 2818 ACATGAATTTAGAAATAAAATGTCGAGGATTCTGAAATCTGATACCTTA
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SEQ ID NO: 2819 ACCTCTTGAACGCAATTGATTCTCAAAATCGAGAGATCATGAAACACCTGAA
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SEQ ID NO: 2820 ACACATGTCATAGTGACCACAGCTTGTGGCTCCTTGAGGGAGGAGATTANC
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SEQ ID NO: 2821 ACTCTTGCTTATATCATCACAGAGCTGGATGAGAGAGAGCGAGAAGAGTTCT
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SEQ ID NO: 2822 ACATGATACAGATTGGTTTTCAGTTTAAATGAAGTGAATAGAAATGTCTA
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SEQ ID NO: 2823 ACAGTCCCTCAACTGGACTAAAATCATGAAGACCAATGTTGATGACCCGTAG
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SEQ ID NO: 2824 ACGGGGTCTCTTTCGGCGGTGCTCGCAAGCGAGGCGCATGTCTTATCCC
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SEQ ID NO: 2825 ACATCTTGCCTAGATGTCGATGACTGCAAGTAATAATACAGTTTATAATGAA
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SEQ ID NO: 2826 ACTGGAGGGAGAGGCGGGCTCTCAGGAAGCAGCAGGACGTGCCAGGTGG
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SEQ ID NO: 2827 ACAAACCAAAATGTTTGTACTATAAATCTTGCATCACAATTAATAATCCAAAC
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[illegible]

SEQ ID NO: 2840 ACGATOGAAGGGACTATGTCTTCATTGAATTTGTGTTGAAGCAGTAAGGA
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SEQ ID NO: 2842 ACTACACGCGCTGGGCAACGACTTCCACACGAAACAAAGCGCTGTGCGAGGA
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SEQ ID NO: 2843 ACTGTCGGTTTCAGAAATGCCTTGCACTGGGGATGTCTCAATGCCATCAGG
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SEQ ID NO: 2844 ACTAACTGATGGGCGGGAGGGGGCATTCACAGTTGCTGGGCGAGCAGTG
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SEQ ID NO: 2845 ACGTATAGTTAAGTGATGAAGAAAGGTTATTTGGTTTGTGTCGTCACTTATA
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SEQ ID NO: 2846 ACGGGTAGTGGGCGACATGTTAGCATTTGAGCATATGGACAACTCCACCTTG
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SEQ ID NO: 2847 ACCTAGAAAGAGAGGCGGGTCAAAGAAAGTGAAGAAGCAATTCAGTTTCAT
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SEQ ID NO: 2849 AATAAAGAACCTCTATCAGTGAGACTTCTCATTTTATAGCAAAATACATTTTG
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SEQ ID NO: 2850 ACTACTGCTGTTTCTGAAGACGCGAGGGCAAGTGCAGCCAGCGTTCTTTT
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SEQ ID NO: 2851 ACTTTTCTTTTCTTTTCTTTTCTTTTNGGANANACAAGGCTNACTATGTTG
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SEQ ID NO: 2852 ACCTGTGACCAAGTGTGTTGGCAGGATGAGATGATCGACGTATCATGGGGTG
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SEQ ID NO: 2853 AATAAAGAACCTCTATCAGTGAGACTTCTCATTTTATAGCAAAATACATTTTG
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SEQ ID NO: 2854 AC GCGGGGAGTCACTCCAGTCAGGACACAGCATGGACATGAGGGTCCCCG
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SEQ ID NO: 2855 ACACGTGTGGTGTATATGGGGATGGGGTCTCGGTAAATTTGTGTTATTTTA
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SEQ ID NO: 2857 ACATTTAAATTTTGGTGGTGTGTTGTTTAAAAAGAAACAGCTTCCTTACG
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SEQ ID NO: 2858 AC GCGGGGAGCGGAAGTAGGAGCTCTCAGAGGCTAAGAAAGTGGAGACCGG
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SEQ ID NO: 2859 ACCAAGGGATGGAAGAAATAATAGCTCAGGTAGCACTTTATCTCAGGC
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SEQ ID NO: 2866 ACAGCAATGAAACACCAAAGGGAGCTTTCTCCAAATTGTGTATAAGCTTG
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SEQ ID NO: 2867 ACATGGCAATTAGAAGTTGTCATGGTAAAAAGAAACCAAGCTGGCCTGCCA
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SEQ ID NO: 2868 ACITTTTTTTTTTTTTTTTTTTTATATCACAAATCGTTTATTATGTGAAT
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SEQ ID NO: 2869 ACAAGGTOTTTTCCAGCTGCTCAGCAAAATGGAAGAGATGTTCACTT
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SEQ ID NO: 2870 CGCGGCGANGTACGCATTNCAATTTTCAGTGCTNNTACAAGGAAAAAGGTG
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GGAAG

SEQ ID NO: 2871 ACGCGGGAGTCGCGCGCTGCAGAGGGAGGGGCACTGGTCTCGAOGTG
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SEQ ID NO: 2872 ACNCGGGGCTCATGAACTCGCCTGCAGCTCTGGGTTTTTGTGGCTTCCTT
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SEQ ID NO: 2873 ACTTGTGTGCTTAAATACTTTATGCTCTGAACCTTCATAGAACTCCTTATG
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SEQ ID NO: 2874 ACAGTTCACTCTGCAAAAAATACCTCTCTCAGCAATTCACATTCCTTCAGCA
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SEQ ID NO: 2875 ACATCAGTGAATTTTAAATGCTAAAAATTTATGATAAAAGAACTAGTAAATC
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SEQ ID NO: 2876 ACCAGAAGTATAAGTTTATGGAACCTCAACCTTGCTCAAAAGAAAGAGGGCT
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SEQ ID NO: 2877 ACTTTTTTTTTTTTTTTTTTGTCTGCGAATCCTAGGACGTTTATTAAT
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SEQ ID NO: 2878 ACGCGGGGACTCAGGGAAGCCGAGGGGACGCGCGGAGGAAAGATGGAAAG
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SEQ ID NO: 2879 ACGCGGGGATCAAGCCTCAAGTCCCTTCATATTACCCCTCTCCTTTTAAAAAT
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SEQ ID NO: 2880 ACAAAAATCCCTTTTGTGAAAAATAAGGGGCTTTCTAAACTAATAAAAAAGG
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SEQ ID NO: 2881 ACTTTTTTTTTTTTTTTTTTTTTTTTACAGCAAGATAAAATGAATCAATTTT
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SEQ ID NO: 2882 ACGCGGATCCACAGCAAAAACAAAATAAGCTTTTATTTTATTAATAATTTGG
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SEQ ID NO: 2883 ACTTTTTTTTTTTTTTTTTTTTTTNGGNAATTTGAATGTATTTTAAATTTAT
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SEQ ID NO: 2884 ACATGAATTAGAAGCGTGCATCTAGGATTATGGCCAAACTGTTTTAAAAATG
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SEQ ID NO: 2885 ACTGATGCCATGGATGTATTGATGGGAAGGGTTATCCAGTCAAACTGGAA
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SEQ ID NO: 2889 ACTACATATTTACGACTAAGGGGGTTGCTTCACTTATATCTATATAAAAA
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SEQ ID NO: 2892 ACTGGAGATGTTTGTATAACCAAGTTTTAGGTAAATTTTCAACGATTTAG
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SEQ ID NO: 2921 GGTACGCGGGGGCTGACTCTCTTTTCGGACTCAGCCCGCTGCACCCAGGTG
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SEQ ID NO: 2922 ACTTTTTTTTTTTTTTTTTTTTTTCTGATGCTTTTCATTATCACAGA
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SEQ ID NO: 2923 GGTACATAGTGTGCGAACTCAAATGGCATTTAGATAGATCCAGTGATTTA
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CATGGAGAAATAGGGGCTGATTTTAAACTGTGTAGATATTAACCAAGCCCGCCTGTATAAA
ATCAAGGAAATCCAAACAGCGATTACACCGATTAAACACCCCTTATATATTTTACAAAAATAC
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SEQ ID NO: 2924 CGAGGTACTTTTTTTTTTTTTTTTTTTCGGANGGTAAAGGAATTTCTT
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SEQ ID NO: 2925 GCGTGGTTCGCGGCGAGGTACGCGGGGACAGCCAGAGCCTAAAGGCTA
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SEQ ID NO: 2926 ACACAATGAATGCTTTTATTTCGGTATGCATCCACATTCAGCATTTAGTGG
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SEQ ID NO: 2927 CGAGGTACANTGTGATGCTCGAGCAATGGCTCTGCTTNAGAGGGTGGCCAG
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SEQ ID NO: 2928 CGAGGTACTTNTTTTTTITTTTTTTTTTTTTTTTGTAAAGAAATGCTTTAATAAT
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SEQ ID NO: 2929 ACTTTTTTTTTTTTTTTTTTCTGTTGCCAGATTTATGAAAAATATACAGC
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SEQ ID NO: 2930 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGGCGGTTCCACACCTGCGCT
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SEQ ID NO: 2931 GGTACCTGCAGGCTCCTACACCTACCTCTCTCTGGGCTCTATTGACCGC
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SEQ ID NO: 2932 ACGGGGGTGTGCCCTGGCGCTACCGGACATCTCTCAGGGTGGCGGCAAC
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ACCCG

SEQ ID NO: 2933 ACTTTTTTTTTTTTTTTTTTTTTTGGCTTTTATTTGGCCAAATCCATAGCG
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SEQ ID NO: 2934 TCNAGCGGCCGCCNCGGNGNACGGGGGCCAGNNANAANCCAGCNGGGC
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SEQ ID NO: 2935 GGTACCCCTTAACCCCTTCTCTTCAACCTTAGCAGCAAGTCCCACTTTCTA
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SEQ ID NO: 2936 GGTACTTTTTTTTTTTATTTTATTACGAAAGTTTCATTCTTTTGAGCAAAAAA
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SEQ ID NO: 2937 GGTACTTCTAGCAAGTGCAACCAAGAAAAACAACGCTGGAATGGGTGGC
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SEQ ID NO: 2943
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SEQ ID NO: 2944 NOGCNGNGACGCAAAACAAATTGCAATATAATGTGATAAGTTCTTTAAAAGA
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SEQ ID NO: 2945 ACGCGGGGCTTGTCCAGTGAAACACCCCTGGCTGGGAAGTCAGTTCGTCTCT
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SEQ ID NO: 2946 GGTACCTACATCAGATCTAACCTTGATCCAGCAATGTGGATTCCCTCTCTA
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SEQ ID NO: 2947 ACCTGCATCAGATTAGTAATCAACCTGTTAATCCAAAGGTCTTTAGAAAAACT
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SEQ ID NO: 2948 NGTACGAAGTTCTCAGTTTCACTTTAGTAGAAAGAGCTCTAGAAATGAGGCT
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SEQ ID NO: 2949 GGTACCCCTGGCCAGCAGACATGTGTCTACAGGCTGAGGCCAGAACAAACA
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SEQ ID NO: 2950 GGTACATCGTGCATGGCGTCCAGGAAGACCTCCGTGTGGATGGCCGTGGCTG
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SEQ ID NO: 2951 GGGTGGGTGCGCGCGAGGTACCTTAAAGTGTCTCACCTAGAAGGCCTCTA
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SEQ ID NO: 2953 GGTACCCAGTAAAAACCAGATGACCCATTGCCAGGACGATCAAAAGTTGAC
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NCANTAA

SEQ ID NO: 2955 ACGCGGGGACCCGACCTTTTTCAGTCTCAGGACGGCGCTTTGGAGGC
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CNANAGCTATTTCCGCAACCAATGAGAAATGACCGGCAAGCATGGGNGATCAGCAGGNAAGGT
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SEQ ID NO: 2956 ACCACCGCAAAGCCCTGTGAGCGTCTACAGACAGCTCACCATTTTGTCTGT
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ACAGCCCATCCTCTGCAAAATCCATCTATGTTGCTTANGCAATCTATCTTGTGCTCAAAATGGTTG
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SEQ ID NO: 2957 GGTOGGCCGAGTACTTTTCTTTTCTTTTCTTTTCTTTGAAAGTAAATGTTATT
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SEQ ID NO: 2958 ACTTTCATNTATTGACACTGAGAGAGGGGCGAGTACCAGGCAGCCTGGAGAT
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CACGGTGANAGGNCCTTATNTTNTGGTAGANCAATTAATNTTACTTTCATNATNATGGGGTGG
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SEQ ID NO: 2959 ACCAAAGGATAGCTGTTCTGTTTAAAGTGGGACCTCATGCGCTACAGGCTT
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SEQ ID NO: 2960 GGTACTTTTCTTTTCTTTTCTTTTGGAGTTTCTAAGTCATTACTTTTATTTT
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SEQ ID NO: 2961 ACACQAAACATGATCAAGGTTGTTACACTGGGCTTCTGTTACAAGATGAGGTC
TGTGTATGCTCACTTCCCATCAACGTTGTTATCCAGGAGAAATGGGTCCTCTTGTGAAATCCGAAA
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CTGAAAAGGAACTGTTCAAGGCTGATGAATAAGATCTAAAGAGTTTACCTTCTCAGAAAGAGAT
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SEQ ID NO: 2962 ACTTTAATAGTTTCTTGAAAAAAAATTTCCAGACACTTAACATTTCAAA
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SEQ ID NO: 2969 ACGCGGGGAGCGGATAGAGGACACGACCAAGATGGCGGCGGTGTCTGGCTT
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NTGCTTTT

SEQ ID NO: 2970 ACAATGACTCATIATTTCTTTATAAAAACTGTGTGTGAAAAATCAACAACC
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TGAAAGCATCCCAAAATNCAATGATGTGAATTTTAAATACCTTNAITTTCTTAACTTAATN
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SEQ ID NO: 2971 ACTTTNTTTTNTTTTNTTTTNTTATATCACAACATCGTTTATTATGTGAAT
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SEQ ID NO: 2972 ACTTTTTTTTTTTTTTTGAGCAGTAAGGTATTATTTATTAAGATCTTAAGCC
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SEQ ID NO: 2973 ACAAAGCAGACTGCCNGCAAATCGACCGGTGTAAAGCACCCAGNAAGCAA
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CAAACTTNCCTTCCAGCGTNTGGTGCNAGAAATGCTNANGACTTAAANACANATTTGNGCTTCA
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SEQ ID NO: 2974 ACTTTTTTTTTTTTTTTTTTGGNGCTTAAAAATATATTTAAATTTTTTAACA
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SEQ ID NO: 2975 ACCAGAAAACTTACATGGACATATGCAGCAAAATGTTGGGAAACATGATCTGT
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SEQ ID NO: 2976 ACTTGATTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAGATTNCAACAGGATC
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TTTGCT

SEQ ID NO: 2977 ACAGCTATTGGAATCAGATGCAAGATGGTGTCTTTGGGGTAGAAAAAT
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CACTCTTAGGGCGAATNCCACACACTTGGGGCGTTACTAGGNGATCCTAGCTCNGGCC

SEQ ID NO: 2978 ACCAACTGCCAGCATTTCTGTGGAGGGTAATCCTGCTTTAATCGTGTGAGAT
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ATAAT

SEQ ID NO: 2979 ACAGGCTGACAGAGAAGATTCCGAGAGTAAATCATCTTCCAAATCCAGAGG
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TCAATAGGAAACATATGCAAGCAACCAANATGCNAATGTTTGAANTGATATGACCNAAATTTT
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SEQ ID NO: 2980 ACAGCTATTGGAATCAGATGCAAGATGGTGTGCTTTGGGGTAGAAAAAT
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NATAATNTTCAAACTTNTTACACTNACAGTGCATGCTCNATCTTT

SEQ ID NO: 2981 ACAGTTTCAGGGCAAGAAAAAGAAATTTGCTAGTGATGATGAACATGATGAA
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SEQ ID NO: 2982 ACCCGGGTCTTGTATCCAGGGCCCTGGAGACAAAGGGGACGTGTTGACGA
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SEQ ID NO: 2987
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SEQ ID NO: 2988 ACTGTTTCTCAGCAGAGGAGAAAACTCAACCTAGTTATGAGACCAACCAC
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SEQ ID NO: 2990 ACCAAGAAAAATAAGAGAGAGGCTGCAAGATATGCTAAACTTTTGGCCAAAG
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SEQ ID NO: 2991 ACATCAATAACCGGGGATTTTCTTTTGTCTACTATTTTCACAACCCAGG
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SEQ ID NO: 2992 ACTTTTTTTTTTTTTTTTTTTTNGAAGGATTTGTGAACTCTTCACATCATG
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SEQ ID NO: 2993 ACATCAGTGAATTTTAAATGCTAAAAATTTATGATAAAGAACTACTGAATC
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SEQ ID NO: 2999 ACCTTTTCTTTTCTTTTCTTTTGGGAANAATCAANAATTAATTCACATATGTG
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SEQ ID NO: 3000 ACTTTTTTTTTTTTTTTTTTTTTTTTANATGCTAANTTNANTNTTTATTNN
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SEQ ID NO: 3002 ACTGGCATTCTCCAGGACATCCCCAGGCTGTCAAAATTTAGCCAAAGCAA
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CTTTTCAGCATCTATATCAGGAATTTCAAAACCAAAATTCGCTTCCATGGCCATGATAATCTCCACT
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SEQ ID NO: 3004 ACTGAATGGAAAGATGAGCATTCTAGTTCTACACTTCTTTTTTCCCCCTCAT
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SEQ ID NO: 3005 ACAATCAATAAGTCTTAAATCTCTTCCATGGAATTCGCCCATCTCCCACTT
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SEQ ID NO: 3006 ACAGCTCATCAGGTTGGCCAGGATGGCATCAGTGGCAAAACACATTCCTGGA
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SEQ ID NO: 3007 ACAGGGGGGGCTACCTCCCGCCGCGGGTCTCTCGGTCTCTCTGTTA
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SEQ ID NO: 3008 ACATGGCAATTAGAAGTTGTATGGCAAAAGAAAAACCAAGCTGGCTGCCA
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AATCCGCTATTGCTT

SEQ ID NO: 3009 ACAGGGGAGTCCAGTCCCAAGATGGGGCCCAACATGAAGAAAGCGGCTGCA
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SEQ ID NO: 3010 ACATGGAGTGTTCAGCAAAAGACCAAAAGATGGAGTGAGAGAGGTTTGTAAAT
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SEQ ID NO: 3011 ACGCGGTGAACAACTGCTGAGCCCTGTGCTCCCGAGTCAGTGCCCGC
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SEQ ID NO: 3012 ACCATTATTTGTCTGCCGCTTTAAAAAATACCATGGCTATGCCACTTGA
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CAAGATTAGCAAAAGATAAATGCCGAAGTCACTTCACTTGGACACAGTTGGATCAATCTGAT
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AGAGAAACACTTCTTGTGCTTTTCTTTTGTGAGGTANAAGTCTCACTATGTTGCCAGACTAG
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GCCCACTCACTTGGCAANAATCACTTTTATAAAGCGTNAGNCTGCTTNCACAAGAAGCANCA
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SEQ ID NO: 3013 ACCACAGTATCTCTCCTCTCTCGGCTCTCTGTTTTGTCTTGCTTATGCTTC
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SEQ ID NO: 3015 ACAGGTTGTGTCTGCCAGTTCAAGTCCACAGCTCAGAGTATCACTTGTCTCA
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SEQ ID NO: 3017 ACTCAAAGGTGATATTGCTTTTTCATGCTTCAGGGGAAAAATCCTTTTCT
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SEQ ID NO: 3018 ACTACTGCTGCAAGAAGGACCTGTGTAACCTTAAAGCAAGCTTGAAATGG
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SEQ ID NO: 3020 ACAGAGATTTAAATGAAATCTTCAAGAAAGATAAATTTGCTTTTCAAGTCCACTG
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SEQ ID NO: 3021 ACCTTTTGGTGCCAGGCTTTCAAGGAGCCCTCACCATGAAAACAGTCAACCC
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SEQ ID NO: 3022 ACTGTTTATTAACCAACCAGCTTAGAAAAAATATCATGGTAGACACCTTAGTT
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SEQ ID NO: 3024 ACCCAGAACATCTTCCCTGGAAAGTTTGAAGCTGGGATTAAATCTGGAGC
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SEQ ID NO: 3026 ACCAATGGCTCTGGAGCTTGGAGGAAGACTAAAGGAATGTGTAGTGATTCTG
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SEQ ID NO: 3027 ACCGGAGCCTAGGCGACCTGGAGAGGATGTCATGCTTCTGTCAACACGC
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SEQ ID NO: 3029 ACTTGATTGGTCATTTGAAAACTGCAACAGTGAACCTTTTGCACTCAAGAA
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SEQ ID NO: 3030 ACCATTCTGAACGATGTTAAAGCAAGTGTGGTTATTTATGACATGAACCATG
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TGTTAGAAATATATTGGCAGCCAGGACTCTGAACCTCTGCAGAAACATTTGTTTCAACCCAGACTTCA
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SEQ ID NO: 3031 ACAGAGAGCATAGAAATAAAGCAAGATGTGAATGTCTCTACCAGACAGAG
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CAAGCCATCAACAGGCAACAAAGTCTATGCTTGGGCTCTTCCCTGCTCTGTCTTGGAGTCAATGAC
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SEQ ID NO: 3032 ACTTTGGATTAGAGCCCTTCATAACATCTTTGAAAAAATCTTCTTGTCTCT
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GATCTCTGAGAAAGTGGAGGATCACTTCAAGCAATTTACCAAGCTTCAGGTGATTCATGGCTAT
AGTTAGTCTGATTTTGTCTTAAGCATCTGTATGATGTGTGAACTTAAACTTCTATCTGTAGGCC
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SEQ ID NO: 3033 ACGCGGCCACAGAGAAAGGAGGAAAGACCTAAATTGACTCCCTAACAC
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SEQ ID NO: 3034 ACAAAACATCAGAAACCAATATAATCTGGCAATCTTTTAGGAAAGGGGTGT
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SEQ ID NO: 3035 CGCGGCGAGGTACTGTTGTGTAAATTGAOCCAGTGACCACAGATGAGG
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SEQ ID NO: 3036 ACATAGTGTGCGGAACCTCAAAATCGGCATTAGATAGATCCAGTGGTTTAAAC
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SEQ ID NO: 3037 ACGAGTCAAGCAACAACTGCTGCGCCAGGAAAAAGACAAGGCTAATTGGGCC
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SEQ ID NO: 3038 CGCGGCGAGGTACACCAATCAAACGTAGATTGCTCTTTTACATAGTCTCAT
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SEQ ID NO: 3039 GTTCGGCGGAGGTACAAGTGAAATCTTAACGAGACTTGCCGCAGAAATG
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CCTTTCACTCATCACCAGTTAAATTAAGCATTGCAATGATGCTTTCACACAAATTAATCAAGCA
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SEQ ID NO: 3040 ACCTTGTGGAGATGCCACCTCAGAAATTCACACTGTGACGGAAGAGGTTT
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SEQ ID NO: 3041 CGCGCGAGGTACTTTTTTTTTTTTTTTTTTTTGTAGNAAAAATATCT
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TCNAAATGNCCTTTAGGAAAAAATGGCAAAANTTAATGGTCCATTG

SEQ ID NO: 3042 AGTCCGGGCGAGGTACTGTCATGACGAGAGCGGCTTGAACAGGCGGCACA
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ACACTCTCACCTTGAAGGAACGGGAGCGGCTGAAGAAAGGATTCTGGATGAAATTTGAAGACA
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SEQ ID NO: 3043 ACAAGGCGATATTTAAAGGATCTCAGTTACACTTAAAGAGGATGCTGTG
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GAAGCTCTAAGTTTGAATTCAAACCCACAGGTTATGCCAACACTTTGAGGATGACAGTCA
AAATGTATAAGGAAGAGGCTAAAGCAATCTCAAGGGGTGTGCTCTTGGATGACAGATC
CATACATGATGAAGTTGCTGTGTGAACGTANCTNGCGGNAACACGCTAANGCN

SEQ ID NO: 3044 CGCGGCGAGGTACGCCCTTCTGTCGACAGCTGCCGGGAAGAGCACAAGAG
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SEQ ID NO: 3045 ACAACAAAGCAATGTTACCTTACCATAGGCTTAATTCAACTTTGATCCATT
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GACTTTTTCATTTCTACTGNGAANATAAACTAGAGGCTTATAATAAGTNTGGATTGGGGNGAAA
AACTGAGTAAAAAAGCTGGGGAAGGAACTTGTGAAGTACTTATTTGNA

SEQ ID NO: 3046 ACAATTOGTATTGCTTTCCTCTTCTTCTTCAGACAAACACCAATAAAAT
GCAOGTGAAAAGAGATGAACCAAGACTAGAGGCTGACTTAGAAATTTATGCTGACTCGATCTAAAA
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SEQ ID NO: 3047 ACTTGAGCTGTGAGGTCAATCGGAATCCGACACCTGTCTCATCTGGAACAA
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SEQ ID NO: 3048 ACTTTTTTTTTTTTTTTTTTTTGGTNATATTTTTATTTTCANAAAAACAGAGT
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SEQ ID NO: 3049 ACTTTTTTTTTTTTTTTTTTTTAACTNAAAAAGTGACATTATTTCAA
AGAAAAAAATGACAAAGATGTCCATCCCTGGCTCCCTTCCCTCCCTCTCTGCTGNTCNCANC
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SEQ ID NO: 3050 ACTTTTTCTTTTTTTTTTTTTTTTTTGGACAGAGTTTGCTCTGTCAOCC
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SEQ ID NO: 3051 CCGGCGAGGTACGGCGGGAATTCAGAAGAGGAAAAATGTCGCCAGCTGC
CTGGAGAAAGCGTCTGCTCTAGCCAAGATCTCTCATCAAAAGTAATGTGGCCAATGAGT
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SEQ ID NO: 3052 ACCTTGCTCACTAGAGCAGCTAAAGGAGGAAGAGCTGAACCCCTGATTTCAT
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SEQ ID NO: 3053 CGCGGCGAGGTACTTTTTTCTTTTTTTTTTTTTTTGGAGCTAGCCTCCCTCG
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SEQ ID NO: 3054 ACTTTTTTTTTTTTTTTTTTTTTTGGCATACAAATGGCTGGTTTAAATTTT
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SEQ ID NO: 3055 ACTCANATTGTGAACAGGCATATTTCACTGATTTAGACTTANTACTTGATG
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SEQ ID NO: 3056 ACTTTTTTTTTTTTTTTTTTCTGATGGCTACTTATAATTTATTTAAAAACAT
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SEQ ID NO: 3057 ACTGAAAGAAAATGTCATGCTGCAGTCACAAAAAGGGGGCTCTCCTCTTCA
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SEQ ID NO: 3058 ACCAAATGGGATGTTTCAACAACCAAGCTCGAGTGGCAGCTGAGAAAAAGC
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SEQ ID NO: 3059 ACTAAATATTGCTGAGAGCATCCACCCAGGAAGGACTTTACCTTCCAGGAG
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SEQ ID NO: 3060 ACATGGAGTGTTCAGCAAGACCAAGATGGAGTGAGAGAGGTTTTGAAAT
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TNTTTANAAGCCAACTATGANTATTAAAGATGTNCACCTGCTGGCCACAGGGTCTTTTGACA
CTGCTNTAACANCCCTCCTCTGNCCTCCCTGACACACCCNGGCGCTAATTCNAGGAATTTCTAA
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SEQ ID NO: 3061 ACCTCTGCATGATTATCTTACGTGGGGCAAAATGATTCATGTGTGATGAGAT
GGAGCGCTCTTACATGATGCACTTTGTGTAGTGAAGAGAGTTTTGGAGTCAAAATCTGTGGTTCC
CGTGGGGGTGCTGTAGAGCAGGCCCTTTCATATACCTTGAAAACATGCAACCCAGCATGGGGT
CTCGGGAACAGCTTGGCATTGACAGATTTGCAAGATCCTTCTTGTATTCCCAATACACTAGCAG
TTAATGCTGCCAGGACTCCACAGATCTGGTTGCAAAATTAAGAGCTTTTCATAATGAGGCCAGG
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AACAAACCAAGCAGGGGTGTTTGAACCAACCATAGNTANAGTAAGATTNGAAATTTGCACAGAAAG
CTGCAATCANCAATTTGJNATGNGATTTTAAATCNTTCAGAAAG

SEQ ID NO: 3062 ACOCGGGGGAGGTGAGGTTTGTACCCGNATTCGAGAGGTGGGCTTTTGT
CCCTOCANACCTCGGNTTATAGNGCTGTCTCCGCTTTCTTCACTTCACAGAGGTTCCGGTCTCC
TAAAAANAAGGTTTTATTTGGGAGGTAAAGGTCAATGCGTAGGGGTAGAGTAATGATGCTTATGGT
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TNAAGTCACTCCACAGAGTCTGANTNTNACATCATAGAAATGCTGATTNTCAAGAAACCCAG
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SEQ ID NO: 3063 ACACCTGTAGTCTTCTGACCTGTATGTATCTTGAGGTGGGTCCGAGGTTGC
TGGGATCACTAAAAAGCCTTGCTACAGAAATCACACTTGTGGGGCTTCATACCCATGTGAOCATAA
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CTGGTCAGATGGGCTTTGAACTCTGTGTGAAGAAATGCACTCCTTGCCACAGTTACAGAGATGCACA
TCTGGGTGTTACAGGACACCAATCTGTTGAGCATANCTCGGCTATAATAAAAAACAGTTTCAATTC
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SEQ ID NO: 3064 ACTTTTITTTTTTTTTTTTTTTTTTGGCTGCCCTAAATGTTTATTAAGTATGAA
TTTTACAACTTTACTTATATTAGCGGTAAACGNGGAGCTGGAGATTGGCCCTTCTCCAAAGCT
GCCCGGCGAGAGCCACCAATAGTGTGGGAATTTGGGCCCTTCCAAAGGCCAGGCTCTTTCCG
GGCTGCAAAATGAGGCCACCGCATNCCCTGTGCTTGTGGACTGGATTGGAGACCACTGGGTGTNA
GGATTTCTTCGGATNGCTTTATGG

SEQ ID NO: 3065 TCGCGGCGAGGTACTTGGCTTTTTGTGCACTCTATGACATGGAAATATTG
AAGAAAGAGCTTTCTTGGCTTGGAAAGAGATATAACCCAGAGTTTCCGGGAAAAAGGCAAGGCT
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AGCTGACTAAAGAACCAAGCCAAAGCCTTAAATTTGTGCAAAAAATACCTGTGCTATGATGTAATG
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SEQ ID NO: 3066 ACTGCGCCTTCCTGCACTGAAGCAACCCCTGCAGGGCTCAGTGACCAAGGAAG
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AGCTCCTGCATCCAAATGGATGCTGCCAGANATCCGACGATATCAAAATCGTGCAATTGAGGCCAT
GAGAAAGGACATGGGCTCTCAATTTGCCCGTGACGGCAACAAGGACATGGTGTGGGATCTGCAT
GGAGGTGGTCTATGAAAAACCAACCCCAAGTGAGCTCCGTTTGGGATCTCTCAACTGNAACACA
CCTATGCTCTNAAGTGCNTCCAAAGTGGAGANNCTANCAATTTGAGAGCAAAACATAAAGNGAGCT
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GGACGGATTAAATGATGNNTTTNTTAACTGGANNTTTATGGGGATCTTTTNGTTNACTACTC
TAGGTNGTGGCA

SEQ ID NO: 3067 ACCAACCTATGCAGCCAAGCAACCTCAGCAGTTCCCATCAAGGCCAAGCTCCA
CCACAACCGAAAGTATCATCTCAGGAAAGCTTAATTCCTGCCGCTCCTGCTCCTGCACCTCTTTA
TATAAGTCCCTCAGTGAATTTTAACTCTTTTTCGAAATGTCTTCAGGGAACGTAGCTAATAC
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GGGAAATGCAGTAAAGCCAAGGAATTTACATANCATTCCGTTTCAATTGAAATAAGTCTTATTC
AGNNTCNGGGAGGTAAAGCAATAATGATTTTGGACNTGTATTGNANTGATCTAAATACCTGG
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SEQ ID NO: 3068 CGCGCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTGTAGTTCAAGTTA
ATACAAACTACAAAAGATTAAATGGTTGCTCTACTAATACATACATACAAAACGATAGCTGCCCA
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GGCCTGCTTGTAAACACCAACAATTGGGCTGAATCTGAAGNCTTGTGTTTTTACTAATGGAAAAA
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NAATCCAAANGGNCACAGGNGGTATTTNANGATTGCGGAAAAATCCCTTTATTTAAANAA
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SEQ ID NO: 3069 ACAGCAATGAAACACCAAGGGACGTTTCTCCAAATGTGTATAAGCTTG
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CCTTTGAGCAATGAGCCTTAGTTCAATGTCAGAACATTAGCATCAGAAATTATGCTGCCACACT
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GATGTTGGCTCTCTGCTGCAAGCAAAACCACTCNTTTGCTAAAAATCCCAACAGGTCTGCAAT
GTCCAATAGCTTCCATGGCATAATCAACTTGTATANCNGACCTTTGGANAAAAATAGNGGTCC
TGGAGTCATATCTNGAACATTGTTCTGACTTATATAGTTCANATGGAAACCTGGAAGACCTG
AGATGTACGAGCCTTACTTCAGGGAAGANTAAACCAACCGTTAACNATACCTGNTATTTCC
CGGACTNGCGGAC

SEQ ID NO: 3070 ACCTCTGTTCTGGATCTGGGCACTCAGCACTCTTTTATGATCTTTGTGTGGCTC
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AATAAGACTATTTTGACAAAAGATGCCATTAAATTTACAGCTGTAGAGCCACTTACAAATACCT
CAGGCTAATTACTGTTAATTTGGGGTTGAACCTTTTTTTGACAGTGAGGGTGGATTATTGGATTGT
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ATTCT

SEQ ID NO: 3071 GTCCGCGGAGGTACAGTCCAGTTATTTACACTCAGATATTACACCTGT
GTAATAAGTAGAACTAGATCACTCACTGAAATCAGAAAGCAATTCAGTCACTGATAATGATCA
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SEQ ID NO: 3072 ACTTCTTTTTTTTTTCTTTTTTAAATGGCAGCTAAAGATATACAGATTACTG
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GGAAATGTATGTCTGGAATTTTCAAACTTTACATTGAAACATAATTCCTTGGAACAAAACCATAA
CCTGAGGAGGTTTATCAACTGGAAATGCTTATATTAGTTGGTTTCACTGNCCTGGCCGGACCCAC
TAAGGCN

SEQ ID NO: 3073 ACAACACCGAGGTGGGAGACAAGTGGATCTGGCTGAAGTGAAACGGGCCGCC
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GCTTTAAAGATCGGGGAGGGTAAATGCAAAAATTTGCAAGATGGGAAGAAAGGGGTCTCAAAA
AAGCAAATCCATCCTGTAGTATAGGTAATGGAGATTGGGGGAAGCAAGCTTCCATTCTGGATGTTTGA
ACCTTTAGCTTTGTTTGGAAATGGGCCACCAATCTCACTGGAAACAGTGGTCTGTGTGAAAG
GCCAGCTCTCGGNAAGCCCTGTGGTTTCAGCGCTGCGCTCTGTGTATTGATTGTCACATTG
TTTTTTCTGACTTCANAAATAAAATGTTTCCATGGGAAAAAAAATAAAAAATAAAN
TCTNNGCGGGANCA

SEQ ID NO: 3074 ACAACCTTGTCAACCTCTCAGGGGAGAGCACTCACTGATGATGCCAA
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AGACAAACATTCAGCCGCTTGAAGGCTCACTCAAGAGATGAACCTTAAAGGCAAAAGCTCTCC
ATATCCCATCTCCGTGAGAAAAATCATTAACTCCCTGTTGTTGACTTCAAGGAAATGATGTCCA
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ACTGAAAAACAATNACCTTTTCTCAAGTTTAACTGCTTACCTGATGAAATGGAACCTTTTCT
TNNTGGATCTCTGACAAACAGAAATGNAATGTTTCTCTGTGCAAAAGTAAAAACCGTGTAAANAAC
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CGTTATAGGTCC

SEQ ID NO: 3075 ACAGCAGCAGTTGTATCTTTATTAGCTTGGTAGATCAATTTCTCTGCTCTT
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OACTGGGAAACCAATTGCTGTTAACTGGTGAAGATAAAAAAGAAATCTCTCTGAAAGAACGAA
TGAATGGCAAGAAAGTGTTTATCTGACTTACACCCCTGAAGATGGCCAAGGGAACCGTTCACT
NGAACTGGAGANTAAATAAACTTTGGNATTGATTACAATAAANCTCTGTTGCCGNAAGGGCNC
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GTTTATTGGAANAGGGNATGGTGGAAAAANNTTCTTTCTNNAGGGATTAAAGGNACTTAAAC
CTTCANCCNGGATATGGGATTTCCCATNANGGNCGAANGGNAATAAGTNCACCAANTCAAN
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SEQ ID NO: 3076 ACTTGGTGAATATGAGGATATTAATAAATTTCACTACCAAAAGTTT
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GGGATTGACATCAATCCCTATAATGATCTGCCCACTGGAGGGTGTCTTTCAGGATCCAAATGTTG
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TGGGATGCGGGANCTTTGGCCAAGCNCAGNTCTNTTNTTGTGTTGNATANAACAGGATNGCC
CAANTGGGAGATGGTTGGCTGTGANTNTNAAATGGCANCTGNTTNAGCTCCTGGGAAGGCCTT
TTTGGGCTATCTGGNT

SEQ ID NO: 3077 ACCCTTAACTGGCAGGACATTTTGAATCACAATTTGACATAAAGAAAT
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SEQ ID NO: 3078 ACGCGGGAGCAGCAGGAGGAGGACAGCAGCATCTCGGACCAAGACT
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SEQ ID NO: 3079 ACCACGCTGTGCTAATGCANAAATGGAGATTGCTACAAAGGACCCCTTTAAAC
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GCTGAATAATTTGGCTGAAAGTTCTAGGCATATTTGGCTATGATTGACGAAGGGGAAACCGACTG
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SEQ ID NO: 3080 ACAAGTCCAGAGAACACATTTATGATTACGATCCAGGAAAAATCCACT
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AACNTCCAAAAAATCCCCCCCTTTTNGGAAAAAANCCGAAAAAGGCAATTCCTCAAGG
GNAATTCAAAAANTAAAGGGGAACTGNACCAACAAACCTTTTTCACCGGGCCAAAGAGACC
CCACAACGACAGACAGGCCCCGAAANTTCTTCCAAAACTTTNTTTTGACCCACNNCNTTTC
ACNCGGGGCAAGCAAGTCCAAATCAAAANTGTTTNAACCCACCCCTTANGTNTNAGTTAAA
ACTCAAGGGCTACANNAAGTC

SEQ ID NO: 3081 AATAAAGAACCTCTATCAGTGAGACTTCTCATTTTATAGCAAAATACATTTTG
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TATTTTATACATTAAGATTTTGGTTGAATATCTTCAATTTAGGTTTCTAAAAAACACCATTTATCTG
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ATTCAAGAAATTCCTGTTTGTCTCTCAAACTTTTATCTTCTCTAAAGCATCTTGCCAGAGACTACAAA
GGGAANGGACCAATACAGAGCACTATAACATGCTTTGGACAGTAAAAAAGATTATTTCTCTAC
ACTCTTGGATTTTCCAATCATATCTTCTCAAGCATGTTCTTTTGGCCCATTTGGGGCACTAAAC
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SEQ ID NO: 3082 ACAAGATGTGTTACTATGCTTTGGACAGGTTTACACAGAAGCCAAAGCGTCC
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ANAATGTCTGGAAGTTTGTCTTGGGCCATGATGGGCTGGGCCAATTAAGAAATGATTTTATTAAT
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GTTTGGAAACCTNTACT

SEQ ID NO: 3083 CCGGGGTATTNATTCGCCCNACCCGGANTTGGGTGGGGTTCTGTTGT
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NCCCTCAAAA

SEQ ID NO: 3084 CACTTTTGTACAGTTCATATATGAATAGTTAGCAGAGGGAGAAAACCTCCCG
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SEQ ID NO: 3085 ACTCACACAAGTTGTTCAAAAGATGATATTCTGTGACAGAGAGGCCATGG
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ACTNGATCTTATGATNTAAAGGAAATTTTAAATATGATTATNTAGGTTGATTACAAAAANCC
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SEQ ID NO: 3086 ACATGTTTGGAAATGAGTTAGATACTTGAAAAGTCTAAACACACTGATTAG
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CTNNAAAAACCTTTTAAATCATATNTATGGGGNTTTAANAAGGGGGGNGAGCCNCAATTTT
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SEQ ID NO: 3087 ACTTGCCCTTCGCCAGAAAAAGCGGACTTGCTGCTAAGGGTGAAGGACCAA
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SEQ ID NO: 3088 ACAGATGTCAAGTGAAGAGACTCTTACTGACACTCAAGTGGTTCTTTTCAGG
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SEQ ID NO: 3089 ACTTNTTTTTTTTTTTTTTTTTTGGGATTAGTGGCTATTTCTGCTAGGGG
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GAACCAAAAGGATTTAATTCCTACCCCTTTTAAACCNATNAACANTTGAATTAAGTTTGTANCGGN
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TGAAATTTTTTCCAAAGNGNAATTTTTTNAATGGACCTNTTACCAACAATGNTACGGGATTAAT
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CAATCCAAAAAANA

SEQ ID NO: 3090 ACTTTTTTTTTTTTGGGTTTGTGTGANACAGNCTGCTCTGTACCAAGG
CTGGAGTGCAANNGGACGANCTTGGCTTACTGCACCTCTGCTCCAGGTTCAAGCGATTCTCT
GCTNAGTCTTTTGTAGTGTGGGACTACAGGATGCACCAACACACTTGGCTAANTTTTTTTGT
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SEQ ID NO: 3091 ACTGTTGGCTTTTCCGAGCAGAGTNGGAGAACTTGTGAACCAAGGCTGCT
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CAAGCGGATGTTTCCAAATTTGGAATGAGTTAAAAAGCTTGGAGTTTNACTANANNNGNAACG
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SEQ ID NO: 3092 ACOCGGGATTTAATCATTATTTTGGCTGTCATAAGAAAACTTTAGCTGAA
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SEQ ID NO: 3093 ACTGGATTCTGTATCTTCTGCTCATCAAGAAATGGAACAGAGCTGTAAATCC
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SEQ ID NO: 3094 ACTTTTTTTTTTTTTTTTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTT
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SEQ ID NO: 3095 ACTCTNNANGTGACANTNATGATCANTGAGNGGTGTNATANATGATGAA
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SEQ ID NO: 3096 ACAGAAATATCTGGTGAGGGGCCCGCATGGTCCGGGATGTGTCCGCCCTG
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SEQ ID NO: 3097 ACCACCAATCAATGCCAGGAAGAGAGTAAATGCACCTTAGACTCATTTTGGC
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SEQ ID NO: 3098 ACCTTAACAGCTCTGAAAGCTTCTTCGATTTTGAGAGTCTTCGTGTATTCCA
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SEQ ID NO: 3101 GTACCGCTGAGGGAAGGAACGGGACTCCGACCTCCAAGAGTGCAAGGAT
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SEQ ID NO: 3102 ACGCGGGACAGACGAGATCTGGATCGAAGGCGAGATGGCGGACGTGCTAG
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SEQ ID NO: 3103 ACACAATGGGTTTGTCTTCAAAAATGCTGCCCTTATTGGAATCATGGTTG
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ATGT

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SEQ ID NO: 3105 ACANCCAGTGTGGGATGTGATGANGGCCCTGGGCCAGAACCTCAACCGC
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SEQ ID NO: 3106 ACGCGGGAGTCAGACCCAGTCAGGACACAGCATGGACATGAGGGTCCCCG
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SEQ ID NO: 3119 ACTTTTITTTTTTTTTTTTTTTTTTTTNGGTAACCTAATGGATCATCAATTGTG
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SEQ ID NO: 3120 ACCTTTGATCTCAAAATACTTTGTGAATTGGGCCCCGGATTGATTGGATGGGT
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SEQ ID NO: 3121 ACOCGGGGGGGCGAGGGGAGCTTGAGGAAACCGCAGATAAGTTTTTCTCT
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SEQ ID NO: 3122 ACAAAACCGGATCTGTGTGAGAAACACATGTTGAGACTCTCCATCTCTC
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SEQ ID NO: 3123 ACATATTTTGGTTGAAGACACAGACTGAAGTAAACAGCTGTGCATCCAAAT
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SEQ ID NO: 3124 ACCTATTCTTTGCACTGCTCAGGAATTGTTGACATGCTCACTATCTGGTCAGC
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[illegible][illegible][illegible][illegible][illegible][illegible]

TCCAAGACCCANCANCTNAAAANCCACCCCTAAAGCTTT

SEQ ID NO: 3131 ACTGGTTCTTAAACAGCCCATAAAAACCCATTGGGCTGAAGCTTATATCTCAG
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SEQ ID NO: 3134 ACCAAGTCCCTTCCATCCTCTGGGAGAAAGGATGGAGGACAGAGGAAAGG
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SEQ ID NO: 3135 ACGGGGGGACCGACCTTCAGCAGGGCTGTGGCTACCATGTTCTCTGGCGG
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SEQ ID NO: 3136 ACCCATTCACCTAAGAAGCAGAACTTTTTCACAGCATTTGTAATAGGAATGG
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SEQ ID NO: 3138 ACTGTGTAGTGTATCACTGTAAAAATGGAAGATCATTATGAAGAAACAAT
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SEQ ID NO: 3139 CCCCAGGGCTCTGCCAGGGTTCTCTGTGGGAANTGANATTCCTCTTTAAC
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SEQ ID NO: 3140 ACAAGTCCAAATCTTACTTTATGGATGTAATAATGCCAGGTGTCTACAAGA
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SEQ ID NO: 3142 ACOCGGGGGTCAOCCTGAAGTTTATTTCTTACCTACAGGCTTGGGAATAA
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SEQ ID NO: 3145 ACCOCTGCTGTTTGGCTTTGGTAATGTGATGTGTGTTCTCCOCTACCCCA
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SEQ ID NO: 3146 ACAGAAATGGCACAGGGAATGCATATGAAGAGGAAGCCAAACAGCAGTCATG
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SEQ ID NO: 3147 ACAAACTAGGCAATAAACCGTTACCTGGGATCAGTTCAGATGAGACAGTA
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SEQ ID NO: 3154 ACAAAGCAGCAACTGCAATCTCAAGGTAAAAACATTAGAAAAACATTTGTG
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SEQ ID NO: 3155 ACATAAAGTTTATTAATATCTGATTCTGTTGATAGCTTTTATGGCAGGA
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SEQ ID NO: 3156 ACCAAAGGGCAAACCCCACTATGGCTTGTATGGCTTACAAAGAAAACT
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SEQ ID NO: 3157 ACTGTGTGGAACCAACCACTGATACCTTGCAGAAATGCACATTAGAATA
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SEQ ID NO: 3158 ACGCGGGTATGCTATAAATCAATAACAGAAAGCACTGGAAAAACCCAA
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SEQ ID NO: 3159 ACGCGGGCTCCTCTCTCTCTCCGCCATCGTGGTGTGTCTTGAACCTG
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SEQ ID NO: 3163 ACCCTCAOCCNCTCCGCCCTCCCTCTCTAGATGGTCAACCATAGGGCAGTAA
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SEQ ID NO: 3167 ACGGGGGGACTTTGTTCAATACAAACTGGCAGAGAAATTTGTGAAACAAG
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SEQ ID NO: 3168 GGTACGCGGGCTGAACCGGAAGCTCACTGGCATGGGCTTCCGTGTCCGAC
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SEQ ID NO: 3169 ACGCGGGGATCAGATTTAGAGGCACAGTGGACCAAGTGGAAAGCGATGCA
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SEQ ID NO: 3170 GGTACATCATGGCTGGACTTGGTCAAGCTCTTGGCAOCAAATGCTGGCAT
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SEQ ID NO: 3171 ACACCTTGAAACCAAAATTTCTAAAACTTGTTTCTTAAAAAATAGTTGTGTA
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SEQ ID NO: 3173 ACTGAAAAACATAGCTAGCCAAACAGAACTTAAAAAATACCTTTCCAAATGC
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SEQ ID NO: 3179 GGTACAGCTCTTCATTAATAAGAATACTTACACATACATTTTCAGATATTTCTACCTTCTGTATGTGTGTGGAAATGTATGTAGGTAGCCACTGAAAGAAATTTGGGCCCTTGGGAGGATGGCAGTGGGAAGTCCATGAAGTAAAGAGCAJTCTTTAAAAAGCAGATTGTATGCATACCTTTT

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CATGGANCAAT

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SEQ ID NO: 3181 GGTACACTGAAACCAAAATTTCTAAAAGTGTCTTCTTAAAAAATAGTGT
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SEQ ID NO: 3183 GGTACGGGGGGAGTGGAGAAACCGGGAAACCATGGCGCTGTGTTGCTGTT
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SEQ ID NO: 3184 ACACAAACCATGGAGGAGAGTAAGAGAAATAATTAACAATGCTGTTGG
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SEQ ID NO: 3185 ACAGTTGTTTGGGCTACCTGATGCTATCTCTAAACTCTTTAAAAATGAAGAC
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SEQ ID NO: 3186 CGAGGTACTTTTGTGCATAGAGTCCGGCATTATCAAAATCTGGATTTTAAG
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SEQ ID NO: 3187 ACAGATAAAAGATGTAAATCTGGAGGTTACGGCCAAGCCAGTCCATTAAAT
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SEQ ID NO: 3188 GGTACAAAACCAATGTTTGTACTATAACTTCTGCATCACAATTAATAATCCA
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SEQ ID NO: 3189 ACTACTTGGTTCGGATATGGATGATGAAGAGGAGAGGAGAAAGAGATG
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SEQ ID NO: 3190 GGTACGAGGACATTTTGGCCGGGCTGTTGGGCTCTCCTTTACCAATGTTG
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SEQ ID NO: 3191 ACATAAAGTAAGTGTATATGTGCACAGCATATGCAATTTTAAAAAC
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SEQ ID NO: 3192 ACGCGGGGGGGATGGCTTGGTAGTGGACTTCTGGGGTTGCTGTTAOCG
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SEQ ID NO: 3198
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SEQ ID NO: 3204 ACTTCATAAAATCTCTTATAGAGTTACTCTTGGCCTAGATTGTAAATTAAGT
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SEQ ID NO: 1205

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[illegible]

SEQ ID NO: 3207
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[illegible]

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SEQ ID NO: 3211 ACAAGGAATCCTTTATTGGTAACATCTTGGTGGCTGGCTAGCTAGTTCTACA
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SEQ ID NO: 3212 ACCGACATAGAGCAAGAAATCAAGATTCTGTAACCTCTGCAAGGCCGCTC
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SEQ ID NO: 3213 ACGGGACACACATCAAGCTTTAAAGAAAGTGTGCTGAAAAATAAGAA
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SEQ ID NO: 3214 GGTACTGATACACCATGTTGGCAAGCAAGTGGAGGCAGTCTCAGAGAT
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SEQ ID NO: 3215 ACACCTGAAACCAAAATTTCTAAACATGTTTTTCTTAAAAAATAGTTGTGTA
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SEQ ID NO: 3216 GGTACTGCTCCCACTAGTTCTTCAACTAACATAGAAAAATGTCGAAAA
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SEQ ID NO: 3217 ACGCGGGAACCATCAATTGACATTTCTAACTAAGCGAAAAACAATGCACAGCGTCA
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SEQ ID NO: 3218 GGTACGCGGGCCATCCATCCCAAGGAGAACTTCAGTTGCTTGACTGTTGG
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SEQ ID NO: 3219 GGTACAACCGGGAATTTGCCAGATTAACTGACCACCAACAGATTGC
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SEQ ID NO: 3220 ACGCGGGGGCCAAATGTGCCAGCAGATCTGAGCTGAGAATCACTCGTGGTGG
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SEQ ID NO: 3221 GGTACTTTTTTTTTTTTTTTTTTTTTTTTAGGACTCAACTCATGGAANAA
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SEQ ID NO: 3222 ACCCTCAACTCAAAAGGAAAAAGGTTATTTGGGAATTTAAATATCTTTT
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SEQ ID NO: 3223 ACAAGGACCACTCTTCAGAAAGCAGAGCTCTCTCTCAGTCTCTCAAAAGGT
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SEQ ID NO: 3225 GGTACAAAGGACGGAGCACCATAACCCGTCOAAGGCCAGCACAAACCCAG
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SEQ ID NO: 3226 ACAAGGAGAAATTCAGGAAGTAAGAAGTAAGAGTGACCTATTATGCTTC
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SEQ ID NO: 3227 ACTTGATCAAAGACGACATTTAGATTCTTCAGCTTTGAAGCATTTAGTAACA
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SEQ ID NO: 3228 ACCTAGAAGAGAGCGCGGTCAAAGAAAGTGAAGAAAGCAATTCATGTTTCAT
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SEQ ID NO: 3229 GGTACGCGGGGCGCGTGGAGCCCTTGACGCGCTGCTCTGTGATGCTTCTCT
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SEQ ID NO: 3230 AOCACAGAAAAGCCTCTCTGTCTACGGGGTGTCAATTTGACACCCCTCCCA
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SEQ ID NO: 3231 ACGCGGGGGGTGAGCTGACGGTAAACGGGCGAGAGGGCTGTTCCAGAGC
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SEQ ID NO: 3232 GGTACGCGGGGGGAAGGTGGCGGTGTTGAAGTGCAGGCCCTTGGGCGCGC
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SEQ ID NO: 3233 GGTACATGGAGGAGATGACCAAGCTCAAGAGGGAGCTGCTGTTGACGGAG
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SEQ ID NO: 3234 CGGTACAAAGATGACTATAAACAGATGCAGGCCCTGGTTCCATGAACAGC
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SEQ ID NO: 3236 GGTACAAAAATTGAAAGTGTGACAAATTGAAATCCTGTGACTGA
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SEQ ID NO: 3242 ACGCGGGGTTCCGAGCGCGCGGGAGCTGCCACGTCCGAGACCTGGAG
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SEQ ID NO: 3244 ACGCGGGGGAGGGGGGGCGGGCTTGGGGCTTGTGCAGCAATGGCCAAG
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SEQ ID NO: 3245 ACAGAGAAAGTTTAAAGTCAAGGCCCTCAACCAATTCCTACAGTATTAGTATGT
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SEQ ID NO: 3248 GGTACGGGGGGGGAACGTCTTCTCATGCTCGTGATGCATGAGGCTCTGCA
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SEQ ID NO: 3254 GGTACGACAATAGCAATCTTTCTCTGATAGGACAGGGGAGGAGTCCCTA
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SEQ ID NO: 3257 GGTACCGGATTCCTCTTTAAOCCCTCCCTGCTGTTTCCOCCAAATGTTAAAA
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SEQ ID NO: 3258 ACOCGCGGGGGTGGAGCTCGTCTGAGGCCAGGGTGGCACACACT
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SEQ ID NO: 3259 GGTACAAAGCGGGAGCACATTAACCTGGGCTGCGACATGGATTTCGACATTGC
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TACT

SEQ ID NO: 3260 GGTACTTTTTTTTTTTTTTTTTTGTGCTGNCCTAAATGTTTATTAAGTATGA
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SEQ ID NO: 3261 GGTACTTGTACAGTAAAAGAGGTATAAAGTCTGTTTCCAAAGTCCAAACCA
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SEQ ID NO: 3272 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGGAGATCCATGCTTTATGAACACAT
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SEQ ID NO: 3302 ACGGGGGGGCGGTTCTGAGGACTGGGTTGGGTGACAGCGTTGCTTGGG
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SEQ ID NO: 3303 ACATAGGAAAAATGATTGAAGCATTTCTCAAATACATGGCTCTGAGGGTGA
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SEQ ID NO: 3304 CCCAAGCATCTAGTCTGGAAGTACAGAGATAAATGAGAAAAATGTTCCAAA
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SEQ ID NO: 3305 ACATTTAAAAATAGTCCCTTTATGCAATTTTACTCTACATGTGTTATCCTTGCA
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SEQ ID NO: 3306 ACATCCATGTGGCCAAAATCATCAAGCCTGTCTGACACAGGAGTCAACAC
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SEQ ID NO: 3307 GGTACAAAAAGAAAAAGAAAAAATCAACCCCAAAAGCTCTTAAAAAAGG
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SEQ ID NO: 3309 GGTACGGGGGGCTGATGTGGCAAGAATGGTCTCCACATCTCCCTCCTGCAQ
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SEQ ID NO: 3310 GGTACTATGACTGAAAAGATTCTTCATGGCTAAAAAGCTCTGCATCAAACTCA
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SEQ ID NO: 3311 GCGGNGCCCGGNGCGNGCCNGGGCANTCTTANGACGGGGGCTNTGGAG
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CACATGGGGACCCAGGCTGGCCAAAGCATTTGCTCTCACACTAGATAAOCAGNTTCCAGTTGAGA
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NCANCACTACAACTCTNCCCCATGATTTGGAGACTGNAATTTCCCATAGCCCTTACTGCTCTTT
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GCATTACTGAAAAANACCAATNTACGCTTATCCACTATCCATCTTNTGTATGGAGAGAGAGG
GAACAGGAAAAACNTAACCTCANCATGHNATTGATTTCTTGCGCNANAAANAGACTGGGGG
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SEQ ID NO: 3312 GGTACACAGGCTGCTACCCAAATTTGTGAAATTTCTGAAACAGAGTAA
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GCATATGGCTTTCAAGGCAACCAAGAGAGATCCAGTATGATCTGGAACTTGAGATTGAAAAATA
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SEQ ID NO: 3313 GGTACATGGGCCAGATCATAAOCCAACTTTTGTGAAATCATGAACAA
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SEQ ID NO: 3314 ACTAAAAATACAAAAATTAAGTGGGTGTGGTGGGCTGCCCTGTAGACCCAG
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SEQ ID NO: 3315 ACCTGCAAAATGGATCCAGAGGCCAAAGCTGTGGAGCACACATGGAATCT
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SEQ ID NO: 3316 ACTTTTTTTTTTTTTTTTTTTTTTTTATAGGTTGACGGGCTTTATATTTCAGCA
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SEQ ID NO: 3317 GGTACCGACCATAGAGCAAGAATCAAGATTCTGCTAACTCTGCAAGCGGCC
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SEQ ID NO: 3318 ACTTTTTTTTTTTTTTTTTTTTTTTTGGANGAAAAAGGCTAAACGCTTNTGA
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SEQ ID NO: 3319 GGTACCTTTGGATTCAACAGTAACTGGGATGTAACAACTTAGTTCCT
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SEQ ID NO: 3320 ACTCCGTGAAGTCTAGGGATAGGAAGATGGTTGGCGAGCTGACCGGGGCCA
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SEQ ID NO: 3321 ACGCGGGGGAACGGAAAGTGAGCGCGGGGTCCACTGACGGTAACGGGGCA
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SEQ ID NO: 3322 ACTGCAAGCCTGGATTACAGAGACTTGTCTCTTAAAAAACAAAAACCAACT
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SEQ ID NO: 3323 ACTGATTCACCTTCAGCTCCCAAGTCCAAAGCGGTAAACATCAAAAAAGCGA
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SEQ ID NO: 3324 GGTACCTACATCAGATCTAACCTTGATCCCAAGCAATGGATTCCTCTCTA
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SEQ ID NO: 3325 CGAGGTACTCAGGCCAGCATCCGCCCACTTGATTTTGGAGGATCTCCCTCC
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SEQ ID NO: 3327 ACOCGGGGGOCCTCTGTCTTCTTCCCTGGTGTGGTGGTTAGTTCTGGGACTTG
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SEQ ID NO: 3328 ACOCGGGGAAGTGGAACCAATGCACTTCTGCAAGCCACCTGGGTTGCAAGCTGA
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SEQ ID NO: 3329 CAAGACACTACGGGAACAGTTTGGCTCCCTCCAGCTCAACCCAAATCTTCT
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SEQ ID NO: 3330 ACOCGGGGGGTGGCGGCGAGGCTTTGGCAGCTGGGACTGAGTGCAAGAA
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SEQ ID NO: 3331 GGTACCCCAAGATTACAGAGCTTTGAACAAAGTGAACCTATGGTTACCAAC
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SEQ ID NO: 3337 GGACCGCGGGGACTCCGGCAGCTTATCGCCAGAGTCCCTGAACTCTCGCTT
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[illegible]

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SEQ ID NO: 3343 GGTACTTTTTTTTTTTTTTTTGTATGAAAAAGGCGCTAAACGGCTTCTGAT
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SEQ ID NO: 3346 ACGCGGGGGGGGATGTGGGACCTCAATTCACAGCCCGGCTTCAGCTCTT
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SEQ ID NO: 3351 GGTACTATAGACAGATTGAAATGATGTTGTGACAAATTGTGATGCATATCT
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SEQ ID NO: 3352 ACGGGGGGGGGGAAGAGGGGAACATGGACATGAAGAGGAGGATCCACCTGG
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SEQ ID NO: 3354 ACTGAACTTCCGGAGCAAAGAGACTGTCTGAGGTGATCTTCTCCGTCTCA
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SEQ ID NO: 3356 ACTGTGGAGAAAGTAGAAATATATCCGTCTTTGAGAGTGGACTCAAACTTT
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SEQ ID NO: 3365
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[illegible]

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SEQ ID NO: 3382 TNGCGGGAACCTACGGCAAGCCTGCCATCATGTGTTAAACCAAGCTAAAGTT
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SEQ ID NO: 3384 ACTTTTTTTTTTTTTTTTTTTTTTGGGCAGATTTAAGGGTTTATTTAAAG
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SEQ ID NO: 3385 ACGGGGGGAAACGACAGGGGAAAGGAGGTTCTCACTGAGCACCGTCCCAACA
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SEQ ID NO: 3386 GGTACACTTGAACCAAAATTTCTAAAAATGTTTCTTAAAAATAGTGTG
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SEQ ID NO: 3387 GGTACCTTCTGGGGCATAACAATGGCAGCAGGGGCTCGGGAAGAGGGGTA
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SEQ ID NO: 3390 ACAGTCTATAATACTOCAAACAGTCTCCCATCTGTATTCAATGGCGCCACCCAA
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SEQ ID NO: 3391 GGTACTGGCCCTTCCCGAGAAAAGGGGACTTGCTGCTAAGGGTGAAGGAC
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SEQ ID NO: 3392 TCNNTTACAGTGAATTAATTTGGTGTCTGCTACAGTTTTTCTGAACAC
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SEQ ID NO: 3398 GGTACCGGGGGGAGACAGACTGACGGAGCAGCCAAAGTGTGGAGCAGCT
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SEQ ID NO: 3399 CGAGGTACCGGGGCAAGACCGGCGAGGCGAGACCATCAACGCCACTACT
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SEQ ID NO: 3400 GGTACACGTCTGTCTGGGCTGGGCAAGGTTGCCAGGGCCAGCATGAC
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SEQ ID NO: 3401 GGTACCACTGTGGCTGTCTCTCCACCGGAATGATCCGTGGAATCCAGGCTA
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SEQ ID NO: 3402 ACOCGGGAGGGCGGCAAGGGCAAGGGGAGCGGAGCGGAGGAGCAACAAATTTATC
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SEQ ID NO: 3403 ACOCGGGAGGCGGCAAGGGGAGGCTGTGCTGGGAGGTTTTATACACCTGAAA
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SEQ ID NO: 3405 ACTTTCCTGGAAATAAGTGAAGTCAAAGCCACAGGCTCTCCAGGAAGCTCTG
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SEQ ID NO: 3412 ACGNCGGGGGGATGTGGACCTCCAAATCCCAAGCCCGGCTCAGCTCTTT
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SEQ ID NO: 3413 GGTACTTTCTGCAGAGCTACATTCACCTGCATAGCGCATAAACTCATTOCTGGA
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SEQ ID NO: 3414 ACGCGGGTTTTTGTCCCTGTCTGCTGCAAGCATGCAGGACTTGACTCAGGAA
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SEQ ID NO: 3415 GGTACACCTTGAAGCCAGGTTAATTAATCTGTGTGAGTTTGAAGGGCC
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SEQ ID NO: 3421 GCGTGGCNCNGGCCGACGNCACTCTATAATACTCCAACAGTCTCCGATCTG
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SEQ ID NO: 3422 GGTACGGGGGGACTCGGTCCCGACATGATGGGGAGCATGGGAGTGGTGAAG
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SEQ ID NO: 3423 GGTACGGGGGGGCCAGATATCCACAGTCAAACTGGAGCCAAAAAGGACA
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SEQ ID NO: 3424 CGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTNGGGTTACCAAAACAGCTATTT
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SEQ ID NO: 3425 ACCCGGGGGGAACTGTGGCTGATGGCCCGGGGGCTCTCCAGAACATCATC
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ATCTGGGCTACACTGAGCAACAGGTGTCTCTCTGACTTCAACAGGACACCCACTCTCCACCC
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GGGT

SEQ ID NO: 3426 GGTACTTTTTTTTTTTTTTTTTTTTTTTTGGGAGTTTATTAATATCGGAG
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SEQ ID NO: 3427 ACAGCTACNGCTTCATCAACCTTAGAACGGANTGACTCTGGAGACTGGAGCA
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TATCCCTCN

SEQ ID NO: 3428 GGTACGGGGAGTCAACCGTCAAAGGTGATTTTGACCTAAGCAATTGGAGATGA
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SEQ ID NO: 3429 GGTACAGNCTGTCTCCACCCAGGAACCCCTCTGCCTAATGACAGGACCT
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SEQ ID NO: 3430 TGAAGGTTCTGGGAGCTCTGGAGTTTTCCTCTCTTTCTGGAGCAAGGGAAAG
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SEQ ID NO: 3431 ACCCTTAACCGCTTCTCTCAACCTTAGCAGCAAGTCCGACTTTCTAGGG
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SEQ ID NO: 3432 CGAGGTACAGGACAGATTGGAGATCTTTATCCTATCCCTGAACTAGCTGC
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SEQ ID NO: 3433 ACACGAGAAAGCTCCGAGGATGGCTGAAGTCCAAAGTCTCTGATCGGTGGCT
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SEQ ID NO: 3434 GGTACGCGGGGAGCAGCCCTGAACAGAGAGTTCTTGGAGGCCAAGCTCTCT
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ATCNAAN

SEQ ID NO: 3435 GGTACACTTGAAACCAAAATTTCTAAACCTGTGTTTTCTTAAAAAATAGTTGTT
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SEQ ID NO: 3436 ACGGCGGACTCAGAAAGCTTGGACGCGATCCTAGCGCGGACTCACAAGGC
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SEQ ID NO: 3437 ACGCGGGGCTAAATCTGCTCAATTTTACAGAGGGGAAACCTAGCAAACTAA
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SEQ ID NO: 3438 ACGTGGCCTATTTTAAACTAGTGTAAATCAOCCATGTCATACCAATTCAGTATG
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SEQ ID NO: 3439 ACGGACCATAGAGCAAGAAATCAAGATTCTGCTAACTCTGCACAGCCCGTTC
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SEQ ID NO: 3440 GTTACGCGCGCGCGCGCTGTTGGGAGTTGCTTGGAGGTTGGCGCGCGCGCGCG
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SEQ ID NO: 3441 ACTGTGCANACTCATGTANAAACCAAGTCTGCTAATTCCTGAAAAGTTGCA
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SEQ ID NO: 3442 GGTACGCGGGGAGAAAGCTTGGAGCGCATCTAGCGCGCGGACTCAGCAAGGC
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SEQ ID NO: 3443 GGTACGCGGGGACTCAGAAAGCTTGGAGCGCATCTAGCGCGCGGACTCAGCA
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SEQ ID NO: 3449 CGAGGTACTTGGCCCTTCCCAGAAAAAGGGGACTTCTCTCTAAGGGTGAAG
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SEQ ID NO: 3450 AC0CGGGGGCTGACTCTCTTTTCAGACTCAGCCACTTGCACCCAAGTGAATT
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SEQ ID NO: 3451 AC0CCTTAA0C0CCTCTCCTTCAC0CCTTAGCA0CAA0TCC0CCTTTTCA0GG
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SEQ ID NO: 3452 GGTACACAAATGTTTATTAAGGAATGTATGGCCACATCAACCTAGCAAAG
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SEQ ID NO: 3453 GGTACTGAGACTATTGGAGCTTGTGGCAGCATCCCATGCAACCGTTGTC
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SEQ ID NO: 3454 ACATGGCCTTCTGGAATACATG0CAGATCGGGAATACCTGCCAACTCCTG
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SEQ ID NO: 3455 GGTACAGGGAAGCTGGTTGAAAGAGCTCTTTGTGCTGTAGTAACCTTCTTC
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SEQ ID NO: 3459 GGTACAAGAACATCAAGCTTCACTGTGTGGAGCTGGGTGGCCAGGACAAAGAT
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SEQ ID NO: 3460 ACACAAAGGTGCTGCTCAAGAGCAAGGCCAGGGCGAAGATCCAGGAGTCAT
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SEQ ID NO: 3461 ACACTGGCCCGGCTGTGAAAGCCAGAAATGTGTGTCTGTGTGTCAGCGCTC
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SEQ ID NO: 3463 GGTACTTTTTTTTTTTTTTTTTTTTTTTTATAGGNTTTTTTATGAAAA
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SEQ ID NO: 3464 AAGCGGCGCAGAGAGAGGCCATCACCTGCAATGGCAGGAAAAATCAAGTGT
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SEQ ID NO: 3465 ACAGCTTGTCCAGTTACTCTGGAGAGGCTGTCCAGAGCTGTGATGAAATG
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SEQ ID NO: 3472 GGTACAAGACCAGCAAAAGCCAGCTTCTGGCTGTGAGCTCTGAGAACTGG
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SEQ ID NO: 3473 ACBCGGATGGATGTTGTTTCAAGTTAAGCTACGGCAATCTGAACTCTCGT
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SEQ ID NO: 3474 GGTACGCGGGGGGTCCGCTGTGCTTCTATGCTAATACCATGAGCTCCCTC
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SEQ ID NO: 3487 ACTTTNTTTTTTTTTTTTTTTTTTTTTTAAAAAATAAAAAATGATTTTTATTAGTT
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SEQ ID NO: 3488 ACTTTTTTTTTTTTTTTTTTTTTTGGATAACTCAGTTTCAGATAAACCATCTTGG
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SEQ ID NO: 3489 ACGCGGGGGAGGCGAGCCATGTCTTATCCCGCTGATGATTATGAGTCTGAGGC
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TNAT

SEQ ID NO: 3490 ACCGACCATAGAGCAAGAATCAAGATTCTGCTAACTCCTGCACAGNCCCGTC
CTCTTCCTTTCTGCTAGCCTGGCTAAATCTGCTCATTATTTAGAGGGGAAACCTAGCAAACTAAN
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TCTCTGGCTGTCTCGAGCAGTCTAGAAGAGTGCTCTCCAGCCTATGAAACAGCTTGGGGTCTTT
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SEQ ID NO: 3491 ACACTTGAAACCAAAATTTCTAAACCTGTTTTTCTTAAAAAATAGTTGTTGTA
ACATTAACCATAACTAATCAGTGTGTTCACTATGCTTCCACACTAGCCAGTCTTCTCACACTTCT
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AGCTTCTTCATATGTCTGAGTCCAAATCCCCGCGTTACCTCGGCCGCGCCACCCCTAAGGGGGA

SEQ ID NO: 3492 ACTTTTCTTTATTATTACTTTTNTTTTCTGCAAGTCANTAAAAGGATTTAAG
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SEQ ID NO: 3493 ACTTTGTAGGCTATACGTTTTAAACTCCTGTAAAGAACATTACAAGCTATTTT
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CGGGAAA

SEQ ID NO: 3494 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTGNGTAAAAACAAAAATTCCT
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ATCTATTTTTTTTAAAGTCTCAACTTCCAAAAATCANTAATCCTTTCTGTAAANTCAGGATTGTAA
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CTTG

SEQ ID NO: 3495 ACCATTTGGAAGAATGGAAGCTGATGCATCTGTTGACATGTTTTCCAAAGTCC
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SEQ ID NO: 3496 ACCTCTCAAATTGCTCATCAATATAGGAGATAATTGTCTTAAAAACAATCTCTG
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SEQ ID NO: 3497 ACCTTAACATCTGTTGAGAAAAATACAAATAAATATGATGCTAATAAATGGCC
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SEQ ID NO: 3498 ACACTTGAAACCAAATTTCTAAAAACATGTTTTTCTTAAAAAATAGTTGTTGTA
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SEQ ID NO: 3499 ACTTTTTNTTTTTTTTTTTTTNTNTTTTTTTTTTAAAAANTTGCANATCTTTAATA
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SEQ ID NO: 3500 ACCCCCATGCAATATATGGCTCTACAATCCTCANCATGTTAATCGAANCCTTG
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SEQ ID NO: 3501 ACAAATATCCATTGCTTCATAGGTTCAAGTTACATAAAATTAAGTCAAATAAT
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SEQ ID NO: 3502 ACTCCAGCCTAAGCAGTAATTCTCTAAGTTTCGCAAAAACTCCTTCTTTGG
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SEQ ID NO: 3503 GTACACTTGAAACCAAATTTCTAAAAACATGTTTTTCTTAAAAATANTTGTGT
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SEQ ID NO: 3504 GTACAACGCTTCAGCCTACTGCAAAATCCAAACACAGGTTTGGTGGAAGATT
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SEQ ID NO: 3505 ACTGGAAGCATGCTCCAAAGACCTGTAAGAACTTTGCTGAGTTGGCTCGTCG
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SEQ ID NO: 3506 ACCATAATAAGTTTGTAGTAGTATAGGCTAGGCTTAAAACTGCACCTCCTCTG
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SEQ ID NO: 3507 ACGCGGGGAAAAACAGAGTAGCAGCTCAGACTGCCAGAGATCGAAAGAAGG
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SEQ ID NO: 3508 GTACTCGGGACTGTGTAGGAATGATGGAAACCAATCAGGGAGAGTTTCTT
TGGCAATTTCACTTCTGCANAGAAAGATTCCGGGACAGATTCTCANCANCGAGATGGCTGTCTTT
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SEQ ID NO: 3509 ACTCATGTATTTTTTTCCAGATCTCTTTCCCAAGTTGCTATTGTAAGAGTAT
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SEQ ID NO: 3510 ACGCGGGGACATGTGTATGTGCCAGCTCACACCTAGGGGCGGGCTGCCTCTC
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SEQ ID NO: 3511 GGACGCGGTGAATACATTTCTACTTTATTTTGAACATTTGCCAAACTAAAT
ACTGTAACACTGTATAACATTTAAAAATGTTAAAGAACTGCTTAGTATTAGAAGCAGATCATTTCC
CAAAATCTAAGAGCAGCAGCATATGTTGTTGCTTGTATAAAGCCTAGCGATAATTTTLAGACTAA
CTTCCATGGTGCCTGTTGGCATTAGCACTACCATTTG

SEQ ID NO: 3512 ACGCGGGTGAATACATTTCTACTTTATTTTGAACATTTGCCAAACTAAATAC
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SEQ ID NO: 3513 ACATTTACATTCAAGTTGATAACACCGGTGGTTTTCAATTTCAATACAAATTATG
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GGTGATATTTGCGTCAAAACACNNATAGNACGANACNAGCNAACTACAATNACNAAGATNTCNNA
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SEQ ID NO: 3514 ACCACAAAGGAGAAGTTGATAGGGAATCTAATTTTAGAATGTGCCAAATGGT
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SEQ ID NO: 3515 ACGGATCACGCTTTCCCAGGATGACCTCTGCCAGTATATCACATCAGATGA
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SEQ ID NO: 3516 GNGTACGCGGGGACGCGCGGGGGCATTGCTATTGCGCGGCTAGAGGTGAA
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SEQ ID NO: 3517 GTACTGCAGCATGCACTGGCATACTATAGCTTGGTCCAGCTCTTCCANAGCCC
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CTGCCTGGCAG

SEQ ID NO: 3518 ACGCGGGATAACCATGCACACTACTATAACCACCCTAACCCCTAACCCTA
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SEQ ID NO: 3519 ACTGGCGTGGATTCTGCATAATGGTGATCACACGTTCCACCTCATCTCAGTG
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CNNATTCACTTATNAANAAATACCAGCTTATCTTGATGATCGATATCCATATAAGTAAAAATAA

AAT

SEQ ID NO: 3520 ACGAGATCCTTATGGAAATCGTCCCTTATGCATTGGTCGTCTTATCCAGTGT
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SEQ ID NO: 3521 ACCTGAAGCTCAGGAGGAGATGAAAGAAGTAGCCAAACACCCAAAGAATCC
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SEQ ID NO: 3522 ACGCGGGGAGATGGCAGATGAGATTGCCAAGGCTCAGGTGCTCGGCCTGG
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SEQ ID NO: 3523 ACTTTTTTTTTTTTTTTTTTTTTTTTAACTANATTTTTGAACTTTTTATTTAT
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TTTTATGCAAGTGCATTCAATTGTAAACTATAAAATAACATTTGTATTTAAAAANAAGCTGGGAATAC
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SEQ ID NO: 3524 ACTTTTTTTTTTTTTTTTTTTTTTTTGGATAAATACATGCTGATTTATTACA
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TTNTCTGGCANTNCTCAACTTTTGCTGGNCCTCTTGCTGGNNCAAACACACCGGGACCCACCAN
GATT

SEQ ID NO: 3525 ACAAAATGTAGATCTATTTATTTAGCACTTTGTTCACTCAGATAAAATTTATAT
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CCAAACANATTTGCAGATCAAGGANACCCAGGAGTTCAAAAAACNCTAGTAAGNNTTTGANACCT
TGCNCTCTACATCTCAGGGTAGGAAGAAAAGGNTTCCAAACATGCGGTGNTCNATTGTTGACT
CCTGCCAAAACAGGATNCTGG

SEQ ID NO: 3526 ACGCGGGGGCTTTCCACTATGGCTTCCAGCACTGTCCCGGTGAGCGCTGCTG
GCTCGGCTAATGAAACTCCCGAAATACCGGACAACGTGGGAGATTGGCTTCGGGGCGTCTACCGC
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TAGACAAATGGAATCCTGTGCTGAACCCGAATCTTCCAAAAAACAGCCTACAATCTGTGACCACC
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TCCTTTTGTTCTTGATCCACGCANAAATTCATTCTCTGGTCACAACAGGCTAACTAAAGNTTGCTCTA
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TGAAAAATTTANT

SEQ ID NO: 3527 ACAATTACCCACCACTGGATTGACTCAGAGAGGACCCCCAGAGGGTGTCTC
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ACCCGCGT

SEQ ID NO: 3528 ACGATAATCCACACCATATCTTGGATTCTTGGAAATTGACTCAACTCTCCA
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SEQ ID NO: 3529 ACTTTTTTTTTTTTTTTTTTTTTTACCACATATTTATTAAGACAATCATTTAT
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SEQ ID NO: 3530 ACTCTCTCAGCTCAGGTCTCTTAGCTTTTAGTGTGGTGTGACGCAAGTCATTTT
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TAGTTAGTCTACT

SEQ ID NO: 3531 ACTGCTTGTCTCTGTGGAGGAGATGATTAATAAATAAAAAATCCAGAAAGGACA
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ACATCAAGGAATGGGTCTGCCCGGCGGCCGTCAAANGGCN

SEQ ID NO: 3532 ACTTGAAGTGGAGGGCAAGAAGTGGAGAGTGGAAAAATCAGGAAAATGTTTN
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SEQ ID NO: 3533 ACTTAGCATTGATCAAAGAAATTTCAAATTACGATCAATTGGGTGGGGAGAA
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SEQ ID NO: 3534 ACATGTTTACAATACCAAAAAAGAAAAATCCACAAAAGCCACTTTATTTTAA
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SEQ ID NO: 3535 ACGCGGGGTGTATNATGCCTGTTACTANTATTCACATGGAACAAATTGCTGCC
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TGAGATAATTTGAATGAAAGTTTCTCTTATGCTTCTGGTCTTTCCAANCTATACAAGAGATAG
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SEQ ID NO: 3537 ACACTTGAAACCAAATTTCTAAAACCATGTTTTCTTAAAAAATAGTTGTTGTA
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SEQ ID NO: 3538 ACACTTCTCGAAATCTAATTGGGGGCGCTGACATCATTGTGATCAAATACAA
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SEQ ID NO: 3539 ACCATGGAGAAGGAGTCGAAAACCAACCCGATTCTGTCTTATCTGTAACTATG
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SEQ ID NO: 3540 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTCGATTTTTANAAAAATCAAATAATCTT
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GTATATTA

SEQ ID NO: 3541 ACAGACAAAACAAAATCTGCCTTAGGCTGTGTGATAAACCTATCATACCTCC
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AGATTGATGGTCTGACAAGTCTTCAATGACTCACTGGACAGTCTCTGCTGAAAGTCTGCTCTCATA
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TTNCATCCACT

SEQ ID NO: 3542 ACATTTTCATGACTGGGGAATGGATTTTCTGAAGTCATCTTCAATAGGGCAAA
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TACAAGCGNNGGGTGTTCANACCCAGGCANCGGNNNTACTGNNTTGGGCTTACCTCCATCTT
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SEQ ID NO: 3543 ACGCGGGGAGAAAGCTTGGACCGCATCCTANCCGCCGACTCACACAAGGCAG
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AGCT

SEQ ID NO: 3544 ACGCGGGGGTCTGGAGCTGCCTGAGGATGAGGAGGAGAAGAAGAAGATGGA
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SEQ ID NO: 3545 ACATAATCGTTTTGTGGAGTCGGCACAGTTTCAGGTTATGGAGGCACGTAATTC
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CATGGTAATGATACTCCCGTTAGGACCTTAGGGATGAACCAAGGCCCAAGATCCGACNANCCC
ANACCGCTCTCCATGAGAGCCAGTGAGGGCGTGATCCCNCTGNCCCCGCTGACGCCCCCGNTCTGC
CGGCGGCG

SEQ ID NO: 3546 ACAGATTGCCTATTTGAGGACCTTGCCGCTCTGTAAGCATCTGACTCATCTC
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SEQ ID NO: 3547 ACGCGGGGTTGAGGCTTTGCAATTTCACTTGTTAAAGGCTCTGGCATTTTT
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SEQ ID NO: 3548 ACAGCCTTGTGGCCAGCCTTGACAACGTTAGGAATCTCTCCACTATCTTGAAA
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CCCTGGACTTGATTTCTGCAGACCAATGTATTAATAAAATTATTTCTGCAGTCAGANGGGCTCCGTG
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ACTTTGGAATGCAGAGTTCCACTN

SEQ ID NO: 3549 ACGCGGGGACTGCGATAGAAATCATGTCTGGTCGCGGCAAAGGCGGAAAAG
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SEQ ID NO: 3550 ACGCGGGGACTCAGAAGCTTGGACCGCATCCTAGCCGCGGACTCACACAAGG
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SEQ ID NO: 3551 ACCACAGTTCACAAGTGCAGGAGAGAATTTTGATAAATTGTTAGCTGGAAAAG
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SEQ ID NO: 3552 ACCCTTTGGATTTCAAAACAGTAACATCGGATGTAAACAACTTAGTTCCTTTT
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SEQ ID NO: 3553 ACTTCAGACAGGATCCCAACCCCAACCAAAATCAATGTCGACCGTCTGAGC
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SEQ ID NO: 3556 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTCAAAAATAACAAAAAATATTTTACTAAAA
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AACTA

SEQ ID NO: 3557 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTCGACACCTGCCCTTATTGGTCTCTTCT
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SEQ ID NO: 3558 ACAGCCTGTCTCCACCCAGGAACACCCCTCTGCCTAATGACAGGACCTTCCT
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SEQ ID NO: 3559 ACGCGGGCTCATTTTAAAAATTGGTGCTTTCCACAACATGCATCGAGACCATCT
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TCAT

SEQ ID NO: 3560 ACAGTCATTAGATAGCCGGAGTGTAAGTGAAATCAATTCAGATGATGAATTG
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SEQ ID NO: 3561 ACAATGTTGAACAAAAGACCACAGGGGGACCTTTTGTTCAAAGTAGCACCAA
TCCACACCTGATTGTGTTTCCAACATTAACCTTCCTGTTGACTCTATCAATTGGCACTTTGAATGGAA
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SEQ ID NO: 3562 ACACTGAAACATAAATCCGCAAGTCACCACACATACAACACCCGGCAGGAA
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SEQ ID NO: 3563 ACATGACAAGGTGCGGCTCCCTAGGCCCTCCCTCTTCAAGGGGTCTACAT
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SEQ ID NO: 3564 ACTTTTTTTTTTTTTTTTTTTTTTTTTTCTAGGANAATTTANCTGTTCTTTATTGA
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SEQ ID NO: 3565 ACCATAAGGAGACACAAGAAGAAAGGTGACACTAAGGCTACAGTGACACAGA
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CAAAAAGGGAGTATTTAAAGGAAACTCAAATCAGGAGAACCCGGTAGGCATCAGAGGTTCAAGGG
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SEQ ID NO: 3566 ACAGTCTATAATACTCCAACAGTCTCCCATCTGTATTCAATGGCGCCACCCAA
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TGGCA

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CTTNACCCCGANG

SEQ ID NO: 3568 ACCCACCACCATGCCTGGCTAATTTTTTGTATTTTAGTAGAGACAAGGCTTC
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TGTCAT

SEQ ID NO: 3569 ACGCGGGGACAACATGAAGAAAGCTCTCAAGTTGCTGAAGACTGAATTGTAA
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SEQ ID NO: 3570 ACGCGGGGATCCCGGAGTTGGAAAAACAATGAAAAGGCCCCCAAGGTAGTTA
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SEQ ID NO: 3571 ACAGGCTGAACAGAATTGAGAATGCCTTGAAGACAATAGAAAGTGCCAACC
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SEQ ID NO: 3572 ACTTCTCAGAGGTATTTGCAGCTTGATGCAAGTAGTCTCTAATGAGTAGGCA
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CACCA

SEQ ID NO: 3573 ACAAACATATGCATATCATAACTACCAGCTTCATGAGGTCAAGACTAAATCAA
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SEQ ID NO: 3574 ACGCGGGGCGGCCAAGGTGCCGGCCGACACCGAGGTGGTTTGTGCTCCCCCT
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SEQ ID NO: 3575 ACTGAACACTGTAGGAAATGTAAACAAAATGTAAAGTATTTATGAGTCTAAA
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SEQ ID NO: 3576 ACTTGCCATGAAAATGCCCTGGGGACCCCTCTGACGACACTGTTGGGATGGCT
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SEQ ID NO: 3577 ACGCGGGACACTTCTGCTGGGATCCGAGTGAGGCGACGGGGTAGGGGTGG
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SEQ ID NO: 3578 ACGCGGGGTCCCATGGCTGGCCAGAGGAGGAACGCTTTGTGTTCTCATCGGA
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AANC

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SEQ ID NO: 3588 GTACTTTTAAATCATGTTCCCCCTAAACATGGCTGTTAACCCACTGCATGCA
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SEQ ID NO: 3589 ACGGGGCAGGATTATGTTTGTGACCCATCTCTGACAGTTAGAGCCGATATCA
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SEQ ID NO: 3594 ACAAAGATAATCAATGCTGATTTCGGAGGACCCAAAATACATTATCAACGTAA
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SEQ ID NO: 3596 ACAGCTACTATCCAGCCCAGTCAACAAGCCCAGATTGTCACTCGGTCACTGT
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SEQ ID NO: 3597 ACGCGGGGAGCAGCAGGAGGAGGCAGAGCACAGCATCGTCGGGACCAGACT
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SEQ ID NO: 3598 GTACCGACCATAGAGCAAGAATCAAGATTCTGCTAACTCCTGCACAGCCCCG
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SEQ ID NO: 3599 ACCGTTTTTTCAGGCACAAGGAAGGTTTCACCCCGTTGCCGAAAGACTAAGC
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SEQ ID NO: 3600 ACGCGGGCGGGAAGGGCCTGTCCAGTCGGCTTTACCTATCGACGCAGCGT
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SEQ ID NO: 3602 ACTGTGTCTCAGCTCCAGCAGTCTCAACTGGGAAGACCCAGGACTCCTGCTCT
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SEQ ID NO: 3604 ACTTTTTTTTTTTTTTTTTTTTTTTGGGTTTATTTTTATTAAGCACTACATAACAC
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SEQ ID NO: 3605 ACGCGGGGGGGCTTGACGTCTGCAGAGCAGGGAGCACAAACCTGCTCTCTC
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SEQ ID NO: 3607 ACCGCTGTGTCGGGTGGGTGGTTCAGAATGCCGTGCTCCAGGTGTTTCACAGC
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SEQ ID NO: 3617 ACTTTTTTTTTTTTTTTTTTTTTTTTTTAGCANATTTTAAGGGTTTTATTTAA
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TNAAAAATGAANTTGGGAGAAACNACCCTTCCGAAAGGCGCATTNCTCGGGGTGNTGCCCGGG
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SEQ ID NO: 3618 ACACAAGATGGTGGCCTTGGCGGTTACTCTTCCAACCACTTCCACAATTCCAG
AGATTTCTTCATCAAGGGGTCCATCAACTCGATGGTCCATTTTTCTTCTCCATCTGAAAGAAT
AAACATTTTTCCGGTGGGATGAATCTTTCCAGCCTCCCTACGAAGCANACAGGCTTGTGATGAA
TTGAGCTAGCATGCCGGCGTTGATGCGCGACCTGGGCAAGTCCATCATGTACCATGATTATGGTC
CAAAGACTCCCCGCGTCAACATCTACAATGTTGGCTCAAGTGTGCTGATTANACGTGGAACATCTG
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GAATCTTGCTTACGGNATTTTAANGGTAATTTCTTTTNTGAATGG

SEQ ID NO: 3619 CGCGGCGAGGTACTGGAGATGTATTTGATAACCAAGGTTTTAGGTAAATTTTC
ACCAGTATTAGTTCTATTTGCAAACTGAAAAATGTTGTAGGCTTAATGTAAAAATAACCACATTAGT
GAACATTATATCTCTTAGAAGAAAGGCCATATTTGCTCCTGCTTCTGTAAAAATATTATTTGTTTG
AAGGGGAAATAATGGTANNTGTGACCTTTCACCTAATTCCTACTCCCTTAATGTGAGAGAGACAA
ATTGAGCTGAAGAAGGAAAAATCTGGANTTACACTCCACAACCTTGAACATACTGACGGACATCT
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SEQ ID NO: 3620 CGCGGCGAGGACGCGGGGAGAGAAAGTTTGTGATGCAGGAGGAGTTCTCGCGT
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GTCTGAACCTATCCCANAGAGCAATGATGGGCCGTGGAAGGTAAGTGATGACAGANAATTTTGN
ANATATTGAATTATGANAATAAANATGTGCTGATTGAATTTTATGCCCTAGGTGTGGTCATTGTA
ANAACCTGGANCCATTATAAAGAACTTGNCGAGAANNTCAGCNAAAGACCCAANTATNGTNAT
AGCCAAGATGGATGCCNCANTCAATGATNTGCCCTCTCCAT

SEQ ID NO: 3621 ACCAAGGCTTTAACGTGTCTGTGCAGGGTATTATCATCTACCGAGCCGCCTAC
TTCGGTATCTATGACACTGCAAAGGGAATGCTTCCGGATCCCAAGAACAATCACATCGTCATCAGC
TGGATGATCGCACAGACTGTCACTGCTGTTGCCGGGTTGACTTCTATCCATTTGACACCGTTTCGC
CGCCGCATGATGATGCAGTCAGGGCCGCAAAGGAACTGACATCATGTACAAGGTGGGAGGAGAA
TATGCCTCATTCACTCAATCAATTTCTTGGCCTTGAAGAAGCGTCGAGGTANAAGACCTGCC
AGGTAGCTAGTCCAATGAGACAGAACATTGAANAGATGCTGAAGTATAGGACCCGAGTGTGTTGTT
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ANGGCTTNNAGCGTNNAANTCTACCTTAATGGNNTANCTTTCAAATTTNGGAATNTNNNAATTT
ACNCCCCCTCCTGCTTAGTTAGGAACNAAAT

SEQ ID NO: 3622 ACAATCTATCGACAAAACAACTCCAAAAGAAGGTGTGAAAGTTAACAAGG
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AATAC

SEQ ID NO: 3623 ACGCGGGGAGTGAGGAGGAACGCGAAAAAGGTAACGCCACTCATGGTCAAAG
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CGCCNTCATTTGGNGATGTGNTGGTGTTAACNATACCTNTANGAACCAATTTNTNCAAATGNCC
TCATTNGCTGGNTTAATCCTTGAAAGANGTAATAANNTTTTNTATGGGTNNTCTACNTACANANT
NGGTAAC

SEQ ID NO: 3624 ACAAAAACCCAAATTGATAAATCTGCAAAATCTTAAACTTCTTAATCCATTGA
TAAATATTAAGGAGTAGCTGGTCTTCAAACACCGTAAAAAGTTAAAGGGTTGAAAACATGTTAC
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CAAGAAGGTATATATATGCAATTCTNAANANAGCTTANAANGTTACAGTTNACTTCTATTCAGNATT
GGTAAAGTTGACTANGGATGGCT

SEQ ID NO: 3625 CGCGGCGGGTACAGATCTCACAGGGACACTCCTTATCCCTTGACAGAGTTCCA
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GTGTCCAGCAGAGCTTCCACTGCCCTGTAGGCTGCAGGCAGCTGCTCAGTTGAGAGATACACTG
AGCTTCCTAAAGAATTCCATTTTAAAGTTTAAAGCTATGAGCATAGATGGAAGAGGTGGCTGTGTAT
TGGATCAAGGATATGAGCAGAGATGGATGAGGCAGCGGCTGTAATGGATTAAGGCTATGAGCATC
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SEQ ID NO: 3626 ACGCGGGGAGGACAGCATTTTCATATGTAACCATTTGAATGTTTTGCTGTTT
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TGGGTCTCGAGGGTCAATGGCTGTCCCTGGTCAGTCTGTCTGACTGCCTNANGGCCTACCTCTCT
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GATTA

SEQ ID NO: 3627 ACAAATAAAATCAAAAAGAGCAGTGTTCTGTTGTATTCTATTTCTGCATGTATA
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NTNGGTCGACTTATTTATCACACANCCGTGAATATGCAATGTTCTGAAAAAAGGGACCTTTNTG
CCCACGTTATTTTANAA

SEQ ID NO: 3628 ACGAGACATGTCATGCTGCCCAAGGACATAGCCAAGCTGGTCCCTAAAAACC
ATCTGATGTCTGAATCTGAATGGAGGAATCTTGGCGTTCAGCANAGTCAGGGATGGGNCCATTAT
ATGATCCATGANCCATAACCTCACATCTNGCTGTTCCGGCNCCTACNCAAGATNCCAANGAA
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CTGATAACATTATTATTATCCCTTCTGTNTNTTACTTTNGATATTTAAAAAGATGTA

SEQ ID NO: 3629 ACCACAGTTCACAAGTGCAGGAGAGAATTTTGATAAATTGTTAGCTGGAAAG
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TTCCAAAGNCTG

SEQ ID NO: 3630 ACAGATACTTATGAGGCCAGCTGGTCTTTAATTATGTGGGTCCGAAGCAAATT
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TGTAGNTGGATCACCCCGNTGGTGGCTANGATGTCTTTTGGAGATGATCNCCTTCCCTTGAT

SEQ ID NO: 3631 ACGCGGGGAAGTATGGAATAAACTACTGATGCAGTGAANACAGTTGAAAA
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AGGACATCAAAGAAAGTCANGCAAAAACCTCATCTTGACCCCTGTTGCATGCTAAGGAACNCAGCTTG
GAAGAAAAAGATGATATANCAGTTAACAGCGNTGCATACNTGGNAGANGNTTNCNTAATNATCTNN
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SEQ ID NO: 3632 ACCTTTCCTTTTCCAAATCTAGCTGAAATTTCTCACTTGTTTTCTTTTGATGA
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GAGAACATCTCCTCAGAATGTCATAGGCTGCTTTATCTCCTCTAGGGGAGCTGGTCTCTGGGCTAGN
GCTCTGACATCNAANTGGATCCA

SEQ ID NO: 3633 GGGTACCAAAGTACCAATGGGCTGCAAGAGGTTTAGATTATTGCTACCCAC
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TNCATCAAGTAATNCTCAGGAACCCAAGTANCTTNTCNTTGTCTTTATCCTTCATGAAATAATTTA
ACCATTCTTCNACNTANATNTGNTTTTTGCTNAAAGCCAT

SEQ ID NO: 3634 GGGTACAGGCGGCAACTTCCAGAGCTTCCCCTCAGTGCTTGGTGACTGGCAC
AGACACGATGCCATTTGCTCATGTTCCCCTAATACAGACTGGTAGAGCTGTGGTGGATCCATTGTC
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TNGAAATNAAATGANTTCCAAAGNTAACCTATTATGAANTATAAATTTTTTCTTGG

SEQ ID NO: 3636 AGCGGCGAGGTACCTGCAGGCCTCTACACCTACCTCTCTCTGGGCTTCTATT
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SEQ ID NO: 3637 ACGCGGGTATTACAGAGTGATAGTTTGTGGCTTGTAANAATTCTATGCTCCATGG
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CAAAGTTTGGTGCAGTTGATGCAGATNAGCATCATTCCCTAGGAGGTCATTATGGTGTTCAGGGAT
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GNCGAAACCTNTGTNGATGCTGCTCTGAATTGCTTN

SEQ ID NO: 3638 ACTTTTTCTTTGAAGTTTGTAGCGGTCAATTTGCCTTTTTAATGAACATGTGAAG
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NGGCNAAATTCCAAGACATTG

SEQ ID NO: 3639 GCGGCGAGGTACGCGGGGGCTGTGCGCGGTGGACTCGTGGAGCCGCGGGC
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TGGCGG

SEQ ID NO: 3640 CGGTACCCATGCACAGCAGCTGTGGGGTGTGGGCATCTTCAGGTGGTGTCT
GGTAAAAATCGTTAGAATAGCTGTATGAAGGAAACCAGTGGGAGGAAATGAAGTTTTCAAGGATGGT
GGGATGTGATTTAGACAGTGCACATGCTGTTATGGCTGTCACTAGGGAGTGGCCTTNATGGAGGG
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SEQ ID NO: 3641 TTACACATTGCCTCACTTTATATTTTAAATGAGAATCTTGTTTATTGTATTTGA
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CTTTGAAGAATGGGAAGAAATTACGTGAACGGTCTTNATATCACCTCTGGGAANCAGGTTATATT
GTNACGGACNCTTTCAATCTAGAATAAAGCAGGANTAAGTTGCTAACAGTNTATACCCTGTGGCA
NATTGATTTTTGTAGCATAT

SEQ ID NO: 3642 ACACTTGAAACCAAATTTCTAAAACTGTTTTCTTAAAAAATAGTTGTTGA
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TCTGGTTTCAAGTCTCAAGGCCTGACAGACAGAAAGGGCTTGGAGATTTTTTTCTTTACAATTGAG
TCTTCAGCAACTTGAGAGCTTTCTTCATGTTGTCAAGCAACAGAGCTGTATCTGCAGGTTCGTAAG
CATAGAGACGATTTGAATTTNTTCCAGNNGATATCGGGCTCTAAGTGTGAGAGATGGGTCAACAT
AACATAATCCTGGGGACATACTGGCCNTCATGAGAAATGTGTTTGTGAGATGTTTCATAAACCAGA
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SEQ ID NO: 3643 ACGCGGGGGCTGACTCTCTTTTCGGACTCAGCCCGCTGCACCCAGGTGAAA
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CCCTGAGAAAAAGATCCACCTACGACCTCNTGTNCTNATACCGACNANCCCNINANNCATNTTNAC
CATTATCAAATCATGGNANCAACCTNTTTTACTCATNTNCTNNAACNTACCTCACTATCCCTNAAC
CACTTTCTCCTTTAAATCTTGGCACTACNCATTTAATCT

SEQ ID NO: 3644 ACAAATAAAATCAAAAAGGGCAGTGTTCTGTTGTATTCAATTTCTGCATGTATA
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SEQ ID NO: 3645 ACACATCTTATAGCTGAACGCCTATGTAAGAGTGAAAAATTTTATGACAGCTTG
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SEQ ID NO: 3646 ACTGTAAAAGTTCTGACACAAGACAGTGGCAGTGGTTACTTTTCATCGACTTT
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SEQ ID NO: 3647 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTACCTCAGTCTTTTANACTCTCAGCTG
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SEQ ID NO: 3649 ACACTGTTGGAGAGATGAGACAGTCACACCAGCTGCCCTAGTGGGGCTCTT
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GCCCTTNTC

SEQ ID NO: 3650 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGCCCTTATATCAGTTTTATTGGTGGGTTT
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SEQ ID NO: 3651 ACAGCATAAAGTCTACTTTCCTCTTGAAGAAACCATAAGCTACCAGCTGTTGG
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CCGGCCTNNGCTGA

SEQ ID NO: 3652 ACGCGGGGGTTGTGAGTTTGTGGACCTGGAACAATTTAACCAGCAACTTTCC
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SEQ ID NO: 3653 ACGCGGGGAGCGGTAGCTGGTCTGGCGAGGTTTTATACACCTGAAAGAAGAG
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SEQ ID NO: 3654 ACGCGGGAACGAATAGAATCGAATGGAACAATCATCGAATGGACTCAAATG
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SEQ ID NO: 3656 ACGCGGGGGACACAAAGGACTCTCGACCCAACTGCCCCAGACCTCTCCAG
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SEQ ID NO: 3664 ACAAATATCCCCACTTCCCTTGAGAAAGAGTATATCTAAAATACACTTTGAT
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SEQ ID NO: 3667 CGTNCGCGGGGACGCTGAGGGGTCCGAGGAGACCGTGAGGCTNTGGCCTG
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SEQ ID NO: 3669 ACTCTTGATGAAAGACCGTGAAACCAACAAATCAAGAGGATTTGCTTTTGTG
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ATCACTTTTG

SEQ ID NO: 3674 ACACTTGAAACCAAATTTCTAAAACCTGTTTTTCTTAAAAAATAGTTGTTGTA
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SEQ ID NO: 3681 ACCCAAACCTCCAATCCCCAACGCGGTCTCAAGTTCAGACTGGGCTCCAGC
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SEQ ID NO: 3682 ACGCGGGGGTGATTGAGAGAGGGGTTAGAGGCGGGTCCCAGCGCTGCCGCA
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SEQ ID NO: 3683 ACTATCTAGTGTCTAAAACATTATTCTCCAGAAAAATCAATCATTTTCTAGCC
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SEQ ID NO: 3684 ACNCGGGGTTNTGAAGCACTTTTTACCAACGGNCAGTTTTTACATTTTANANC
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SEQ ID NO: 3685 ACGCGGGGGGAAAACCTCTGAGGACATGAATAGTCGCCAGGCTTGGCGGCTCT
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SEQ ID NO: 3686 ACCNTNNGCNNAACANAAAAAGCGTNTGATNATAAACTACATCAACACGGT
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CNAAG

SEQ ID NO: 3687 ACGCGGGGGACGCTGAGGGGCCCCGAGGAGACCGTGAGGCTCTGGCCTGCAG
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SEQ ID NO: 3694 ACCATGATCCTGACCAATTTGACGGCGCTGCACAGGGACCCCCACAGAGTGGG
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SEQ ID NO: 3696 ACGCGGGGGTCAGACCCAGTCAGGACACAGCATGGACATGAGGGTCCCCGC
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SEQ ID NO: 3697 ACACTTGAAACCAAAATTTCTAAAACCTTGTTTTCTTAAAAAATAGTTGTTGTA
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SEQ ID NO: 3698 ACTTTTTTTTTTTTTTTTTTTTTTTNGCTTACCATTGCTTATTAATCTTCTCC
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SEQ ID NO: 3699 ACTAATTGAACCGATGTTGACAGTTGTGGTTCTGAATTCACCAAGTTCTCTTC
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TTT

SEQ ID NO: 3700 ACGCGGGGGGCTTCCTCCTCCTGAGCAGTCAGCCCGCGCGCCGGCCGGCTCC
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SEQ ID NO: 3701 ACGCGGGTCAGCATTCTTGCTCCTTGCGCCCTCTCCTACACTCTGGCCAGAG
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SEQ ID NO: 3702 ACGCGGGGGCCAAACTTGACCGCGCTTCTGCTGTAACGAGCGGGCTCGGAG
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SEQ ID NO: 3703 ACAAAGCATTCTGCTTCCAAGAGAAATATCATTGCTACAAAAAACTGGCAC
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SEQ ID NO: 3704 ACGCGGGGACATATCCACTCCTGCTCTCCCTCCTGCAGGTGACCCAGCCATG
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SEQ ID NO: 3705 ACGCACCTGGGNTNAAAAATGCAGGCGATTCTGAGGACGCCATCCCTGAGGA
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SEQ ID NO: 3706 ACCTGTATTGGGGAAACATAGCATACAAGCAAGAAGCTTACAGCCTCAGTGG
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SEQ ID NO: 3707 ACGCACCTGGGGTCCAAATGCAGGCGATTCTGAGGACGCCATCCCTGAGGA
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SEQ ID NO: 3708 ACGCGGGGGGAGCCAGGGCCGGAAGTAGAGCGGAGGTGGTGGCGGCGGAGG
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SEQ ID NO: 3709 ACTTTTTCTTTGAAGTTTTAGCGGTCAATTTGCCTTTTTAATGAACATGTGAAG
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SEQ ID NO: 3710 ACCGACCATAGAGCAAGAATCAAGATTCTGCTAACTCCTGCACAGCCCCGTC
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SEQ ID NO: 3711 ACCCAAGGGGGTGAGGATGGCATTGTGGGCGATCAGCTCCCATCTTCCCTCT
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SEQ ID NO: 3712 ACTTGCTGGTCTCAAATTTCCACAAGGAGATATCAATGGTGATACCACGTTC
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SEQ ID NO: 3713 ACACAATGTGCTTCCTTGTGTATTATAACACATTTCAAATAGGGACCTTTG
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SEQ ID NO: 3714 ACATTTACCCTGATCATAAAAGAGGGACAAGGGAGCACTGGGCTCTACTGG
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SEQ ID NO: 3715 ACGCGGGGACTGCGGGCTGGTCCGGGCTCCTCAGGTTTCAGACCCGACCGTTA
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SEQ ID NO: 3716 ACGCGGGGGATGCTGCGCCTCTCCGAACGCAACATGAAGGTGCTCCTTGCCG
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SEQ ID NO: 3717 ACCCTTGGAAGATGGGAAAGGTGAGGGAAATATTTGAAGCAGGGTCAGAAC
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SEQ ID NO: 3718 ACAGAAAGTAAAAATGCTGTTACAATCTCAGTGTAAGTGGTAGCCACAGACG
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TACAATTTTGTGGGGTGAAGTCCACAAGCTTGGTGGTAGATTACCAAGAGGGACTACATGGAAG
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SEQ ID NO: 3719 ACTCCAAGCTGCAGGATTTATAACTGGGGCAATTGTGGTTGGATTTCATCCC
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CNCGGAACTGGGTTTCAACCACCGTNGGCCAGGATGGTCTCGATCTCCTGACCTCNGANANCCCG
CCNCCTTGGCCTCCCAAAGNGCTGGNATTCAGGTGTGAGCCACTTGTGCCTGCCANATTCTTNN
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SEQ ID NO: 3720 ACGACTTANATAAATATGATGAGGAAGGTGACCCAGATGCTGANACTCTTGG
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SEQ ID NO: 3721 ACCACGAAGTCAATACTTCTCAGTGAGTAGGGAAGGCAAAATACTTCTCAA
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SEQ ID NO: 3722 ACTGGGATAAATGAAGAAGAAGGCATAAGGACAATAAACATGGAACTCCAC
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SEQ ID NO: 3723 ACCACTGTCTTGAAATACAGCTTTGAGACACCAAATAAGATGTCAGAAGCC
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AATGGCAAACTTCAAAATGAAAACGAAAGGAAAAATACAGTTTCTATGTCATGTAAATTTTCAG
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GGGTGCAGAGCTGTGTCTGGAACACGGNTAGAGCCACGGCCGAAGTGTGCACANATCCTTCTC
TTNCGGCTNATACTTCACTTTGTTCTTNTTCTTCTC

SEQ ID NO: 3724 ACTGAGACCTATTGGAGCTTGTGGCCAGCATCCCATCTGCACCGTTGGTCAGG
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GACCGTCTTCTTGGTGGTGTGACGATGATGAAGGGGCANGTGGATGACTGAGTTGGGTGGCGG
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SEQ ID NO: 3725 ACGCGGGGTGGCGATGGATATGTGGTTCATCTGGCCCCTCCAAGTGAGGTC
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ACTCAGGATTGGCTAAATGCCATAATTATCAGCACTGGGAATATGAACAACCGCTGGAATTTCTT
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SEQ ID NO: 3726 ACTTTTAATGGAAACAACTTGACCAAAAAATTTGTACAGAATTTTGAGACCC
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SEQ ID NO: 3727 ACGCGGGGATATTGGAGCAGCAAGAGGCTGGGAAGCCATCACTTACCTTGCA
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SEQ ID NO: 3728 ACTTCCTGTTCTGGCTTCCAGAAAGTGACCTCAGCTTCATTCGGTCCTTCTGGT
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NTTA

SEQ ID NO: 3729 ACGCGGGGGTGGTGGAGAAGGACGTGCCGTGCCGCTGGGTTCTGAGCCGGA
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ATATNNAATTTGCTGNATTCAATAAATNTGTTTTGAGTAAAAAAAAAAAAAAAAAAAAAGTNC
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SEQ ID NO: 3730 ACCACCTCAGGTGTTTGTGCTTTTCTTCAGGTTCTCTACTTCTTCTCAGAC
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SEQ ID NO: 3731 GTCGGCCGAGGTACCAAGAAAAGGGTGTCCGTTGCTAGAGAACTTGGTGTG
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SEQ ID NO: 3732 ACACAATGGTTTATTAAAGGAATGTATGGCCACATCAACCTAGCAAGGATT
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CCTTTGAAATATGAANCANATTTACCCNTGTAGCACAAAATGAAGAAGGACGGGGCTGTNCAGG
AGTTAACNANAATCTTTATTTCTAGCTNTATGGNCGGTCCTGCCCCNGNCGGCNNCTTTAAAGGG
CAANT

SEQ ID NO: 3733 ACATCATCTGGTTCTCCAGACCCCTTTTAGGACTGAACTGTGCTTTAAATAGT
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AACATGGCCAGGGAATTGACNNTGACCCCTNGAAGGCTTTTTTCTTGNAAACC

SEQ ID NO: 3734 ACATAGACAAGTTTCTTGTAAAGACAGAAAAACAGAGAAATCCACAGTAACTCT
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GAAATTGAGGAACTAAAGGAACTGCTACCCGAAATTAGAGAGAAGATANAAGATGCAAGAGGAGT
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SEQ ID NO: 3735 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGATATCGATCTCTTTTAAATTTTAGGCC
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GACNGTCGATGGTATTAGGNTANAAGCACCAGGGGACCCACNNAACNGTGTNTNNNAACACC
ANCCCTTATTTACACACTGGGAGGGGNTNNCNCNTGAAAAACACAATTTCTTTCTTTTACGGGGG
GCCNACTGGTACCTCTGGNCNTAACNCNCTAATGGCGA

SEQ ID NO: 3736 ACGCGGGATCCCAAGTCCAGCGTGAAGGGCCACAGCCCCTCTTGGCTGCCAA
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AGTTGGTTTCCAGCCCCAGTGTCTGACTTCTGTCTGCACATGAGGAGGGAGGCCCTGCTGTGT
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SEQ ID NO: 3737 ACAGCGGGGGCTTTTGTGTGTCCCTGGCCATGGCGCTGCAGCTCTCCCGGG
AGCAGGGAATCACCTGCGCGGGAGCGCCGAAATCGTGGCCGAGTTCTTCTCATTCCGGCATCAAC
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AATTGGTTATACAAGTGTNAGNTCANAAACCTGGTTGTANTTATCTCAAAATTGAAAGTAGGTG
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SEQ ID NO: 3738 ACCGACCATAGAGCAAGAATCAAGATTCTGCTAACTCCTGCACAGCCCCGTC
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TAGTGGCTTCTAGCTCTAAATGTTTGGCCAGCCATCCCTTTCCACAGTATCCTTCTACCTCCTCC
CTGTCNTGCTGTCTCGACCAGNCTATAAAGAGTGCATCTCCAGCCTATGAAACAGCTGGNTCTT
TGGCCATAAGAAAGTAAAGATTGATGACATGATGGAAGAACTCAGGAGTNNGCTTCTAGACCC
NTTCAAGCTTNTACACCCTTNTGCCCTCTTTCATTGGCTGCNCCNCCANCCAGCCTCTCAACTCT
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SEQ ID NO: 3739 ACGTCAAGCAGGAGTGCAATCGCACCCACAACCGCGTGTGCGAATGCAAGG
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TGCAAGCTGGAACCCAGAGCGGAAATACAGTTTGCAAAAGATGTCCAGATGGGTTCTTCTCAAAAT
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TCAGAAAGGAAATGCNACACACNACAACATATGTTCCGGAACANGTGAATCAACTNAAAAAAT
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GCCTAACCTGGCTTAATTGTCTATGGTAGANAAATNTGCCCTGGCACCAGTAAACGCAGAANA
GTGTTANAGANGGATTTAAACGGGAATCAGCTTCACAAGNAACAGTACTTTCCANCTGCTTGAA
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SEQ ID NO: 3740 ACCATTGGTGGTGGTATCTTTCAAGCAATCAAAGGTTTTGCGAATTCTCCAGT
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CTGGTATCTTGTGACAAGATTGCCCTCTGCACAANTTTCCCCAATGGTCTCANTTTGCAAAAAA
NCCCTCCAGTTGCCCTCAACTCANTTACCTTCTCACCTTTTGGAACTANTCGACAATNTCAGT
AGGGACTTCTTNTCTAANGATTCTTTTAAACAAAACAAGTTGTGGGTTCTN

SEQ ID NO: 3741 ACAATTCCTTGTTTTCAAGGGTAAGTTCCAAGACTTCCAGACTCAGGTTTGAA
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GTGGGCCATCTCTTTGGTCAGCTCATCTGGTTCATANCTACTCTCNGAGTCTTNCACATCATGTGG
CTCCTGCNCTTNAANGGGCACTGGNAACAACCACTGGCATAGNAGGCCGGCTCCTNNCTANAGT
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SEQ ID NO: 3742 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGNCANCTATTTAATTAGGTTCT
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SEQ ID NO: 3743 ACTGTATTTATTTCTTATTTTATACAACTCTTACTCTTTACAAAAATGGTTATA
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SEQ ID NO: 3744 ACTGGAGATGTATTTGATAACCAAGGTTTTAGGTAAATTTTACCAGTATTAG
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SEQ ID NO: 3745 ACACGAGAAGCTCCGAGGATGGCTGAAGTCCAACGTCTCTGATGCGGTGGCT
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SEQ ID NO: 3746 ACTTTGTTTGTGATACAAGGTGAGCCAAAGGGGTGGTGAAGAAGACACACN
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SEQ ID NO: 3747 ACTTTCTTTTTTTTTTTTTTTTTTGTGTTGTCCAGATTTATTGAAAATAATA
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SEQ ID NO: 3748 ACTGGCCAGGAAGGTGGAGTAGGTTTCAGGCCCTGGGGATTTCAAGTGCAGA
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 ACTTTCAG

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SEQ ID NO: 3750 ACGCGGGGGCATCCTANCCGCCGACTCACACAAGGCANGTGGGTGAGGAAA
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SEQ ID NO: 3771 ACCGGCTTCTTCTCTGGGGTAGGGGTAGCCTCGCCCGGAAGCAAGGCCTCTG
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SEQ ID NO: 3783 ACTGATTAAATCAGTATAAAATCGAAAGAGCTTTAGATCTGTAATAAAAAATC
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SEQ ID NO: 3784 ACTTGTGACAGGCAGACGTGATTGCAGCCACGAACACGATGAACTCACTGAA
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SEQ ID NO: 3785 ACTCCCTGTCGTCAAAGTGCTTCCTCTGGTAAATACACGGGTGCCAACTTAA
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SEQ ID NO: 3786 ACCGACCATAGAGCAAGAATCAAGATTCTGCTAACTCCTGCACAGCCCCGTC
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SEQ ID NO: 3787 ACTTTTAAATCATGTTCCTTAAACATGGCTGTTAACCCACTGCATGCAGA
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SEQ ID NO: 3802 ACGCGGGGCTCTTCTCGGCGCTGCCTACGGAGGTGGCAGCCATCTCCTTCTC
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SEQ ID NO: 3816 ACCTGTGGAGCGAAGGAGAGGTTGTCTATCTGGGCCCCGTGTTTACCAGTCAA
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ACGGCACTGGGTTGGGAAGGATGAGAAAGCCAAGACAGGTGGGCCAGGTTCTCCGAACATGGGG
CAACAGTGACCTGGGCAAAAGCCTGGAAGTGAAGGCTGATAAGGCCACAATTACTGCCACCACC
TCTCAGTATCTACAGGGGGCAGACGTTAGGCAGTGGGAACTGAGGACTGGAGGGCGTGTGGCAA
ACACGGGATGGATTTATCAGAAAAGAGAGGACACCCAAACAGTGCCTGCCCTATTTATCTTGC
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SEQ ID NO: 3817 ACCCATGATTTGGACACTTTGTGCGGGCCCATTTACTTATACTGCAAAGCGTCC
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TATACAAGACTGACAATCACCTGAACATTATTTACATATCATTGAAAAACAAACCCCTGTATCCAG
TTATCTATGATAGCAATGGTGTCTGCTTTCAATGCCTCCCATCATCAATGGGGATCATTCCAGAA
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SEQ ID NO: 3818 GGTACATGGGTGTTTCAATGCCTCCATTCTAAACCTGAGCAGTTGTACAGCTG
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CTCTGAGTTTCAGAGTCCTTTCCACTAGGTATACAAATGAGGATCCTTGAGCAGGAAGGATCCAGTT
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SEQ ID NO: 3819 GCTTTTTTTTTTTTTTTTTTTTTTTGGTAACTTTCCTTCAGGATTGTAATCTG
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CGATAGCCTTCATCTTGCCACCTGCTCTGGAGTTGCCATGATTTTTTCAGTAAAGGGCATCTTCT
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CATCCAACCTCTTCTCCTGTGGCACCAAAGCCACAAAATAAGGAGGGATGTTCTGCGGGGTGTGT
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SEQ ID NO: 3820 GGTACTACGATGGAAGATGCAACCCCAATATTAGAAAGGCAGCTTGATGAGC
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AGGGACAGGTCTGCTCCAGAAGAGGGCATAAAGACACTGCTCAAGCTCCAGAAATCTTCCAGCGT
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AGAGTATGCCAAAAAATAGAAAAGCTATAAATATTTCAAATAAAGAAGAATCCACATTGCAATT
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SEQ ID NO: 3821 GGTACTCAGCAATTCACAGACATGACATAAACATGACATTTTTAAGACATAA
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AGGTCTTTTTTACCTCTGACAACCCAGTGCATTGACGTCTTCACTGAGTCATTCAAAGCTTCCCACT
GCTGGAATGGCATCGACATCTGGCTCCTTCGCCAGTGGTCATA

SEQ ID NO: 3822 AACTAACAATTTGGATAACTCGGAAAGATGGATTAATTCCTACAAACATAT
AATCTACCAAGAAATGAATCATGAAGAGATAGAAAGTCTGAACAGACTGATAATTGGTAAGGAGTT
TGAATGAATGAAAAAACCTTCCAAAAAGAAAAGCTTAGGAATATATGGCCTTACTGGTGAGTT
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SEQ ID NO: 3823 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTGGATAAACAATACTTTATTA
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SEQ ID NO: 3824 GGTACAGTATGGGGGTGTAAATTGGCATGGAAATTTAAAGCAGGTTCTTGT
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CTGCATATCATAATGGGGGTAAAGTTAAGTTGAGATAGTTTTCATCCATAACTGAACATCCAAAAT
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SEQ ID NO: 3825 GGTACACATANTGCTTCTGCCACATGATAACGAGCGCGGTGAAACCGATGAA
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SEQ ID NO: 3826 ACGCGGGGACGTAACGGAGTGGCCAACGGCCTGCAGAGCAACATGCCCAAG
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GCTCCTCCTCTGCAGGGGCGATGATACCACCTCCCCCAGCCTTCCGGGTCCTCTCGCCCTGGT
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ATGATGCCAGTGGGGCCTGCTCCTGGAATGAGGCCTCCCATGGGGAGGCCATATGCCAATGATGC
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SEQ ID NO: 3827 GGTACAGCGTCCTCGAAACCACNAGCAAGTGAGCAGATCCTCCGAGGCACCA
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SEQ ID NO: 3828 ACCCAAATGCTACCACTGGAGAAGGAATGAGAGATAAAGAAAGAGACAGGT
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SEQ ID NO: 3829 GGTACTTCTTGCCCTGTAGAATTTCTGAGGTTTTCTTTCTGAGTCTGGTTAA
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SEQ ID NO: 3830 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATGTTTCTTTGGTTTTATTATTACA
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SEQ ID NO: 3831 ACGCGGGGGAAGAGGCCGGGCTACGTCGTGCCCTGCGCGTGAGCAGCTGCA
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SEQ ID NO: 3832 ACTAAGTTGTAGCAACCACGTGTCCGTGCAGTGCCAAGGAGCTAGAGCAGT
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SEQ ID NO: 3833 GCGTGGTCGGGCCGAGGTACGCGGGGCTCTGCGAGCGTTATTTCAAAAAGAAG
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SEQ ID NO: 3834 GGTACACCATATAAACAGCAGATGAAGTCGGAGAGATAGTCTAATACACTTA
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SEQ ID NO: 3835 ACCGCGCTTGGCGGTAGCTGGCCCCAGACTTCTGTCTTTTCAGCTGCAGTGAA
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SEQ ID NO: 3836 ACTTGTTGACTAGAGTTCATCTAGGGTGATCTATCTGTGTCATTTGCTGGGG
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SEQ ID NO: 3837 GGTACTACTTCTCCAAACTCATAGAATTTATGGACACTTCTTCTTCTCATCCTGC
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SEQ ID NO: 3838 ACTCCTTCTGAACTGCCTCCAGGTCAGCCCCTGCCACGGCTGGATGTCTTCC
AACAAGACGTTGCGGACTCTCACTTCAGAGAGAGCAGAGCAACTCTCCAACACACTGAAAAAAT
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SEQ ID NO: 3839 GGTACATGTCACATATATAGTCAATGTAAAGCAATTCTACTTTGCATCCCTTA
GCCACAGGCATAAGGCAGAACACAGATATTTCTGTGTTCTGTGAATATCTGTGGAATGATACTTGA
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SEQ ID NO: 3840 ACACTGGCTGTCCACAAGGCCGCACCTCACAAATCCGGGTTTCTTTCACAAG
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SEQ ID NO: 3841 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGNATATAAACTATTTATTAAC
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SEQ ID NO: 3842 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTGAANAATCAGAATTTATTTCACTATGTG
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SEQ ID NO: 3843 GGTCGGCCGAGGTACTTTTTTTTTTTTTTTAATGTTGCACTTGTTAGTTTCATT
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SEQ ID NO: 3844 ACTCTGCCAGGCATTTAACATACATTATTTCACTTGTTTTCATGATTAAATTC
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SEQ ID NO: 3845 GGTACGCGGGGCTTGCGGTGCTGGGCAGCAGACCGTCCAAACCGACACGCGT
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SEQ ID NO: 3846 GGTACTTGACAGGAAGTGTGGCGCTTGTTGCATTGTTGCTGCTCCAAGTT
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SEQ ID NO: 3847 ACATAATCGTTTTGTGGAGTCGGCACAGTTCAGGTTATGGAGGCACGTAATTC
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SEQ ID NO: 3848 GGTACTCTGTGAAGAACAGAAATGATCATATTCTTATGCATCTATCTGTATGG
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SEQ ID NO: 3849 GGTACCAGGTATGTCACCTTTTGGGTTCCGTCCTTGGTGTGATAGGTTATCTC
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[illegible]

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SEQ ID NO: 3889 GGACTTTTAATCACTTACTGAGAATATTTCAAATTTATATTCTCATCAGGAAA
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SEQ ID NO: 3890 ACTTGGGGAAGCCATCTCTATCATTTTTTCTTGTAATCTTTTCGGGTCCATGC
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SEQ ID NO: 3891 GGTNCAACCAAGTTACTTTTCTCTTACTGAATTTTCAATATGTTTTCATATTT
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ACCCTGCAAGGAGCTGGCCAGCCAGCCGNGNGGATGGGTTCTTGGGGGGGGGGGGGTTNC
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SEQ ID NO: 3892 ACTGTGCATTTCTCTACTTGCATGGCCAATAAATACAGCTACGACCTGTTTG
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SEQ ID NO: 3893 GTACGCGGGATTGGCACATGGGTGGACACGGATCTGCTGGGCTCTGCCTTAA
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SEQ ID NO: 3894 GGTACCCCAATCTGAAGTCAGTAAATGAACTAATCTACAAGCGTGGTTATGG
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SEQ ID NO: 3895 GGTACTTATNGGAAATNG
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AAAACCTTNGGGNGCCATGGGAANTACTGGGCTTGANACCNTTGCCAACCTTANACCAANGTTTTT
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SEQ ID NO: 3896 GGTACTGTCTGTCTTCACATTTCATATCCAGATTTATATTTTCTGGAGTTAAAT
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SEQ ID NO: 3897 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGATATTTTCATTTGGTTCTTTTATTAG
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SEQ ID NO: 3898 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGAAAAATGTTTATGGTTTATTTTTC
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TTTTAGGTCG

SEQ ID NO: 3899 TACAAATATTTAAGAGTGTGATTGGGAGTAAGGGAATGTCAACTGCCAATA
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SEQ ID NO: 3900 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGAANAATGTCATTGGTATTTTT
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SEQ ID NO: 3901 ACATGGCCGCGCTCCTGGAATACCTGACAGCGGAGATTCTGGAGCTGGCTGG
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SEQ ID NO: 3902 GGTNCTTTCCTGCCTTTTAGTTCTGTGCACAGCCCTAAGTCAACTTAGCATT
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SEQ ID NO: 3903 GGNACAGTGATTTGGCTATAGACTCTCGCCCTTCAGGGCANACTGTCCTCAG
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SEQ ID NO: 3904 GGTACTTCTTTTTTTTTTTTTTTTTTTTTTTGGTTTTTTTTTTTTTTTTTTTTT
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SEQ ID NO: 3905 GGTACACTGCCAGGCAAAGCGTCCGGGCAGCGTAGGCGGGCGACTTAGATC
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SEQ ID NO: 3906 ACTTTTTTTTTTTTTTTTTTTTTTTCAGNCTTGATGTGTGATCTTTATTTTGT
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SEQ ID NO: 3907 ACACAGAGTAAAATGTTTTTCTTTTTTTCAGGACCTTGAACCTGAATCTTGCACT
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SEQ ID NO: 3908 GGTACTTTTTTTTTTTTTTTTTTTCATANAAAGGAGGAAAAATTTTATT
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SEQ ID NO: 3909 ACGCGGGGGCAGAGCTGCGGAAGATGAATGCCAGAGGACTTGGATCTGAGC
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SEQ ID NO: 3910 GGTNCCATCTGCGCCATCCTGGAGAACTACCAGACAGAGAAGGGCATCACTG
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SEQ ID NO: 3911 ACACAAAGAGGGGGTGGGTGTGGATGCAGAGTGTGTGGCCTGATGCTCCAC
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SEQ ID NO: 3912 ACCTTTGGGGCATGGGGGCATTACATGGGATGCTTGTGTAATCGACCACCTA
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SEQ ID NO: 3914 GGTACAAAATTCAAATACCAACAAAACCTGATCTGTGATGATAGAAAGCATAT
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SEQ ID NO: 3915 ACAGTGTTCCAGCCATCCTGCTGTTTTTCCCTCCAATACCTCCAGAACAG
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SEQ ID NO: 3917 GGTACAAAGGCAAAGTAGAATAACAAAAATATTTTACTAAAAACATAAGATT
 TACAGAAGTTTCCAGACAAGCCATACAAAATGGTCACAAGCTTTTTTGAAGGGGGGAATCTACA
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 TTAGCTGCTTTTAAACCAATGCAATTAGATCACAAAAAAGGGGAAAGGAGCCCATAAAAATTA
 CTACTCCCCCTCAAAAAATAAAATAAAATAAAATAAAATAAAAAACACCCACACCCCTGCAGCTA
 ACCTGACAACTACCTTCATTACAGTGCTTTATACTTAAACCAGGATGGGGGAAATGAATAAAA
 GCAGGGANGGCCNCTGNTTTTNAACGTTTCCAACAATCCAATGATCTTCTACCTTGNTATGCTTT
 ATGACGGGGATNAGGGCAGAATTAATTTGTAT

SEQ ID NO: 3918 GGTACTTGGATTATGGAGAAGAGAATTGGAAGAAACAGACATCTCAGTGCTT
 GAAGAACCTGAAAAATTCTGTGAGGAGACCAGGAGGAATTTTGAAGCCACCTTAGGTTGGCTAC
 AAGAACATGCTTGCTCAAGAACTTATGGTCTAGGCACTCACTTGCCTTGGGATGAGCAGTGCGTGA
 TTGAATCACTTTCTGACTCCACTATTACATGGCATTTTACACAGTTGCACACCTATTGCAGGGGG
 GTAACCTGTCATGGACAGGCAGAGTCTCCGCTGGGCATTAGACCGCAACAGATGACCAAGGAAGTT
 TGGGATTATGTTTCTTCAAGGAGGCTCCATTTCCTAAGACTCAGATTGCAAAGGAAAAATTAGAT
 CAGTTAAAGCAGGAGTTTGAATTCTGGTATCCTGNTGATCTTCGCCGCTCTGCGCAANGATCTTGT
 TCCAAATCATCTTTCATATTANCTTTATAATCATGTGGCTATGTNGGCCGGACCAAAGNGNTNAAT
 GGNCTNCANTTGGANANCNAATNGGCATTTTCTTCTTGAA

SEQ ID NO: 3919 ACATCTTCCAGAACGTAATGGTCATGATCCTGGTCGTGGACACCAAGATCTTG
 ATCCTGATAATGAAGGTGAACCTTCGACATACTAGAAAGAGAGAAGCACCATGTTAAAAATAAT
 GCAATAATTTCTTTGGGAAAAGATCTAAATGAAGATGACCATCATCATGAATGTTTGAACGTCCT
 CAGTTATTAATACTATGGTCATGGTGCCAACTCTCCCATCTCAACTGATTTATTACATACCTTT
 GCCCTGCAITTTATATCAAATCGACAGCAGACTTTGTATTGAGCATTTTGACAACTTTTAGTTG
 AAGATATAAATAAGGATAAAAACTGGTTCTGTAAGATGAGGCAAATATAGGGGCATCAAGCCTG
 GATTTGNGGTATCATTTCTATCACTGNCAATAGCCTGCTTTNCTTGCTAGGCGTGACTTGGTTCCTA
 TCATTAACCAAGGGTGCTTCAAATTCCTTCTTACATTCTTGGTGCATTANCTNNAGGAACAAATG
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SEQ ID NO: 3920 GGACCTCTGGACCCACTCCTGCTTGGGGTCGCCACAGAAGCTGCTGGCCCTTCT
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 GGTCTCAGGAATTTCTTGGAAACAAAGACATGCAGCAGGGAGAGGGGATGACCACAGAGCC
 CGTAGGGATGATGTGGTGGGCACAGACCAAGGAACAGAAGGCTGGTTACTATGGTCATCAGGC
 CTGCCATGTCTCAGAGAGCAGAAGCAGCTCGGGGCTCAAAGCTGACGTGCAGGAGGAAAGG
 ACCCGGAGGTAACAGGGTGACAGCCTTGGTGCCAAGTGACAGAGCAGAAATGATCCCCCGT

SEQ ID NO: 3921 ACTTTTTTTTTTTTTTTTTTTTTTGGGGAAACCATGATTTTATTAAATTTTATA
 ACTGGGAAATTCATGTGAAAGTGAAACAAGCATGAGTCAAGTCAACCAGGGAAGGAATCTGGG
 GACAGGCCAAGGAGCGGGAGGTGGGGCAGCGAGGCANTCCTGCTGGTAGGAGCCCTGAGGATTT
 CCCAGCTTGTGTGCGCTGCCTCTGGCATCCTANAGACCCGGATTTACTCAGCTAGGAGAGAGGATG
 GATCACAGGGTCTAAGGGTGGCCATTACAGAGGTAGAAGATGGAGGGGCGGCAGATTCTGGCAGG
 GCAGCANAGGGCTCANTGGCCATGGCTTGAGGGGTAAAAAATTNAGGACATCCCCCAGTGCTGCC
 TCACCAAGGCTTCTCCGAANAAATNATTTGAAAAATTNGTGNGNGGGGACCTTTCTTCAAGGG
 GCCTTTTTCNGGAGTTTTTTTCAACCANAACCAANCANGGNTTTAAAAAAACCCCANCTTTCC
 CAAANCCCCTNAAAAACCTTGATTTTCCNTTCAAAGGAA

SEQ ID NO: 3922 CTTAGCNTGGTGC GCGCGCGGCGGNCGCGGGTATCANANCCATGCGNAGAGT
 CCGGAAGACAGACAATAATCGCATTGCTAGAGCCTGNGGGGCCCGGATAGTCAGCCGACCAGAG
 GAACTGAGAGAAGATGATGTTGGAACAGGAGCAGGCCTGTTGGAATCAAGAAAATTGGAGATG
 AATACTTTACTTTTCATCACTGACTGCAAAGACCCCAAGGCCTGCACCATTTCTCCTCCGGGGGGCTA
 GCAAAAGAGATTCTCTCGGAAGTAGAACGCAACCTCCAGGATGCCATGCAAGTGCTGCGCAATGTT
 CTCCTGACCTCAGCTGGTGCCAGGGGGTGGGGCCTCCGAGATGGCTGTGGGCCATGCTTGN
 AGAAAAATCCAAGGCCATGACTGGTGTGGAACAATGGCCATACAAGGGCTGTGCCCCAAGCCCTA

NANGTCATTCCCTCGTACCTTGCTTATGGCAAGCATTNGTCTATTTTGCANAATGTTCCATGTGTAA
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SEQ ID NO: 3923 GGTACGCGAAGGATATCGGTTTCATTAAGTTGGACTAAATGCTCTTCCTTCAG
AGGATTATCCGGGCATCTACTCAATGAAAAACCATGATAATCTTTGTATATAAAATAAACATT
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SEQ ID NO: 3924 ACAAAGCTAAAGAAAAATTGTGGTCATTGATGATGGAATATATGACTTGCAG
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TTTCTAAAATCGCATTTTGTANCCNAAAAAAAAAAAAAAAAAGGTCAGTCTATAATACTC
CAACAGTCTCCCATCTGTATTCAATGGCGCCCCAATACAGTCCTTTGTTGGATGCTGGGGAGAG
TAATCCCTACCCCAAGCNCCATATAGATAAGAAAAACCTCTCCAGTTGAGCTGAACCACANACGG
TTGGCTGATGTTCCCCCACCCCATGACACAGTTNCTTGAATNGGAAGAAGGNGGACAACAGGNG
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SEQ ID NO: 3925 GGTACAGACAGCTGGTGTCTTTTGACACCTGGGGCCACACACAAAGAAAGC
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GGCATCGTTTACGACAGATTGAGCTTCTGCATAAGGTANGCCACANTCCAGTGACTGANCGGT
AATGCCAGCCAACNTTGTACNTAGNTAACCAAAAGTATATAGCTTATTTGGNGAATCTTCATCCT
TATTACGTTTTCTGGACACCCACACGGATTCCGTTNTGGCATTCTTATTCCTTTTGGCCCAAN
ANNTTTTTNACNTTGTNTNANTNCCCCAATTTTGGG

SEQ ID NO: 3926 ACTTACTTGGAGAGACATATGTCTGAATTTATGGAGTGTAATTTAAATGAACT
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CATTCTGGAAGGTCTTGAAGAAAGACCACAGAGAAAGGCACAGCCTGCTCAACCTGCTGTAGAA
CCTGCAGAAAAGGCTGATGAACCAATGGAACATTAAGTGATAAGCCAGTCTATATATGTATTATC
AAATATGTAAGAAACAGGCCACCATACCTGATGACAATAATCTATCTTTGAACCAAAAGTTGC
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AAACCTATATAATGGGAATACCATTTTTCTTTGAAANGGGCTGTATATAATCATTTTTNTAAAAA
GGATGGGGTTCTAAACCNAAGGTTTTTTTTNTAANAAAAATANG

SEQ ID NO: 3927 ACTGGATGTCAGGTCTGCGAACTTCTTAGATTTTGACCTCAGTCCATAAAACC
ACACTATCACCTCGGCCATCATATGTGTCTACTGTGGGGACAACCTGGAGTGAAAACTTCGGTTGCT
GGCAGGTCCGTGGGAAAATCAGTGACCACTGATCAGATTATCAGAAATGGTGAGACTCATCAGA
CTGGTGAGAATCATCAGTGTCTATCATCATCAGAGTCTGTTGAGTCAATGGAGTCTGGCTGTC
CACATGGTTCATCATCTTCTCATCATCCATATCATCCATGTGGTCTGCTTTCGTTGGACTTACTT
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GATTCTGCTTCTGAGATGGGGCAAGGGTTANCCATGTGGNCCCCACATCTGGGTATTTGTTNNAA
AGCTGCTTTTTCTCAAAACTTTTCAAAAAANACCTGTTTAACTNGGTTTGGCNCACGGNAATGCCT
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SEQ ID NO: 3928 GGTACTGAGGAGAACTTCATGATGCTGCCAGCAAGCTGCTTAACACAGTTG
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TGGCTGTCAATTTCTCAGTGGCAACTATTTACTGTTGAAAATGGGAAGCAATAATATTCATCTGA
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SEQ ID NO: 3929 GGTACTGGGAAAAGATCTAATCTGCGTGGGCCTGTCGTGCCAGTCTGGGG
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CAGCCTGTGGTTACAGTGCAGACAGGCCATGTGAGCCACCGCTGCCAGCACAGAGCGTCTTCCC
CCTGTAGACTAGTGCCGTAGGGAGTACATTATTTCCAACAAGCTTAAGACTTACCATGAATGGCT
CATTCATACAAAAACACACTCACACTAATCTTTTAAAAACAGTAGTGCATACATTATACTCCTCCT

ATAAAGCCAACCTTTGATTAAAAACCACTNGTTTTCAAAGCTCAAGTCTTTGATTTTGAAGAAGAAC
CAAGATATCCCCCTATGATCCTACCATCTATTTTANGNCTTTTGGACCATTCTTGACAGCTTNCAG
GGCAAATGGTTGCAGCCCAANATTAACNCCCCACTNATTGGNTTTTGG

SEQ ID NO: 3930 ACATCTCCGCTGCAGATCGTTTCACACCTGCTTTTCCTCGGTTCACTTNTGGCT
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GGGGAGGGGAGAAGAGATTNGNTTCTGAGTCTNCTACTCCCCGGGTCTGCNTNAAAAAACCCCTCT
GCTGGTTGGAGGCCGNAACGCGGCCCAAACGGTTANNTTTTNGCNTTTTAAAAAANTNCCCGGG
NCCTTNTTTTNTTTTNTTNTTNTTAAAAAACAGG

SEQ ID NO: 3931 GGTACTTTTTTTTTTTTTTTTTTTTTTGGTCACTAAATTTATTTTAAAAATCATA
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CACAATAATTACATGGGGGGAATTTTTTAAACCACCAACAATAACGAAAAATAAAATCCACTCAC
TCTGCTGCTGTTTCAAAATTTCAATGTAGTTTTTGACGCCCCCTCCCCCCCCAACCCCTGTTTGT
AGGAACTAAAACATTACATNTGGTGAACAGCAAAGATTTCACTNCACCTCAAATGCAGAACACCT
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CAGTTCTTCACTTGTCTTAAAAAACTTTCCANAATACTGNTTCACTTTAAAAAAGAAAAAA
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SEQ ID NO: 3932 GGTACACCCCAACCCCAACCTCAGTGGAACAATGCCAGGGATTAGGCT
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TCTTTCCAAGATAATGCTGTAGGTGTACACCCCAATCTTTCATGTNCACATCTGCAAGGNTCCT
TGCTTAATAACTTNTCATTAAACNGNCTTGGAGTTTNTGA

SEQ ID NO: 3933 GGACAGACTGTTTTCCGGATGGACTGGTTTGGGAACACTGTGCTGGGGGAAG
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SEQ ID NO: 3934 GGTACTTTTTTTTTTTTTTTTTTTTTTAACTTTCAATCTTTATTTAAATGC
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AAAAGCAGNGATCTGCTCTCCAGCATATNTGTTCCAACTTATCATCTTCACTACNCACTGTAT
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AACGTTCTTCCCTTANCCCTCTTGCTTCTTCACTTTCTCTCATCATCAAGACCCAAAGAGGGNCA
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SEQ ID NO: 3935 ACCTGTGAACCAAGTGTGTTGGGCAGGATGAGATGATCGACGTCATCGGGGTG
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ATCTGACAAGAACAATCAACCTCTGGGTGGCTTTGTCCACTATGGTGAAGTGACCAAAATGACTTTT
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SEQ ID NO: 3936 ACAAGCTGAGTATCCCTTATCCAAAATGCTAGGGACCAGAAAGTGTGTTGGAT
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TTGCACAANAATTAAGGTTGGAACNTTTGAGCTGGNACCTCANCAAATAAAAGTATATNTTGG
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SEQ ID NO: 3937 GGTACAGATATCTTCAAAGGAGGAAGAAGAAAGGGAAAGCAGATGGTGGAG
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CACTCTCATGAGNGCAACTGTGGCTTACCTAATATTGCAATGNGGTTTGAATGTAGGTAGCATCCT
TTGANGCTTCTTTGAACTNGTATGAATTTGGGTNTGAACAGATNGCCTGCTTTCCCTTAAATAAC
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AAAGGGCTTGAAATTTTTTTTNGTCAAAAAATTAATGCCNCCTTTAANAATATTTTTTTCNCCCA
CTTANAAAGGGTTTTTNTATATTGNTNCTTTGAAAAACC

SEQ ID NO: 3938 GGTACATTTAAGAATAAACTTTTGTAAGAAAAAGAAAAATCTTACAGTGGCTC
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ACCAACTCATTCGAAAAAAGAAAAAAGTCCAAGCCTGGAACATTGAAGGACTCAA
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TAATGGTCTTCAGGTTCTGCCCTTAAATATTTAAAGTCACTTGCTCCATAAACCTTTCCATTAAAGT
CCCAATCTTCAACTATACCATGGCGGATTGGCCACTTTTGTTCATATGTANGGTTTCTTATTGNT
TCATCCCAATGAAGAAAAAGTCTANGNCATCAACACCTTTTATCACCCCTCCTTGANCCTGGTNANCC
CACTTTTNGTGACCTCCTTTATTGNCATCCCGGGAGG

SEQ ID NO: 3939 ACATCAGCAGCAAACCTCCTGTGCATCCCGGTAATCACGGTTCTCCATCTCCG
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AAAATGCCATTGCAATGTTTAACTGTTCTGAAAGCTTTCTTTCTTANAGCTCTGGTGTGTTGCT
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SEQ ID NO: 3940 ACTTGTCTATATTGCAAAAGTCTTGATTGAGGTGGTGGCATTTCAGCTAGTTC
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GACTGAGAAAAGCATGATGCTCGCTCCACTGCTGGAACCGTGCCTGCTGCTGCCTTAATGTTCCA
GAGCGACACTCCCATGTATACGATCTAAAGCCTCCCCTATAAGTAATCCCGAGGGGTTCTCATCAA
TGAAAGCTATTCAAATGTGAAAGGAAGAATGGGGCCCGGGTGTGCAAGTGGCTCTCAAAAANGA
CTGTGGCCCTTCTTTGCACCATGGGAAGGGGCTTCTTCTCCGAATTACAAGCTTTTTCGAAGAAG
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SEQ ID NO: 3941 ACTGCATGTTCTGTTGTGGTGAGGGAAAGAAACATGCTTTGAAGGTTTTCCCT
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CCTTTCANAAATCCTCAGGTTGGGAAAGACCCACACCTTCTTTAAGGATCATTGTCTCGCCATC
ACAGGATCTTGAAATGTTTCTAGGGTGTGTAATAATTAACCAGGGGGGAATGAAGCACATTTT
TCTGGCAACCAAACTTGAGTTCCTCAGAGAACAGATGCAGAAAGACCTGCTCTGCTTGGCCCGG
TACAGGGGCCACTGTGGAAGTCACTGAGGCTGTGACCCGGCCCTTAACCCANGANANCCCGT
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SEQ ID NO: 3942 TGTACGCGGGGCTTTTTCTAACTCCGCTGCCGCCATGGCTCCTGTGAAAAAG
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GAACGGAAAAAGCTGGGAACCTNNGTGGAGGGGGGNGACCATNGAAAGGAGCAAGCAAGAT
CACCGGTGACNTCCNANGNTGTCTTTCTCCAAAAGGTATTTAGAAATATCTCNCCANAAAAATTTTG
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GGATTNTCTTTTGANATTNNCTGNGGGGGATCNANNAAAAATNTGATNATTCTTAGCCTANAT
GTGT

SEQ ID NO: 3943 GGTACAGAGAAGCACCTATTGACAAAAAGGGGAATTTCAATTACATCGAGTT
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CAGTTACATTGTCTTACTCTCTTTTACTTCTCAGACACTTCCCCCACCCTCATAGAACCTGTTCAT
GCANCTTAGTTTACAGCTTTGCCTCTTCTTNTGATGTATTTATCCAGACCTTTCTGCCACTTAGC
ACTTGATAATCANACTGGAAATGGGGATGATGGTGTAATTTGNTTGAAGAAAGATCGCGAATAA
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ANAATNNGTCNANACCCTCCGAATGGTATTTTTGTATTGGGTTCNAAACTCATTTTGGNGGGNG
CTANAACACTGGCTTNGGNTNGATTAATGAATNCCCTGGTTTNGCCANANAATANGAACNCCAT
ACTTTATTTNCCGTATATGGGCTGNNTGNNATATAAANNNCNTTATATAGCNCCANAGGNACCCT
NGTNTGNAAATNAAATTGTNGGGGGC

SEQ ID NO: 3944 GGTACTTTTTTTTTTTTTTTTTTTTTTCTGGAAAAGTGAAGTCTTTAATG
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GCAAGATTCATCAGAAGCCACGTGCAGTCAGATCCAGCTGGCCGGCGGTGCANATCTGGAGTCC
AGCCTCAGGGATGCGCTACTTTCCATTCTCTGCATTGAACATTCGTTCTGTGCAGCATCCGCTCCAGC
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CCCNATGACAATNGGTTTGAACCTAACTTTTNGTANAANTGGANATTTTAGTGACANTNTTACNAN
GGTTTCNAGGGCTANANGATTCTTNCGGGTGGCACNTCCAANAAGGAGNNCCANNAATGGGAA
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SEQ ID NO: 3945 GGTACGTGCAGACGGTGGTAGTTCTGGAGTCTGGAAGCCACGAGGTGCTCA
TCCATCACAAGGCCATCAGGCCGGTAGAAATGCCTGAGGAAAGCAGCGGAGCTGACCGTGCC
AGCATTTACACAGGGAACACTTCTTGGGCAGCCAGGTGTATGGGGCAGAGCCACAGTTCTCTT
TGCGCATCTGTCTCACAGTTCGGTCCGTAGAAAGGAGGGAGGGCAGGCACAAAAGGACCCAG
CATGCAGGTTCCCCATTCAGGCAGCAGGTTCTGTTAGCTCCTTACTGTGCTGTATCCCCATGGGG
GGCACACGCTGGGAAGACCGAGGCCGAATTGCAGGCTCCTCCTGGGGCCAAATGCTGCATCTCTC
CCGCGT

SEQ ID NO: 3946 GGTACAAAAACAACAAAGTTCAAACATCGAGATGTTCCCTTAGCAAGGCT
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TGTGGCACAGTCCATGCTTTTAACCAGATTGAACAGAAGAATGGCCACTTGGCCAGGTAGAAG
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GTGGGATTGTACGCGGGGGAGGCGCTGTTCCAGCCTTCCTTCTGGGTATGGAATCTTTGCGGCAT
CCACGAGACCACTTCAACTCCATCATGAAGTGTGACGTGGACATTTGCGNAAAGACCTGGACTTTT
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NTCCCCCCCCANAATNAAAAATNTGCCNCAGCCCCCATTTTTTNCNTTANTNNCTTNTNCNCAAA
CATNCTGAACAANTNCTCCANANTTCTGCCCTNGCCTTTTGGGAGGNGTCNTTGGGTANCAAT
GGGAAACNNCNGGCNCTTTGGGNAANAATGGAGGGGNTNGGGANTCCTNGNGGNTTATTNNGG
NTTCCCTTGTTTATAGNNNTT

SEQ ID NO: 3947 ACCAAATGTCACACTGGCTGTAATCAAATCGCCCAAGAATAGTCACATTAGA
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SEQ ID NO: 3948 GGTACCTTCAGTCTACACTTAAATCCCCTGAGTTAACTTGCAGCTCACAGCT
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CTCGCGTACCTTGCCCNCGGCGGCCGNTCAATAAGGGNAAATCCANNACACTGGTGGTCTTANTA
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SEQ ID NO: 3949 GGTACTCCGGCAGGGAGGGTGACAAGCACACCCTGAGCAAGAAGGAGCTGA
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SEQ ID NO: 3950 ACAATAGAGTTAGAGCCAAGGTCTAGAGGCGGATAGGTGGATTCTTGAGGG
AGGAGGAAGGGGCTGAGGTTGCTGGAGCCTGGCAGCTTCTTCCGGAGCCATTGGCAGGACTGATG
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CNNACTTGCNCGNTNTAATGGATCNACCTCGNACCAACTTGGCNAATAATTGGCANAATNTT
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SEQ ID NO: 3951 CGAGGTACGCGGGGCTTGCAAGCAAGAGTGCTGGAGGGCGGCAGCGCGAC
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SEQ ID NO: 3952 GGTACGAAAAGCGGCAGAACTAGCTCTGAAAACCTGAGCAAGGTCTGTGTG
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SEQ ID NO: 3953 GGTACGAGATGGCAGCCCTCCAGAGCCCCTTCTATGGAGATAAGATGAATCT
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NAGGTGGGTAAACCGANGCCCCGGANGCCCTGGANTTTGGATTGGAATGNGNAATTTAAGGNA
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SEQ ID NO: 3954 ACGCGGGAGCTCATGTAGGTCTTGATTGGACACAGTGAGTTTCAGATGACAG
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SEQ ID NO: 3955 ACAGACAGGCTTCTCTGCTATCCTCCAGGCAGTGTAATAGTCAAGGAAAAGG
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SEQ ID NO: 3956 ACNNGGGGGCNGCCGAGGCGTGACATGCTCGCCCAGCCACCCCCAGGACG
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TTAAATAGATACAAATGTCTATCAACTTTAATCAAGTTGGAACCTATATTGAAGACAATTTGNTAC
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SEQ ID NO: 3957 ACTTTTTTTTTTTTTTTTTTTTTTTTGGCAAAGTGCTTTATTTACACAGAGC
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GGGATTTGAAGTTGGCTACATGATGATTTCATAAACTNTGGAGTGTGCCCTTTGTGCTACTCCCA
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SEQ ID NO: 3958 ACGCGGGGGCTGACTCTCTTTTCAGACTCAGCCCACTTGACCCCAAGTGAATT
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GGATCTCCTNGGCTTAGTGGCTGAAGACTGNTGCTGNCGGATCGCCTCAGAAAAGCCCCCTGGACC
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SEQ ID NO: 3959 ACTGNTTACAAACACAGCTACTTCTCAAAATAGTCCTTTTCTTTCTTGAG
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SEQ ID NO: 3960 ACGGCACTTGGCGTAAAGCCGCTTCCCTCAAGAGTAACTACAATCTTCCCAT
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TTNTTCCGGCNAAAAAACNCAAAAAAAAAAAAAAAAAAGNTCTTTGGCCGGGACCCNTTANGGG
GAATTCANNACTGGNGGCGGTNTATGGNNCCCTGNNCCAACCTNGGNANTT

SEQ ID NO: 3961 ACGCGGGGATTACGAGATTGGCTTGGATTCTGTGCGGATGGACTTGGGGCTAG
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SEQ ID NO: 3962 ACTTTTTTTTTTTTTTTTTTTTTGGCGTTTCCACACCTGCCCTTTATTGGTCTCTTCT
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SEQ ID NO: 3963 GGTACTTCCCAGGAAGTGGGGACCTACGGGATATCGGGGCTGGCAAAGGCAA
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SEQ ID NO: 3964 CGAGGTACATTTCCCCGGGAGAACTCGTCCATTCGGTGGTGGCGGCCGTTATT
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CCCCGCT

SEQ ID NO: 3965 ACTTGTTGACATTAGAGGAGAAATGCCAAGGAATTTAAGAGAATACATGGTT
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SEQ ID NO: 3966 GGTACATGACAAGGTGCGGCTCCCTAGGCCCTCCCTCTTCAAGGGGTCTA
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SEQ ID NO: 3967 GGTACTTTTTTTTTTTTTTTTTTTTGGCAAGCACGTGCACTTTATTGAATGACAC
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SEQ ID NO: 3968 GGTACTGCAAGTCAAGGGGACTCTTTGCAGGCGTGTCTTTAGAAGGGAGCTG
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SEQ ID NO: 3969 GGTACACTGTAAATGCTCAATAAATATTGATGATGGGAGGCAGTGAGTCTTG
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SEQ ID NO: 3970 ACGCGGGGAAACGACAGGGGAAAGGAGGTCTCACTGAGCACCCTCCAGC
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GGTTCTAGTAACCGGCCATAACCTTGNAACCTTTGGATTCACTGGGCAANNNTTGGNCCTTGNNCT
TGGGT

SEQ ID NO: 3971 AACTGCCCAGGCAAAGCGTCCGGGCAGCGTAGGCGGGCGACTCAGATCCC
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SEQ ID NO: 3972 ACCTGCAGGCCTCCTACACTACCTCTCTCTGGGCTTCTATTTGACCGGAT
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SEQ ID NO: 3975 ACCGACCATAGAGCAAGAATCAAGATTCTGCTAACTCCTGCACAGCCCGTC
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SEQ ID NO: 3976 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGCATCAAAAAGCTTTATTTCCAT
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SEQ ID NO: 3977 CGAGGTACGCGGGGAGATGGCAGATGAGATTGCCAAGGCTCAGGTGCTC
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SEQ ID NO: 3978 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTAGTATCGATCTCTTTAATTTTAGGCC
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SEQ ID NO: 3979 GGTACGCGGGCCTTGCTCCTGTGTGCTGTCTAAACCACTGGTGGATGAATACT
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SEQ ID NO: 3980 ACTGTTGTCCATTTTCATGAGAGTAGGCTTGAGGACACCATGGGCAAGGATCT
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SEQ ID NO: 3981 GCGTGTGCGGCGGAGGTACAAAGAAAGTTTAAAGTCAAGGCCTCACCAATT
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SEQ ID NO: 3982 GGTACGCGGGGGTGGCAGCTTCGGATAAACGCAGGACTCCGCCCGGCAGCCC
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SEQ ID NO: 3983 GCGTGGGTGCGGGCCGAGGTACTGTTTATTAACCAACCAGCTTAGAAAAATA
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SEQ ID NO: 3985 ACTTGTGACAGGCAGACGTGATTGCAGCCACGAACACGATGAACCTCACTGAA
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SEQ ID NO: 3986 ACCGACGTTGAGGTGGCTGCTGACCTTGGGTCTCATCTCCTTGATTTTCTTTAT
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SEQ ID NO: 3990 GGTACTTTTTTTTTTTTTTTTTTTTTCGGTATCATAAAGAGNGNTGAAGTTTAT
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SEQ ID NO: 3991 GGTACATTTTCTCAAGTTAATGTATAAAGAAACTGCATTGATGTAGATAAAT
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SEQ ID NO: 3992 GGTACAGGTGCCCTCTGTGCCTATTCAGCAATTCCTACTGAAGACTGGAGCG
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SEQ ID NO: 3993 ACGAAAACAGAACCAATCTAAAAATGGCTGATGTTACTTTAGGAGCCTGAAA
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SEQ ID NO: 3994 ACATGGCAATTAGAAGTTGTCATGGCAAAAAGAAAAACACAGCTGGCCCTGCCA
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SEQ ID NO: 3995 ACGGGCTCATGAAAGTGTGTGAAGAGCGAAGACTTTTCGCTCCAGCTTAT
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SEQ ID NO: 3996 GCCGTGGGCGCCGNCAGAGNCCAGACATTTTCAAAGTTGCCAGTGTTACTT
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SEQ ID NO: 3997 TTTTNTTTTTTTTTTTTTNTACTTTTTCTTTAGTTTATTGAAAGAAATGTTTA
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SEQ ID NO: 4002 GGTACGCGGGGGCTGACTCTCTTTTCAGACTCAGCCCACTTGACCCAAAGTG
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SEQ ID NO: 4003 GGTACGCGGGGGAACGACAGGGGAAAGGAGGTCTCACTGAGCACCGTCCC
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SEQ ID NO: 4004 ACGCGGGGAAGAACCCCCCTATCAACACCAAGAGTCAGGCAGTGAAGGACC
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SEQ ID NO: 4005 ACTGCTATGAAGCATCCCTTCCACATCAGATCAAAGACATCTTAAAGCCAGA
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SEQ ID NO: 4006 ACTTTTTTTTTTTTTTTTTTTTGTCTGTAAGGCCGGGTGGTTGCTGCCGAAATG
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AATTGACCGTACCCCGCAAAGTGACAGCTGCCATGGGCAAGAAGAAGATCGCCAAGAGATCA
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SEQ ID NO: 4007 ACGCGGGGAAACGACAGGGGAAAGGAGGTCTCACTGAGCACCGTCCAGC
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SEQ ID NO: 4008 ACTTNTTTTTTTTTTTTTTTTTTCTTTTAACTGAAAGAGTTGACAATTTTATTT
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SEQ ID NO: 4009 ACCATCCTTTAATAGATCTCATACACCAGAATTCAGATCATGAATGACTGACA
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SEQ ID NO: 4010 ACACTGCCCAGGCAAAGCGTCCGGGCAGCGTAGGGGGCGACTCAGATCCC
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SEQ ID NO: 4011 GGTACGCGGGGCTCCAGAAGTTCCCCCTTGGGCGGTGGTGGAGGTGGTAAC
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SEQ ID NO: 4012 CGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTAAAGNTAGGAAGAAGAAT
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SEQ ID NO: 4013 GGTACAAAAGCTTTTCTGATGCTTTTCATTATCAGAAACACACCACCTGTAA
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SEQ ID NO: 4014 ACGTAAAGTTAACCTTCCAATTGTCTGAGCTGTCGCTCACTGACTTCATGACAG
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SEQ ID NO: 4015 ACGCGGGGAAACGACAGGGGAAAGGAGGTCTCACTGAGCACCGTCCCAGCA
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NCGNCCATANNNTNNAACTTTGNNTTCACTTNGCAANGNTGGCCTTGNCTGGGGNTGNTGCCN
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SEQ ID NO: 4016 GGTACCATCCGACGTTACAATGGTGGAGTTGGCAGGTGTGCGCAGGCCAAG
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SEQ ID NO: 4017 ACGCAGCCCCTCACACACTGCTTCATTTTGTGATTTCTGCATTTCCAGCTGCC
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SEQ ID NO: 4018 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTACTGGCTAACAGAATTTTATTGT
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SEQ ID NO: 4019 ACAATATCATATATCTGGTATACAAAAAAATCGCTCATTATTTTAGCCCTAC
CCTCCATTTGTCTCTCTTTCTGGGACTCCTATTGATTGCATGACCTTCTGAAGGTCCTTGTGTGTG
TCTTACCTTTTTTTCATAACTTCTCTTAATTTTTTTTTTTTTTTTTTNNANAGTCTTTCTGTACCC
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SEQ ID NO: 4020 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGCCATATCATTCATGACCAAAAAA
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SEQ ID NO: 4021 ACGGAGGAGTTCCTGGAAGCCTTCATGGATCTGAGCCTCCGGAATCTCCGTG
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CTGGCGGTATAGGCTGAAGGCGAACTCAGCCAGGTTGGGGGTGATCTTGTGAAGGTTGGGTGAT
CCTGATCATGGTGGGATGTATCTTGTCTTCTGGGCANNATCTNCNTGGGGATNCTTCATCCANGG
ANACATGNACCAANTAGNCTNNGCCTGCCTACTAANAGGATGCCNCCAGANNGATATCGGNTTT
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SEQ ID NO: 4022 ACTGATTCATCACTGTCAGATTCTGTTCCAGACCCTGTCTCAGCCTGGGGCTG
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SEQ ID NO: 4023 ACAGACATGGCGGCGGCTTTTCGGAAGGCGGCTAANTCCCGGCAGCGGGAA
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SEQ ID NO: 4024 ACGCGGGGGAGTCACTGCTGCTCTTTGAGGCAATGCGCAAGGGCAAGTTTTTC
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CTACACACACTGCCTCTGTGACTCCATCGAGCACATCACTCACTCACTCTGCACCAAGGAATTCCA
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CCACCTGATGGCCATCAACACTTNTGTGCCGGGTGGGAAGTGANTGTGGCACAAACCAACAATG
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TGGCTOGAAGTAATTACGGGTAATTNATACCAANTTTCTGTTGCCAANTCCTTGGGAATTTC

SEQ ID NO: 4025 ACAGGCAGAGCAACCATCCTCTTCGTACCCAGACGCAAGACAGTAAAGGA
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SEQ ID NO: 4026 ACAAGTATTTATATCAATGAAAAATTTCCATTGGTGATTTTTTGGCAGAATATT
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ACAGATTTACCCGTGCCAGTTTTCCAGCTGTCAATACTATTCTNGCATTATCATGGCTTAAATCN
CACAAATTNCTTGACCTTCTGTACCC

SEQ ID NO: 4027 ACCTAAATAATGTCCTTCATTTTGTCTTAGCTTGCAAAGCCTCTAATATTTGCT
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AGNTAAATTTATAAATAAAGGGATAGGAAAAATGCTGATTATTCTGNGTGNCNGNGCTTTNAAT
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SEQ ID NO: 4028 GGGTACTCTGGTGAGTCAACACTTCAGGGCTTTACTCCGTAACAGATTTTGT
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SEQ ID NO: 4030 ACGCGGGGGCGTCTGTTCTTGCTGGTGTCGGTGGTTAGTTTCTGCGACTTG
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AATATGTTGTGTTCTTCTTTTACCCTCTTGAAGCTTACCTTTGTGTGCCCCACGGAGATCATTGCTTTC
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SEQ ID NO: 4031 ACCCTCCAGAAATTGGTGACTTTGCTTTTGTGACTGACAACACTTATACTAAG
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SEQ ID NO: 4032 ACACAATGGTTTATTAAAGGAATGTATGGCCACATCAACCTAGCAAGGATT
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SEQ ID NO: 4033 ACTGCAGCTAAACCAGCGGCTTCAATAACAAGTAAGCCTGCTACACTTACAA
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SEQ ID NO: 4034 ACCTGGGGGGAGTTGTAACACTCCANAAGGTCCAACTCCTCTCTTGGCATGG
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SEQ ID NO: 4035 ACGCGGGGGAGCCAGCGCGGAGCACCTGCGCCCGCGGCTGACACCTTCGCTC
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SEQ ID NO: 4036 CCGGGGGTAGACGGAACCTTCGCCTTTCTCTCGGCCTTAGCGCCATTTTTTTGG
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SEQ ID NO: 4037 ACTACTGCTGTTTTCTGAAGACGCGAGGGCAAGTGACGCCAGCCGTTTCTTTT
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SEQ ID NO: 4038 ACCTAGAAGAGAGGGCGGGTCAAAGAAGTAGTGAAGAAGCATTCTCAGTTCAT
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SEQ ID NO: 4039 ACACATGAGAGAAAAATCTTTCCAATGTAATGAGAGTGGCAAAGCCTTTAAT
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SEQ ID NO: 4040 ACGCGGGGTCCGCCGCTAGTCTCCAGCTCCAAAATGGCGGCTGCCACTGTGG
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SEQ ID NO: 4041 ACTTGCAGCCCTCGGCCAAACGGCCAGACGCCGACGTCGACCAGCAGAGACT
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SEQ ID NO: 4042 ACATGACAAGGTGCGGCTCCCTAGGCCCTCCCCTCTTCAAGGGGTCTACAT
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SEQ ID NO: 4043 ACNCGGGAGAAGAAGAGTAAGAAGGACAAGAAGGCCAAAGCTGGTCTGGAG
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SEQ ID NO: 4044 GTTTTTNTNTTTTTTTGGCCCAAATTTATTTTATTTTGACACATAGGAAAC
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ANATCTGCTTNAAGTTTACTCTGAACACGGACNCTCCGGGAATTCNACACACAGGAGCTGNNTC
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SEQ ID NO: 4045 ACCAAACGGGCAAGGACATCTCTACAAATTACTATGCGAGTCAGAAGAAAAAC
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SEQ ID NO: 4046 ACTTTTTTTTTTTTTTTTTTTTNGCATCAAAAAGCTTTATTTCCATTGGTCCAA
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TNAA

SEQ ID NO: 4047 ACTTTTTTTTTTTTTTTTTTTTNGGTTATTTTAGTTAAAGAAAAACA
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SEQ ID NO: 4048 ACTCTGCCACAACTGATCACACTGCTTCTGGTAAGGGTCTGGCAGGAAGCT
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SEQ ID NO: 4049 ACCGACCATAGAGCAAGAATCAAGATTCTGCTAACTCCTGCACAGCCCCGTC
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SEQ ID NO: 4050 ACTGTTGTCCATTTCATGAGAGTAGGCTTGAGGACACCATGGGCAAGGATCT
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SEQ ID NO: 4051 ACTGAGGACAAATCAGTTCTCTGTGACCAGACATGAGAAGGTTGCCAATGGG
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SEQ ID NO: 4052 ACTTCCCACTTTTCATAACGAGTNGGAGCCTAGAGTTGATCGACTCCAGCGAC
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SEQ ID NO: 4053 ACCAGAAGTATAAGTTTATGGAACCTCAACCTTGCTCAAAAAGAAAAGAAGGCT
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SEQ ID NO: 4054 ACGCGGGGAAGGGGAGAGTTTAAAAACCCAAACCGTTGTGGTTTAAAGGTGT
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SEQ ID NO: 4055 ACAAAAAAATTAAATTGCTTAGTTATAAAAAGAGCTCTGTCAATATACACA
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SEQ ID NO: 4056 ACCCGTGATGCCGTTGACAAGTATCTCGAGACACCTGGGGATGAGAATGAAC
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CCA

SEQ ID NO: 4061 ACTTTTTTTTTTTTTTTTTTTTTTTTCCAAAGCAGTATGTCTCAATAGTGGCCT
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SEQ ID NO: 4062 ACACACACGGGAAAGAACTCTGCGAGTCTGATGTGTGTCAGAGTTCAGTC
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SEQ ID NO: 4063 ACCCAAAGCCTCCCAAGGCCACAGTAGTCATGCTCCCGGGCAGTATCTGCC
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SEQ ID NO: 4064 ACAGTTTGCAGAAATATATTCAGAAAAACGTGCAACTTTATAAGATGCGAAAT
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SEQ ID NO: 4065 ACGACCTCATTCGCGTGTCCAATCATTATGGAGCCATGGGGGTGGCCACTAC
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SEQ ID NO: 4066 ACAGGTTTCACTATTACAAATATATGATGTTAAACTAACAACTCATGACCTT
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SEQ ID NO: 4070 ACTTTTTTTTTTTTTTTTTTTTTTNGCAGTAAGAGTAGCCAGGTGTTAGCCAC
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CATTTCT

SEQ ID NO: 4071 ACATTGAAGCTCGGGTGACAAAAGGTGAGACACTCACCTAGAACAGTGCCGT
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SEQ ID NO: 4072 ACGCGGGAGCCAAGAGGGCGGATAAGTGCCCCACCTTAGAACAGTATGCCAT
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CAGACATTGCT

SEQ ID NO: 4073 ACTTTTTTTTTTTTTTTTTTTTTTTCANATTTTGTTTTATTTTATTATG
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SEQ ID NO: 4078 ACTTTTTTTTTTTTTTTTTTTTTTTCTCAAGCACGTGCACTTTATTGAATGAC
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GATGGNGCT

SEQ ID NO: 4080 ACACAATGGTTTATTAAAGGAATGTATGGCCACATCAACCTAGCAAGGATT
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SEQ ID NO: 4082 ACTAGAGCGCAGAGTTTCAGACTTGGATTTATAAAATGCTTCAACGTGTGGTG
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SEQ ID NO: 4084 ACGCGGGCGGGGAGGCTTTGGAGGGCGAGGAGGCTTCCGAGGAGGCAGAGG
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AGGGA

SEQ ID NO: 4091 ACTGCTATCTCGCATTCTTCTCAGGTTGCCAGGAAATGTTTCTCTAACCCCTTTC
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SEQ ID NO: 4092 ACAGCACTTCGGAAGAGTTTGTAGTTGGCCCTTTGCTGGTTGGGCTGAGTTTTC
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SEQ ID NO: 4093 ACGCGGGGTTGCTTTATTTCCATCAAAGCCCTCTGAGAAGTGAGACCTCAGC
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SEQ ID NO: 4094 ACATTCGTGTTTCATGTTTACAANNCTCTCCATATATTTACAAATTTACGAT
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SEQ ID NO: 4096 ACAGGAGTTGTTGCATATTCCATGAGGCTGGTGTGCGGAAGCAGGGACCCAC
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SEQ ID NO: 4097 ACTTTTTTTTTTTTTTTTTNNNTTGGGGTATAAACTACTATGCTTTAATGAGC
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CCTNAAAANGGA

SEQ ID NO: 4098 ACTTGAGGTAACAGTCATGGAGATCGAGATAACGACCATATCCCTCTTCATCT
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SEQ ID NO: 4103 ACAACAAAAAGATTAGGAAGCAAAATGTGAATAAGCTTGTATTGAGAATATACCTATATGTGTGTGCAAGACAATACACTCATCATATACCTCACTTAGGTTCCCTTTATGATGCATAATTCCTTAATCATTCAATTTGTGAAACAAGAATGAATATTAAGAAACATGAAATCCAAATTGCACTTATTTTACAATATCAATGCTAAACTCAAAATAGCAACTTCATTGACTCTCAATGGTAAATTTCAAAATGGAAGCAATCTTAATTTTTTAACCCCTTTGACTAGGGTCTGTAAAAAACGGTGGATTATTTACTGTACAGCATTCTGGAATAAGCAAGAGTGTTCATTACACACACACAGTAGCTTCAAAACTGTTCGATCTGTTTGTTCCTATGTAGTTTTCTAAAGATGGAAAAAAGGACTTTTGGTCATCAAGACTACTGTGGCCATATTAGATTACTGGAACATCTAAGCATCAGTGTGTGACCATGCGAACAAAAGACTTCGGGGAGTGTCTATTTTTAAAAAGGTTTATGTGTGTGAGGCAGTTGTAAAAGATTTACTGCAGAATCAAGCCCTTTTANGCTTAGGACCAGGTTCTAACTATCTAAAAATATTGACTGATAACAAAAAGTGGTCTTAAATGT

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SEQ ID NO: 4105 ACCTGGCCATCCTGGGCAGTGTGACGTTTCTGGCTGGCAATCGGATGCTGGCCAGCAGGCAGTCAAGAGAACAGCACATTAGTTCCAGAAGAAAGATGGAAATCTGAAAACTGAATGTCAAGAAAAGGAGTCAAGAACAAATTCACAGTATGAGAAGAAAAATGGAAAAAACTTTATTAAAAAAGAAAAAGTCCAGATTGTAGTTATACTTTTGCTTGTTTTTTCAGTTTCCCCAACACACAGCAGATACCTGGTGAGCTCAGATAGTCTCTTCTGACACTGTGTAAGAAGCTGTGAATATTCCTA ACTTACCCAGATGTTGCTTTTGAAAAAGTTGAAATGTGTAATGTTTTTGGAAATAAGAGGGTAACAA TAGTNAAAAAANAAAAAAGGTCCCTGCTATTTTAGAATCCTAGAGAACA TTTTATTGTAANAACTAGTCCATTATTTAAGTGTCCAGTATTTTTTCAATTCAGTGGGTCCAAGATGCNAAGGTTTCCAGACACAATCTTGGTCTCTAATACTGCTCCAGGGTGGGATATCAATCTGTGCACATGATTTGCAATGATGATAACCGTTCCCTTTAATGAAACATTTTTTCCAAATGTCCACATNTCCTGNAACTGNGGAG

SEQ ID NO: 4106 ACAACATGACATTACAGAGTATCTTATAAAATACAAAGACAAATATAAAAGACTATGATGCTTTAAGTCTGAAAACTATTGGCCAAATATTTAGGTTTAAATTTACAGTTCCTGGGTATGAGAATCATATTACTATATACATCTCCCAAACAGTAGGTAGTATTTTCCAATTAACCATGTGTGTGATCATCTTCTACAAAGTCTTTGGCCATCTCTGCTGTGATCACAATATGACTAACCTTATTCTGAACTTTACACCATAGAAATTTGTCAGCTGACTCAAGCAGTTCAGGCCTAAAAGTAGTTGTAATAAAGTGAATGATG

SEQ ID NO: 4107 ACGCGGGGACGGTTCGTTTGTCTTAGTCAGGAAGGACGTTGGTGTGAGGT TAGCATACGTATCAAGGACAGTAACTACCATGGCTCCTGAAGTTTGGCAAACTCGGATGCGTG GCCTTCTGGCCAGGCGTCTGCNAAATCATATGGCTGTAGCATTGCTGCTATCCCTGGGGTTGCAN GCTTTGTATAAAAGTTTCTGTGGCTGATCAAAAANAANAAGGCATACTCAGATTTCTACAGAACTACAATTGTTATNGAAAGATTTTGANNANATNAGGAAGGCTGGTATCTTTNANANTGTAGAAGTAATCTTTGGAATATAAAAGAATTNCTCCANGTTGANTAANCTAAAAATNANTAACTGANCTAGT

SEQ ID NO: 4108 ACTGGCCTGCTGCTGGCCCGCAGGCTTCTCAATAGGTTTGGCATGGACAAGA TCTATGAAGGCCAAGTGGAGGTGACTGGTGTATGAATACAATGTGGAAAGCATTGATGGTCAGCCA GGTGCCTTCACTGCTATTTGGATGCAGGCCTTGCCAGAACTACCACTGGCAATAAAGTTTGTGGT GCCCTGAAGGGAGCTGTGGATGGAGGCTTGTCTATCCCTCACAGTACATCCAAAACCATAAGGAA ATATTCTGATGCCAGATGATGAAGACTGGGGTGAATTAAGTCCACACATTTATTTCAAGTTGTTA AAGAGTTTGTGGGCCACGCAATGGTCCCTCGCATGCAAGAAGTCAAAGAGCTCCTCCGTGCAATC CTCTTCTGTATGTGATCGAGAGGATACACGCTCATCAGAGCTTAGCCGCTCCCGGGCTTTACACATTTCTCCAATGCTCGCATGCTCTCTCACTGTTGTTAGGGGATCCAATAATTCCTCTCTCC TCTTCTCCTCCTNAGGATCTCCGATTCCGTAAGCATCTTTGCTCGTCTCATCCCATGCTTTGG CTACGGTTCTAGATTCAACACGAANCAGCAACAGCGGCACCTACCCANTTCANGATCAAAAAAGG ACTTGTAAGGGTC

SEQ ID NO: 4109 ACGCGGGGGCGGCCAACATGGCGGAACGCAGGAGACACAAGAAGCGGATCC
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SEQ ID NO: 4110 ACAGTAAGGCAGTAATTCATTAGCATCCTGCTGTGGTTTTCTTTCAAGTTA
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CCCTCAAANAATACTAAGCCNGTGGTGCCTTTTATTTCATTGAACACATTAGTTTTTTAATCTAA
CAGC

SEQ ID NO: 4111 ACGCGGGGAGCCGGGTGCTGATGCGAGTCCGTGGCAGCGAGGACATTTCTG
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SEQ ID NO: 4112 ACCATACCATTATAAAGTGGAACTCTTGACCAAGATTTGGATTAATTTGT
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SEQ ID NO: 4113 ACGCGGGGAGGCATTGAGGCAGCCAGCGCAGGGGCTTCTGCTGAGGGGGCA
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SEQ ID NO: 4114 ACGCGGGGGCTGTGCTCACTCAGATTGTCCGTTTGCTATGCCGAATGCAGCC
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CCCCGAATATTGTTAAAGATCGANCAATGGCTTCAGGACATGGGTTCTCTTCTCTGTGATCATTC
AAGTGCTTACTGCATGAAAGACTGGCTTGCTCAAGTGTTTCAACCCCTCACCAGGGGCTGGCTNTT
GGGTCCAAACCTTNGGTTCTGTTAANTGCCGTTNTGAACANCCCCCAATCAAAANTGACCTT
TGNNCC

SEQ ID NO: 4115 ACTAAGAGAAAAGCACGAAGCTGTGGATCATAGTTCCAGCATGAGGAAAA
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 ATGGGACAGATACTTCTTTCTCTCTGGAAGACTTATTCAGTTGCTTTCATCACAGCCTGAAAAATTC
 ACTGGAGGGCATCTCATTGGGAGATATTCCCTCTTCCAGGCAGTATCAGTGATGGCATGAATTCCTC
 AGCACATTATCATGTAACTTCAGCCAGGCTATAAGTCAGGATGTGAATCTTCATGAGGCCATCTT
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 TTCTGCAGTTAAATTCATACCACCAATCCTGAGCAAAACCTTCTGGAACATAATTTGACAGGAT
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SEQ ID NO: 4116 ACTTTTTTTTTTTTTTTTTTTTTTTTGCACAAGCACGTGCACTTTATTGAATG
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 ACTTGGCGGTGGAGGCATAGGCCTGGGCCCGGTACGTCGCCAACCATNTTCTGTCCCTAGACT
 TCACGGAGTAGGCGAATGCTATGAANCCCANACAGCACCAGITCAAGAAGAGGGGTGTGAACAG
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SEQ ID NO: 4117 ACGCGGGTATAAACTATGGAGAAAACTGCTAAAGGGTATCCCTGACCTTTA
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SEQ ID NO: 4118 ACAAAGACAAACACCTAAACACACTGCGTCAAGTGACGACCCGACTTTGGT
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 AGCATCNT

SEQ ID NO: 4119 ACTTGACGCCCTCGGCCAAACGGCCAGACGCCGACGTGACCGAGCAGAGACT
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SEQ ID NO: 4120 ACTTGATATGGAAAGAAGCTTTTTTCTTCTCAAGTTGGATGCAGAAGTGAAT
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 TTAGCAAAACTACCTGATTATGCCCATGTTTCCCAATACCTTGATTTTCTTATATTGACATTTCA
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GGGTT

SEQ ID NO: 4121 ACCTATATGGCTCCCCCAATTAATCACAATTCAGCAGCATCCACTCCCCATAT
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SEQ ID NO: 4122 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGAGACGGAGTCTCGCTCTATTGGCAG
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SEQ ID NO: 4123 ACTTTTTTTTTTTTTTTTTTTTTTTTNGACAGTGCTTTCTACTTTAATAACATCAA
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TCAC

SEQ ID NO: 4124 ACGCGGGATCTGAAGAAAACCAAGAAGAACTAAGCATTGATAACTGCATTGT
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TAATT

SEQ ID NO: 4125 ACAAGTATTTATATCAATGAAAATTTCCAATTGGTGATTTTTTGGCAGAATATT
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CACAGATTTACCGTGCCAGTTTTCCAGCTGTCTACTATTCTGCATTTTCATGGCTTCAATCACA
CAAATTTCTTGACCTTCTGCTACCGGT

SEQ ID NO: 4126 ACTGGTGTCCCTGGGTGCCAGTGAGAACTATCCTTGCTCTCTGCGGGAATC
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SEQ ID NO: 4130 ACCGTGTCCTCGTTCTTAGTGCTCGAATGTCCCAACCTGAAGCTGAAGAAGCC
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SEQ ID NO: 4131 ACCAGAGCTTGAAGAACAGGATTCCACCCAGGCAACCACACAACAAGCCCA
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TATCCGGAAATCTAAGAAATATCCTCTTTGTATCACAAAACAGATGTCTACAAGAGCCCTGCTTC
AGATACTTACATAGTTTTTGGGGAAGCCAAGATCGAAGATTTNTCCANCAAGCACAACCTAGCAG
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SEQ ID NO: 4132 ATGNCAATTGCTTCGNAGCCGGGCCCGCCAGTNGTGGNATGGGNATTATTCT
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SEQ ID NO: 4133 ACTTTTTTTTTTTTTTTTTTTTTTTTTTNTNCCCTATTCTNATTTGAGTTTCCTG
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SEQ ID NO: 4134 ACGCGGGGAAACGACAGGGGAAAGGAGGTCTCACTGAGCATCGTCCCAGCA
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SEQ ID NO: 4135 ACTATTTTCATGGTCCAAACCTGTTGCCATAGTTGGTAAGGCTTTCCTTTAAGT
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AATA

SEQ ID NO: 4136 ACTAGCCGGACTTGGATTTTCTGGAAAGATTTCAAGTTGAGGAACGGGAACAA
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CTATGGTGTCTGGCTTCTTTAACTCANGATAGATCCAGGTGGGGCTCCGNTTCTTAAACTGACA
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SEQ ID NO: 4137 ACGCGGGGAATGAAGGTGATAGAAAACCGGGCCATGAAGGATGAGGAGAAG
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SEQ ID NO: 4138 ACACAATGGTTTATTAAAGGAATGTGTGGCCCATCAACCTANCAAGGATT
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SEQ ID NO: 4139 ACTGTATGTGTTTCTTGAAAAAGTCTTGTATGCATCTGCGAATTTCTTCCTTTT
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SEQ ID NO: 4140 ACGCGGGGAGACATTCACAGCCAAAAGCCTGGGACTCTTTGTGAAGGTCCTC
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SEQ ID NO: 4141 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTACACAAAAACACTTTAATTGACAGTAT
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ATAAAT

SEQ ID NO: 4142 ACTTGGCCAAGCGCTCAGATCGGCAAGGGGCACAGTCTTGATCTGCCAGT
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SEQ ID NO: 4145 ACTGCTACTTCTATAAACGGACAGCCGTAAGACTAGGCGATCCTCACTTCTAC
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SEQ ID NO: 4146 ACTGTTTCTTACATGCGAATCTACAATTATCTCAAAATAAAAAAGTCTAATTTA
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SEQ ID NO: 4147 ACTTTTTTTTTTTTTTTTTTNTCTTTTTTTTTTTTTTTAGGTCCAATGGTAGT
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SEQ ID NO: 4148 ACCTATTTGACTTACCATGGAGTTAACATCATGAATTTATTGCACATTGTTCA
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SEQ ID NO: 4149 ACTGCCATTCCTTAAATTCATTTAGATTACAGTGTGTAATCATAACTTTTGATC
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SEQ ID NO: 4150 ACTTCTTCAGATCGCCAGGATTCAAGAAGCCATAGTTCAAGAAGAGTTCTC
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SEQ ID NO: 4151 ACCAGTAAATCAAAAAAGAGGGAGTATGTCCATTTAATTTTATTGAAGTG
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SEQ ID NO: 4152 ACCAGCGCGGAAGTTGGTCTCGACACCTGGACTAGCCGGGTTGTATTTGGA
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SEQ ID NO: 4153 ACCTTTTCATCTTCTCTGTGGCCAACATGAGGAACAGCAAGCTGAAGGACAT
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SEQ ID NO: 4154 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTGGCTTTCTCCTCTCTCTCTTTGTCC
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SEQ ID NO: 4155 ACAAATGTTTTTTTATTCAAAAATACAAAATAAAATTATCTGTAGGCATGGACA
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SEQ ID NO: 4156 ACGCGGGGAGGAGGGGCTGCTGAGATATCCTGTGCCCTGGCAGTTAGCCAAG
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SEQ ID NO: 4157 ACTTTTTTTTTTTTTTTTTTTTTTTTTTGCATCAAAAAGCTTTATTTCCATTTGGT
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CC

SEQ ID NO: 4163 ACGCGGGGGGAAAGGAGGTCTCACTGAGCACCGTCCCAGCATCCGGACAC
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SEQ ID NO: 4164 ACGCGGGACTCCTCAGCAAATGCAAAAGAACTAAAATCATAACAGTCTCTAG
GGCCACAGCACAAATCAAATTAGAATTCAAGATTAAGAACTCACTCAAACTATACAACCTACATG
GAAACTGAACAACCTGCTCCTTTATGACTCCTGGGTAAATAATGAAATTAAGACAGAAATCAAGA
AGTTCTTTGAAACCAATGAGAACAAAGATATTTGATATAATGTACTCTGACAGCTGTGCCAGATGC
CATCCTTGAGGACTTGGTCTTCCCAAGCGAAATTTGGGGCAAGAGAATCCGCGTCAAACTAGATG
GCAGCCGGCTCATAAAGGTTCAATTTGGACAAAGCACAGCAGAAACAATGTGGAACACAAGGTTGAA
ACTTTTTCTGGTGTCTATAAGAAGCTCACGGGCAAGGATGTTAATTTTGAATCCCAAGAGTTCAA
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SEQ ID NO: 4165 ACTTGCAGCCCTCGGCCAAACGGCCAGACGCCGACGTGACCCAGCAGAGACT
GGTAAGAAGTTTGATAGCTGTAGGACTGGGTGTTGCAGCTCTTGCATTTGCAGGTCGCTACGCATT
TCGGATCTGGAAACCTCTAGAACAAAGTTATCACAGAACTGCAAGAAGATTTCAACTCTTAGCT
TTTCATCCTACTATAAAGGAGGATTTGAACAGAAAAATGAGTAGGCGAGAAGCTGGTCTTATTTTAG
GTGTAAGCCCATCTGCTGGCAAGGCTAAGATTAGAACAGCTCATAGGAGAGTCATGATTTTGAAT
CACCCAGATAAAGGTGGATCTCCTTACGTAGCAGCCAAAATAAATGAAGCAAAAAGACTTGCTAGA
AACAACCACCAACATTGATGCTTAAGGACCACACTGAAGGAAAAAAAAAAAAAAAAAANAAN
AAAGT

SEQ ID NO: 4166 ACGCGGGGAGCTGGAGGCGGCGAGCGGAAGCCCCACCATGGCTGCAATCC
GAAAGAAAGCTGGTGATCGTTGGGGATGGTGCTGTGGGAAGACCTGCCTCCTCATCGTCTTCAGC
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GACGGCAAGCAGGTGGAGCTGACTCTGTGGGACACAGCAGGGCAGGAAGACTATGATCGACTGC
GGCCTCTCTCTACCCGGACACTGATGTCTCATCTCATGTGCTTCTCCATCGACAGCCCTGACAGCC
TGGAACACATTCTTGAGAAGTGGACCCAGAGGTGAAGCACTTCTGCCCAACGTGCCCATCATC
CTGGTGGGGAATAAGAAGGACCTGAGGCAAGACGAGCACACCAGGAGAGAGCTGGGCAAGATGA
AGCAGGAGCCCGTTCCGTCTGAGGAAGGCCGGGACATGGCGAACCGGATCAGTGCTTTGGCTAC
CTTGAGTGCTACGCCAAGACCAAGGAGGGAGTGCGGGAGGTGTTGAAATGGCCACTCGGGCTGG
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NCTACATGCCCTT

SEQ ID NO: 4167 ACTTTTTTTTTTTTTTTTTTTTGAATAACCTGCAAGAGCTGCCTGTATTTA
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TCCATGTCCAAAAAGCTCTTCTTTTTTAACTTCTGTTGAGCATTGTAATTTCTTTCATGATCAGTCT
CATCCCAAGTGATTTCCACCGTTGATGTTCCCATGTCAGCANAAGTGAAATATTTTGGTTTATATG
CTGTTAAATTCATTTCTGAGGCTACATCCTTAGGCTCATCATCAAAAGTAATATCATCTGGTATAA
ACCTTAGATCTATGAAAGAACAACTACTTTCAAATTCAGGCCATCACAATCCTCATAAATTTTAC
TAGCTGTTTCCGGAGAATCACAGTCTACTACTGCATAATAGT

SEQ ID NO: 4168 ACAGCCTTGGCTTCCCCAACTCCACAGTCTCAGTGCAGAAAGATCATCTTCC
AGCAGTCAGCTCAGACCAGGGTCAAAGGATGTGACATCAACAGTTTCTGGTTTCAGAACAGGTTT
TACTACTGTCAAAATGACCCCCATACTTCTCAAAGGCTGTGGTAAGTTTTGCACAGGTGAGGGCA
GCAGAAAGGGGTAGTTACTGATGGACACCATCTTCTGTATACTCCACACTGACCTTGCCATGG
GCAAAGGCCCTACCAAAAAACAATAGGATCACTGCTGGGCACCAGCTCACGCACATCACTGAC
AACCGGGATGGAAAAAGAAGTGCCAACTTTATACATCCAACCTGGAAAGTGATCTGATACTGGAT
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GAACATTCTTCTGTGATGGATATAAACCTGTACAAGCCAGCTCGGTTCAAGGGACTATCCATCAG
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TATAAATTG

SEQ ID NO: 4169 ACAAAAAGACAGCCAGAGGTGTGCGGAGAGGGTGAGGTGGCCGCGTGGAAG
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GGTTTGAGGGATTGCGGGAGGGGGTCACTGACTCAGAGAAGTAGGATCTCTGCACTGGAACCT
GAGGCTTCTGTCTCTCCATGGGCCCCACAGTCACAGGGACATGAAATCCGTGGCCTGGAGGA
GAGGAGGGGAGAGCAGGAGCAGCAGCCACNAGGTGTTCTGAGCCAGCAGGCTGATGCCCTC
ACACTTGACCAAGTTTGTCTCTGAGCACTGTGACGTTCTGGGAGGAGATGGGTGGGGATGGCCAG
AGTGGTGGAGTGACACAGTGTAGGTGCCCTCGTCTTGTAGTGAAGGCGGATAAGTAGAGGACC
TTCATGTTGATTTGCTGGTGAAGTTGTTTGGGAGCGGTATGTGTGCTCAGGCACCCCCACANTG
CCAAANAGCACGTGCTTCTTGTCTACGGGTCAAGGTGAACCTCGTACCTCGG

SEQ ID NO: 4170 ACGCGGGGCTCTCAGAACCTTCCTGCCGTGCGGTTTGACCTCGCTGCCAG
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CCCCATACATACCTTGAGGCGAGCAAAAAATTAATTTTAACCATGAGGGAATCGTGACATC
CAGGCTGGTCAGTGTGGCAACAGATCGGTGCCAAGTTCTGGGAGGTGATCAGTGATGAACATGG
CATCGACCCACCGGCACCTACCACGGGGACAGCGACCTGCAGCTGGACCGCATCTCTGTGT

SEQ ID NO: 4171 ACTTGCAGCCCTCGGCCAAACGGCCAGACGCCGACGTGACCCAGCAGAGACT
GGTAAGAAGTTTGATAGCTGTAGGACTGGGTGTTGCAGCTCTTGCATTTGCAGGTGCTACGCATT
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CACCCAGATAAAGGTGGATCTCCTTACGTAGCAGCCAAAATAAATGAAGCAAAAGACTTGCTAGA
AACCAACCCAAAACATTGATGCTTAAGGACCACACTGAAGGAAAAAAGAGGGGACTTCGAAA
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AAGATTTT

SEQ ID NO: 4172 ACGCGGGGGGAGTTAGGCGACCAAACAGTGAGAGCCCCAATCCCTGCAGTT
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CCTACGAAATCATTTGTTTCTAAGTTGTGTTTATTCTGGAGTGACATGCCACCCGAATGGCTCAC
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TTTCTTTAAAAACAGTGCCAAGAATGACAAGATTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAG
TCCTT

SEQ ID NO: 4173 ACCAACAGACGTGGATAAGTGGTTCCATCACCAGAAAACTAATGAGATTTC
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AATATCAAAGCAGTTGTCAATTTGGAAGTCACTGTGTAATAGATGTGCAAGGGGAGCACATATTGG
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SEQ ID NO: 4174 ACGTGCAACCTTGTGCTACGGCCACTATTCTTCATTTTGGTAGAGCCGAAT
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CTTATGGGCATAAAAAACCTGGGCCCTGGGTTAAAGCTGTTTGTGATCTCCTTATCCAACCTCACATC
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CTCAATGGGTGATCAAAACACTAAGATCCTGTGGCAGATTGCCACGAACATCATCAATGTCCA
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AGTCTTNACCAAAAAATGTTGACACCGTCTNCTGGGAAGCTTATTGGT

SEQ ID NO: 4175 ACGCGGGGAGACGCGCGGGCGGGAAGATGGCGGCTGGGTTCAAAACCGTGG
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CTACTATCAAAAAACAGAGATAATATGTGTTGGCAAGGACCGTGCAAAAAATGGAACCTTAT
TCCTGTGGGTGGGAGTGTAAATTAGT

SEQ ID NO: 4176 ACGCGGGGGCTGACTCTCTTTTCAGACTCAGCCCACTGCACCCAAGTGAATT
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GATT

SEQ ID NO: 4182 ACAAATTTAATAAAGCCTTTGATCACATCTCAATCCATAAGTTAGCTACAAAA
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CCTTCAATAATATTAATACATTCTGTCTTTAAATTCCTTGCCATGTTCCATCANAGTAGAGCACA
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GTTTGCCT

SEQ ID NO: 4183 ACTTTTTTTTTTTTTTTTTTTTTTTCNAATCTGAAGTCTTGTGTTTACTAAT
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TAAACTG

SEQ ID NO: 4184 ACCTGGGTGTTCCCACTTGGGCATCATGCACCACAACAAACAGGCCACTG
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CGGGAAGAGAAGCAGAAGCCCAAGGCTGAGCGGAAGGAGGAAAAAGGCGGCTGCCCTGCTC
CTGAGGAGGAGATGGGGGTCATTAAAGGAACTGAACATTGGATAA

SEQ ID NO: 4185 ACAAGTAAGTGTAGAGCAAGTAAGTAGTTTGGTCCAATATTATCTTAATGT
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SEQ ID NO: 4186 ACGTGCAGACGGTGGTAGTTCTGGAGTCTGGAAGCCACGAGGTGCTCATCC
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CCGCGT

SEQ ID NO: 4187 ACTTTAGGGGCTGCCATTGGGTATTTCTTCTGGAAGGAATAGTTCAAGTTTAAA
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SEQ ID NO: 4188 ACGCGGGGGGATGGTTCATCATGGCGTCAATGCAGAAACGACTACAGAAA
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TTTACCTTGTGGAATGACCTTAGCAATGAACTCTTCTTTTACTGATTTTTTACTCTGTCATCTGG
CGCTGTGATCGTGGTTCATCCAGNCACTNNATGCTTTTTATNTCANTTTATG

SEQ ID NO: 4189 ACATGATCTAAATGTTTAAATGCTAAAGGTATATCGTAAGGGTAGTGTGTTGTTT
NNGAACGATAATTGAGAAGTTCTCATAGAAAGCGTATAACATAGGTCTTCAGAAACTATAAAAGA
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AAACATAAGCTACCAAAATAAAGAGCAATGNGTCTGGCTGTTTTATACTTCAACANTTTCCCT
AAGTGGTAAGCTATTACTATAAAACATATNTTANAAACATTGGTATNGGGAGCTGCTGTNCTACN
GCCAGTTNTCCTNGCACACAATGAGGCTAGGNTTT

SEQ ID NO: 4190 ACTTCGTCTTCTAATTTCAAAAATATAACTTAAAAATGTAAATATTCTATATG
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SEQ ID NO: 4191 ACTTGTCTAGCTCCTCTCGGTTCTTCCGAGCCAGCTCGTCATATTGGGCCCGG
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GTCATCAGCAGCAAGACGGGCATTGTCAATCTGCAGAACGATGCGGCATTGCCACAGTATTGCG
AAGATCTGAGCCCTCAGGTCTCGATGATCTTGAAATAATGGCTCCAGTCTCTGCCTGGGGTCTCT
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SEQ ID NO: 4192 TCGGCCGCCGGGCAGGTACATTTGAGAAGACAACAAATAAAATTACTCTCAG
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SEQ ID NO: 4193 ACATGATCTAAATGTTTAAATGCTAAAGGTATATCGTAAGGGTAGTGTGTTGTTT
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CNTGG

SEQ ID NO: 4194 CGGCCGCCGGGCAGGACGCGGGGACAAAATGGATACATAAAGACTAAGTAG
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SEQ ID NO: 4195 ACCTAAGTATATGATTGCGAGTGGAAAAATAGGGGACAGAAATCAGGTATTG
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SEQ ID NO: 4196 ACTTTTTTTTTTTTTTTTTTTTTTTTATGTTTCTTTGGTTTTATTATTACAAAC
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CATANCA

SEQ ID NO: 4197 ACTTTTTTTTTTTTTTTTTTTTTTTTGCACAATGGTTTATTAAAGGAATGTA
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SEQ ID NO: 4198 ACNAAGGGCTGAGGCAAACTGNTTTTAAGTTGGTAGATATGCTCATGAGC
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SEQ ID NO: 4200 ACAGCCAACGGTTTCCCTTGGGGGCTTTGAAATAACACCACCAAGTGGTCTTA
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SEQ ID NO: 4201 ACGTGGGCCTGTAATGCACCTTCTGAGGCACCTCCAGCTGCCCCCGGCCGGG
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TNTTTANTGATGTCAACCANCTATATCTTTGAAACCTT

SEQ ID NO: 4203 ACGCGGGCACAGTCAAGCTTTAAAGAAAGTGTGCTGAAAATAAAGAAATC
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SEQ ID NO: 4204 ACTACTCGTAAAGAGCTTCAAGAAGCTTCTTCATCCATTAAAGACCTTGTCT
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TACTATATGAAATTTTTCACATTATTTTCACATAATTTAAAAATTACATATTTTCAGGTTTGTCTCT
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SEQ ID NO: 4205 ACTTTTTTTTTTTTTTTTTTTTGGCAGGAAATATTTTATTGACAACCAAGGGACA
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SEQ ID NO: 4206 ACTTTGCCCTCAGCATCTCCCTTCATGTCTGGGTCATGAACCTACGCTGAAAA
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ACACCTAGGCA

SEQ ID NO: 4207 ACATGTTTGAAATGAGTTAGATACTTGAAAAGTCTAAACACACTGATTTAG
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GGGTAGCACCGTATGTGTGTAATATAAAATTATATTAGACATTANCACCANTGCANAACATGCT
CAGCNTCATAAGATCC

SEQ ID NO: 4208 ACGCGGGGCTCTTTTCCGGCTGGAACCATGGAGGGGTGTAAGAGAGAAGAAG
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SEQ ID NO: 4209 ACGCGGGTATGCGGGCCAATATCACAGCCATCCGAGAGTCCGGAAGACAG
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SEQ ID NO: 4210 ACTTTTTTTTTTTTTTTTTTTTTTGTGTTTTTTTTTTTTTTTTTTTTTAGGTT
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SEQ ID NO: 4211 ACTCAGGCTCATCATCTAACAGCCTTCGGGTTTTGTGGCCTCTTCATCTGGA
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SEQ ID NO: 4212 ACGCGGGGCCCTGGAGCTGTCTCTGGAAAGTAGCTGGCGAGGTTACCTTAAC
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SEQ ID NO: 4213 ACTGGAAGGGTAGTGGAACGAGTAAAGGCCTTACCACATTGTTTACACTTAT
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SEQ ID NO: 4214 ACGCGGGGTGAGAAGCTTGGACCGCATCCTAGCCGCCGACTCACACAAGGCA
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SEQ ID NO: 4215 ACCTATGGGCTTCTTGCCACTGTCCCTTCAAAGAAGGAACCTACTCACTGCC
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SEQ ID NO: 4216 ACCGCCTATTCAITTTCTTGAACCTCTCATAATGATAGTCATCAGTTGCCTTCT
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SEQ ID NO: 4218 ACGCGGGGGGAGCGGGCGGGCGGTTGGCGGCTTGTGCAGCAATGGCCAAG
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SEQ ID NO: 4219 TCGAAGCCGGCCCGGGCAGGTACGCGGGGACAGANGGAGGAAGGACAGC
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SEQ ID NO: 4220 ACTAAAGCATTTCATGGAGGCTCTTCAGGCTGGTGCAGACATCTCCATGATTG
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SEQ ID NO: 4221 ACATCAAAGATTACATGAAATCAATCAAAGGGAACTTGAAGAACAGAGAC
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SEQ ID NO: 4222 ACTATGGTAGAAATGGCGCATCTTCCTTTTCATGCTTAAAAACCACCCTG
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SEQ ID NO: 4223 ACACAATGGTTTATTAAAGGAATGTATGGCCACATCAACCTAGCAAGGATT
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SEQ ID NO: 4224 ACGCGGGGCTCACTGAGCACCGTCCAGCATCCGACACCACAGCGGCCCTT
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SEQ ID NO: 4225 ACANAATGGATTTTGGGAAGAGGGAGTCAACCACTGGACCTCCAAGGAAGCCAC
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TGGCTGAAACCAGTTCACAAGGTTACTGTATACATAGCCTGAGTTTAAAGGCTGTGCCACTTCA
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AATCAN

SEQ ID NO: 4226 ACTGTGTGGAAAAGTGGTGTGCTGATTACTTCCTCAACTGTTTACGACTCAGA
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SEQ ID NO: 4227 ACAGATTTTGAATATGGTGACTAGGCAAGGGGCACCTTTGGGCTAATACTCTA
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SEQ ID NO: 4228 ACGGGGGAGGCATTGAGGCAGCCAGCGCAGGGGCTTCTGCTGAGGGGGCAG
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SEQ ID NO: 4229 ACTTTTTTTTTTTTTTTTTTTTTTAAAGTTTAAATGCATTTTATTTTAGACA
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SEQ ID NO: 4230 ACCAACAGAATTATTTGTGAGAAGAATGAACAAATTTTGATAAAGTATGAAT
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SEQ ID NO: 4231 ACATGGCCACAGATCATCAAACCAACATTTTTTGTGAAATCATGAACAAGAT
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SEQ ID NO: 4232 ACTGCTACCATTACATGGTTCCTTATTAATTTGAAAAGTGCCTGAAAGTTTG
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SEQ ID NO: 4233 ACTCCTTACTCAGGTTCTCCATATATTTCTGTAGTGTCTTATGCTTCCAGAGCA
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SEQ ID NO: 4234 ACCCAGCATCAGGTCAAAAACCTGAATCGTTGCAGTGTGCCAGTAGATCAGG
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SEQ ID NO: 4235 ACGCGGGGTCTGCAGGTTGTGCTTCCGGTGCAGGAGGTGAGGACAAAGATGG
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SEQ ID NO: 4237 ACGCGGGGGTCATAGCGACTTTTGGGATAGTTTGTATCGACAAAAGGAGAC
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CGCNACCC

SEQ ID NO: 4238 ACCGGGGGTTAGAGGTATATGAAAAGATGAGAAGCTCACACTGGGCTTCTTC
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SEQ ID NO: 4239 ACGCGGGGCACAAAATACATGCAGAAGATGGTGGCAGATCTGGTGGAAAAT
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SEQ ID NO: 4240 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGCTAGGAAATATTTTATATTAAT
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SEQ ID NO: 4241 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGCATCAAAAAGCTTTATTTCCATTG
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SEQ ID NO: 4242 ACGCGGGGGAGGAGCCTGAGGAAGAGGGCGGCGACGGTGGTGGTACTGAG
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SEQ ID NO: 4243 ACGCGGGGCTGTTTCAAGGATCAAATACAAAATTAATATACTAGGCCGAGCGCA
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CCA

SEQ ID NO: 4244 ACTCTCTCTGAAACAGCTACAAACATCTTGTTTTGCAAAATATACAATGTTT
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SEQ ID NO: 4245 ACTTATACCCCTAAATATATAAAACATTTTTTAAAGAAAAAAGGAAGAA
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SEQ ID NO: 4246 ACATAAGCATAATCAGTTATGGACAGCTTCTTGATAAAATGCTATTTCAGCAA
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GGNGGGGGA

SEQ ID NO: 4247 ACCAGGGCGGCGCGTGGTCTACGCCGAGTGACAGAGACGCTCAGGCTGTGTT
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SEQ ID NO: 4248 ACAGCCGCCACAGCTACACTCCAACCACGTCCCGCTCTCCCCAGCATTTCCAC
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SEQ ID NO: 4249 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGANATGGAGTTTCTCCTGTAAAGC
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TCCAGGAATGCTCTGGTCAGGGCTGCTGTGACTGTTGGCCCTGCTGTCTTCTCTCTCTGTCCCCA
CGT

SEQ ID NO: 4252 ACGCGGGGCTTTCCGGCGGTGACGACCTACGCACACGAGAACATGCCTCTC
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SEQ ID NO: 4253 ACTCTCCTACTTCTGGGCATGGGGTGACTTGAGGAATGTTGAAGCCATTCTGA
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SEQ ID NO: 4254 ACTCTCCTACTTCTGGGCATGGGGTGACTTGAGGAATGTTGAAGCCATTCTGA
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SEQ ID NO: 4255 ACGCGGGGATAAGATAAGGGACCTGTTAGATGTTTCAAAGACCAACCTTTCA
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SEQ ID NO: 4256 ACGAATACACAGAGTGGTCTTTTCAACACTCCTCCCCCTACTCCACCGGACCT
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SEQ ID NO: 4257 ACGCGGGGGATCGCTGCTCCTCTCTGGGGTCTGGCGGCCGACCGAGAACG
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SEQ ID NO: 4258 ACCACATCATCCATGCTGACATCTACCGCTGGTTTAACATTTCTGTTGATATTT
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CGCNACAA

SEQ ID NO: 4259 ACAGATCAGCAGAGCAGGACAGTTGGCAGCAGTGACCTCAGTAGGGAACAT
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SEQ ID NO: 4260 ACATACCCTTTCACTAGTGTGAGTGGCACAAGCCACATTTACCATGAGAAA
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SEQ ID NO: 4261 ACCGCCAGCTCTCTGCTCTCCACAGGGCTCCCGCCCCACCCGGCCTGATAAA
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SEQ ID NO: 4264 AACTAAAGGGTGTTCCTCAAGAATAGAGGTGAAGATATTTTCATTTTGTTTA
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SEQ ID NO: 4265 ACTTTTTTTTTTTTTTTTTTTTTTTTGANACAGGGTCTAGCTCTATGGCCAGGCT
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SEQ ID NO: 4267 ACTATGGCCTCTTCAATACACTGTAGCCAGTGCAGTGGGCCCTTGGGGATGCC
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SEQ ID NO: 4268 ACTGTTCTGCTCTATAAGAAGGTCGTTTGTGGAATAAAAGTCTACATAATTT
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SEQ ID NO: 4269 ACCAAAAAGAAAAAGAAAAAGGAAAAAGGTTTCTACTGCTGTATTATCTATAACT
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SEQ ID NO: 4284 ACTTTTTTTTTTTTTTTTTTTTTTTTGCAGAAAGAGTAGCCAGGTGTTAGCCAC
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SEQ ID NO: 4287 ACGAGCCGGTAGAGGAATCCTGTTTGATCTGGAAATTTCCGTGGAGAGCCC
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SEQ ID NO: 4290 ACATAAGTGGCTATCAGAGAAGCCAGCCGATATGGATTGGCCTGCACGACCC
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GACCT

SEQ ID NO: 4292 ACTTTATGTGTCATTTCATGACTACTAACCACATATATAGAGACTAGGGGAT
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SEQ ID NO: 4307 ACTGAAATAGATGTATAGACCAATGGAACAGAACAGAGGCCTCAGAAATAA
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TCCCTATTTAATAAGTGGTGTGGGAAACTGGCTAGCCATATGTAGAAAGCTGAAACTGGATCC
CTTCCTTACAACCTTATACAAAAATTAATTCAGATGAATTAATGACTTAAATGTTAGACCAAAACC
TTAAAAACCCAGAAAGAAACCTAGGCAATATCATTAGGACATAGGCATGGACAAGGGCTTCAT
GACTAACCAACCAAAAGCAATGGCAACAAAGCCA

SEQ ID NO: 4308 ACTTGCTGGTCTCAAATTTCCACAAGGAGATATCAATGGTGATACCACGTTCA
CGCTCAGCTTTCAAGTTATCCAAGACCCAGGCATACITGAAGGAGCCCTTTCCCATCTCAGCAGCC
TCCTTCTCAAATTTTCAATGGTCTTTTGTGCGATGCCACCGCATTATAGATCAGATGGCCAGTAG
TTGGTGGACTTGCCCGAATCTACGTGTCCAATGACGACAATGTTGATATGANTCTTTTCTTTCCCA
TTTTGGCTTTTA

SEQ ID NO: 4309 ACCACATTATAGTAAAGTATTAGAAAAGTGACCCTCAAGGTGTATCAATTA
TAAAGCAGATGAAAACCTGAATGACAAATATCTAGTAAAAATTTCTAGTAAAAAAGTCGATGCAA
CCCATGTACAAAAATAAAGTGAGAAAGCCATATAAATAAAGCAGAAATAATGTTCTAGGCTTTAA
GGTAATGAAGTTAGTCAAGTTGAAAAATAAAAAATAAAAAAGAAAATCCTNAATTGGAATTA

SEQ ID NO: 4310 ACCTGTGAACCAAGTGTTTGGGCAGGATGAGATGATCGACGTCATCGGGGTG
ACCAAGGGCAAAGGCTACAAAGGGGTCAACAGTCGTTGGCACACCAAGAAGCTGCTCGCAAGA
CCCACCGAGGCTGCGCAAGGTGGCTGTATTGGGGCATGGCATCCTGCTCGTGTAGCCTTCTCTG
TGGCAGCGCTGGGCAGAAAGGCTACCATCACCGCACTGAGATCAACAAGAAGATTTATAAGATT
TGCCAGGGCTACCTTATCAAGGACNGGAAAGCTGATCAAGAACAAATGCCTCCACTGACTATGAC
CTATCTGACAAGAGCATNAACCCNTGGGTGGCTTTGTCCNTATGGTGAAGGACNAATGACTTT

SEQ ID NO: 4311 ACTCGAAGATCTAGATTTCAITTTCTCCATCTACAACTTGGTCAACCAACAAAGA
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AGGAAGTCTCAATCACCATCTCCTAAGAATGAGTCAGCCAGAGGCGGAAAAAATCCCGTTCTCA
GTCCCCAAAAAAGGATATGCAAGAGAAAGGAGCAATCTCAAGTCTCGGTCTCCAAAAAGGGAT
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ACGAAGAAAGTGATNGATATGGGCAGAAAGGAGAAAAAGGAGAAACCAGAAAAGTGGTCT
ANGTCCAAGATCTTATTTCTAAGGTCCCTTNAGATGTANAACNAAAAAGTAANGAGTTCATCATT
TGTA

SEQ ID NO: 4312 ACTAAAATTGTGTTGGGAGCAGGGATTTGGAAATTTCTGAGAGATGTGTAGT
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GTCCTTTGTTGCTCATGCTGTTTAAAGTGCAGGCTGAGACCCACCTCTTTGTAAGTACGCGGGGGA
AGGCAATCCGGCCCTTTCCGGTGGAGGACCCTTCCCCCTGGGTTTGATCTTGAGGAACCTAAGAAC
GGTGTGTTGACTCGACTCTTCCCCCTTTTCTCCGAGAACTTGCTGAAACTCCAACCTCTGAAA
TTACTGGAACCTGCATTCTAACTTGCTGGAACCCACCTCTGGAATTGGCCTGCTTAAAGTGC
CTGA

SEQ ID NO: 4313 ACTTAGCATCGGAACCTGCAATGTTAGGAGCAGGGTTGTGTGTTGGATTGAC
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CATGGTTCAATGTGATGTGTGCTTATTATCTAACAGAAATGTCCAAGTCATTGATACAGTAATTAT
GAATCTCCCTTTGGGACCAAAAAATAAAGGGACAGATATGGCTTTTCTAAAGACTGCTTTGGA

AATGGCAAGAACAGCAGTATATTCCTTACACAAATCCTCAACTAGAGAACATGTTCAAAAGAAAG
CTGCAGAATGGAAAATCAAGATAGATATTATAGCA

SEQ ID NO: 4314 ACCAGTTTTCTGAGGACCATGATGTGGAATATTTTCTTCGGCTGGCTCATGAG
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ACCTGCTTGGCTGCTAGAGAAAGAGTCTATTCTTCCGCTCCTCCGACCCAGATTACCTGGCAGC
TGTGGACAAAGTGGTTGGGAGTCCTTCTGCCCAAGATGAAGCCTCTCCTCTATCAGAATGGAGGGCC
AGTTATAACAGTGCAGGTTGAAAATGAATATGGCAGCTACTTTGCCTGTGATTTTGACTACCTGCG
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CATAAAACATTCTGAAATGTGGGGCCCTGCAGGGCCTTACACCACGGTGGACTTTGGAAACAGG
CAGCAACATCACANATGCTTTCCTAANCCANANGAAAGTGTGANCCCAAAGGACCCTTGATCAAT
TCTGAATTCTATACTGGCTGGCTAAATCACTGGGGCCACCTCACTNCACAATCAANACCGAANCA
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SEQ ID NO: 4315 ACAAGTCTGGCTAGGGCTAAAAATGTGAAGAATGAGAAGATGTTACCTGGGAA
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TGGCATGCTGGGCACAGAGGGCTGTGATAAGTGGTCTGAGATGGCGCTGGAGGTGTAGGGCAG
GGGACAAAGTGGTACTGCATGTTCTGTGTGGTGAGGGAAAGAAACATGCTTTGAAGGTTTCCCTTG
TCAACAGAATGTGTGTCTGTATCTGTGATTGCGCATGTATTCATATATTTTAAAGTTTTCTCCTAA
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SEQ ID NO: 4316 ACTTCAAGAACCTGCACAGATTACTCATATTCCTTCAGGAAAGTGTTAGAT
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T

SEQ ID NO: 4317 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTACAGGAAATCTGCCTATTTTATTTT
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CTTTAATTTTACTCAAGTAAAANCANAATCACATAACGGACATCAAAACTAAATAGTTCACATCAT
TAGTTTAAAT

SEQ ID NO: 4318 GTACGCGGGGACTTCTGAGAAANTGAAACGACAGGGGAAAGGAGGTCTCAC
TGAGCACCGTCCAGCATNCGGACACCACAGCGGCCCTTCGCTCCACNCANAAAACCACTTCT
NAAACCTTCACTCAACACTTCCTTCCCCAAAGCCANAAGATGCACNAGGAGGAACATGAGGTGGC
TGTGCTTGGGGG

SEQ ID NO: 4319 ACGCGGGGGGCTTGCAAATCTCTTGCAATTGAAGGCAGGAAAAAGCAACAT
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TGTGGAAGCCCTGAAGCCAGAGTATGTGGCACCTCTTGTCTTTGGCTTTGTACAGAGAGTTGTGA
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TTGGAGCTATTGTAAGACAAAAAAATCACCAATGACTCCTGAGGCAGTCAANGCTNACTGGAA
GAAAANCTGTGANTTTTGAGAATGCCAGCTA

SEQ ID NO: 4320 ACTGCATTCTGAAGGAAAAAACTGCAGCCAAGGCAAGAACTCTGAAGTTT
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AGGCAATCATAAAAGATTAAATATTGGTAGGCATGTAAGCTTCTTTTAAATAAAAACAAAATAG
TCAATGTCTATTTTAAATAAGTATCCTTTGTTATAGAGTGTTCAGTTTTTGAAGGAGGGCCCT
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NCAG

SEQ ID NO: 4321 ACATTTCAAGTGAATAAGTAATTCTAGATAGGACAATTTAAATTGGATAAT
TTTAAAGTGTCTATAATTGCAGTGGTTTATTTGCAAAATTCCTAAAAGGAAAAATTTATCACTGC
CATCACAGCAGGTTTCTCATCCAGATGAGGAACTAGACAAATGCTAGTGTGTTTTAACTAGCTA
AACAAAATAANTTAAATGAACATTTAAAGTTTCCCTANCGGGCCATTCTTATCAAAATGTTGG
AATCCCTGTNGCTACATTGACTAAAAGGTCAATTATGAATGGAATATGTAAGACTTGGCTCATATAA
ACCTAATCAGATGGTTAGAGGTG

SEQ ID NO: 4322 ACCTCCCATAGTTTGTCCCTGTCTCCACTTCAGCAATGTCAATAAAATGATC
TTCCGATGCTGACGCCAGCATTTTCCCATCATGGCTGAAACTGAGGGTTCTTACAGGCCAATCCAG
CCTGGAAAAGCACCGAACACACACTAATCATCCACATCCAGAGGCTGACCAAAGCATCTGCAC